

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:05:38 ; Search time 61.47 Seconds
(without alignments)
28.137 Million cell updates/sec

Title: US-09-165-546A-8
Perfect score: 88
Sequence: 1 AADHRQLQLSISSCLQQL 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	43	48.9	254	2 H83242	probable transcrip
2	43	48.9	263	2 G87396	spoU rRNA methylas
3	43	48.9	532	2 JN0084	phytoene dehydroge
4	43	48.9	971	2 T03181	hypothetical prote
5	41	46.6	339	2 A83539	hypothetical prote
6	41	46.6	344	2 T42657	hypothetical prote
7	41	46.6	717	2 T27066	hypothetical prote
8	41	46.6	717	2 T27067	hypothetical prote
9	40	45.5	123	2 JC1202	ribonuclease P (EC
10	40	45.5	170	2 D83751	hypothetical prote
11	40	45.5	366	2 D83096	probable two-compo
12	39	44.3	323	2 C82234	conserved hypothet
13	39	44.3	467	2 AB3499	miaB protein limpo
14	39	44.3	502	2 S49113	hypothetical prote
15	39	44.3	709	2 A35364	carcinoembryonic a
16	39	44.3	2014	2 S46622	probable membrane
17	39	44.3	2354	2 T13288	mel-41 protein - f
18	38.5	43.8	278	2 D86277	F14L17.8 protein -
19	38.5	43.8	406	2 H71694	proline/betaine tr
20	38.5	43.8	2843	1 RBHUAP	adenomatous polypo
21	38.5	43.8	2845	2 I49505	adenomatous polypo
22	38	43.2	83	2 C95126	hypothetical prote
23	38	43.2	83	2 G97996	hypothetical prote
24	38	43.2	160	2 F95392	protein [imported
25	38	43.2	205	2 D69804	conserved hypothet
26	38	43.2	299	2 C83595	probable cation ef
27	38	43.2	309	2 E65116	hypothetical prote
28	38	43.2	309	2 D91143	probable transcrip
29	38	43.2	309	2 G85988	probable transcrip

30	38	43.2	309	2 AD0911	probable LysR-fami
31	38	43.2	333	2 G96768	protein transcript
32	38	43.2	343	2 G84371	tRNA intron endonu
33	38	43.2	373	2 I39833	degM protein - Bac
34	38	43.2	417	2 AE2735	conserved hypothet
35	38	43.2	425	2 E97516	hypothetical prote
36	38	43.2	484	2 S73490	glutamate--tRNA li
37	38	43.2	606	2 D95974	probable ABC trans
38	38	43.2	678	2 T23341	beta-catenin - Cae
39	38	43.2	884	2 G96787	protein T4012.9 [i
40	38	43.2	1007	2 G96606	disease resistance
41	38	43.2	1067	1 S62421	endopeptidase La h
42	38	43.2	1208	2 T34469	hypothetical prote
43	37	42.0	200	2 T48038	hypothetical prote
44	37	42.0	247	2 E55545	afab protein - Esc
45	37	42.0	265	2 E64128	lic-1 protein D -

ALIGNMENTS

RESULT 1
H83242
probable transcription regulator PA3220 [imported] - Pseudomonas aeruginosa (strain P
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: H83242
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoquchi, S.D.; Warren, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brödy, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A;Reference number: A82950; MUID:20437337
A;Accession: H83242
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-254 <STO>
A;Cross-references: GB:AE004745; GB:AE004091; NID:g9949336; PIDN:AAG06608.1; GSPDB:GN
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA3220

Query Match 48.9%; Score 43; DB 2; Length 254;
Best Local Similarity 61.5%; Pred. No. 5.3;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 DHRQLQLSISSCL 15
|| || | : ||
Db 20 DHAQLVLGLSGCL 32

RESULT 2
G87396
spoU rRNA methylase family protein [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 27-Nov-2001
C;Accession: G87396
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: G87396
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-263 <STO>
A;Cross-references: GB:AE005673; NID:g13422511; PIDN:AAK23171.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC1187
C;Superfamily: conserved hypothetical protein HI0860

Query Match 48.9%; Score 43; DB 2; Length 263;
Best Local Similarity 43.8%; Pred. No. 5.5;
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQ 16
|||||I: ::::|||:
Db 59 AADHPMLKKAAVACLK 74

RESULT 3
JN0084
phytoene dehydrogenase (EC 1.3.-.-) - Aphanocapsa sp. (PCC 6714)
N;Alternate names: phytoene desaturase
C;Species: Aphanocapsa sp.
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 08-Oct-1999
C;Accession: JN0084
R;Schmidt, A.; Sandmann, G.
Gene 91, 113-117, 1990
A;Title: Cloning and nucleotide sequence of the crtI gene encoding phytoene dehydrogenase
A;Reference number: JN0084; MUID:90382685
A;Accession: JN0084
A;Molecule type: DNA
A;Residues: 1-532 <SCH>
A;Cross-references: GB:M55647; GB:M33237; NID:g141989; PIDN:AAA62573.1; PID:g141990
A;Note: the authors translated the codon CAG for residue 380 as Gly
C;Comment: This enzyme catalyzes the symmetrical introduction of two double bonds at C-1
C;Genetics:
A;Gene: crtI
C;Superfamily: Aphanocapsa phytoene dehydrogenase
C;Keywords: carotenoid biosynthesis; membrane bound; oxidoreductase

Query Match 48.9%; Score 43; DB 2; Length 532;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 ADHRQLQLSISSCLQ 17
|||||I: :||:
Db 374 ADHRQIQVIAQTMLQR 389

RESULT 4
T03181
hypothetical protein 103R - Chilo iridescent virus
C;Species: Chilo iridescent virus
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
C;Accession: T03181
R;Bahr, U.; Tidona, C.A.; Darai, G.
Virus Genes 15, 235-245, 1997
A;Title: The DNA sequence of Chilo iridescent virus between the genome coordinates 0.101
A;Reference number: Z14834; MUID:98141693
A;Accession: T03181
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-971 <BAH>
A;Cross-references: EMBL:AF003534; NID:g2738385; PIDN:AAB94479.1; PID:g2738452

Query Match 48.9%; Score 43; DB 2; Length 971;
Best Local Similarity 50.0%; Pred. No. 22;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 DHRQLQLSISSCLQ 16
|||:|||||:
Db 225 DHNQQLSISKCFK 238

RESULT 5
A83539
hypothetical protein PA0855 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C;Accession: A83539
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pa
A;Reference number: A82950; MUID:20437337
A;Accession: A83539
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-339 <STO>
A;Cross-references: GB:AE004520; GB:AE004091; NID:g9946745; PIDN:AAG04244.1; GSPDB:GN
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA0855

Query Match 46.6%; Score 41; DB 2; Length 339;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 RQLQLSISSCLQ 16
|||I|||I|
Db 176 RQLGLPIGCLQ 187

RESULT 6
T42657
hypothetical protein DKFZp434J1015.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
C;Accession: T42657
R;Bloecker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, November 1999
A;Reference number: Z22230
A;Accession: T42657
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-344 <AAA>
A;Cross-references: EMBL:AL133055
A;Experimental source: adult testis; clone DKFZp434J1015
C;Genetics:
A;Note: DKFZp434J1015.1

Query Match 46.6%; Score 41; DB 2; Length 344;
Best Local Similarity 56.2%; Pred. No. 17;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 DHRQLQLSISSCLQ 18
:|||||: |||I
Db 38 EQRQLQLQEELQQL 53

RESULT 7
T27066
hypothetical protein Y51A2B.6a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C;Accession: T27066
R;McMurray, A.
submitted to the EMBL Data Library, January 1998
A;Reference number: Z20305
A;Accession: T27066
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-717 <WIL>
A;Cross-references: EMBL:AL021493; PIDN:CAA16394.1; GSPDB:GN00023; CESP:Y51A2B.6a
A;Experimental source: clone Y51A2B
C;Genetics:
A;Gene: CESP:Y51A2B.6a
A;Map position: 5
A;Introns: 8/1; 33/1

C;Superfamily: Caenorhabditis elegans hypothetical protein Y116A8C.33

Query Match 46.6%; Score 41; DB 2; Length 717;
Best Local Similarity 52.9%; Pred. No. 36;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 ADHRQLQLSISSCLQQL 18
|| :||: |||||
Db 472 ADKVDNELSVIKLQQL 488

RESULT 8
T27067
hypothetical protein Y51A2B.6b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C;Accession: T27067
R;McMurray, A.
submitted to the EMBL Data Library, January 1998
A;Reference number: Z20305
A;Accession: T27067
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-717 <WIL>
A;Cross-references: EMBL:AL021493; PIDN:CAA16395.1; GSPDB:GN00023; CESP:Y51A2B.6b
A;Experimental source: clone Y51A2B
C;Genetics:
A;Gene: CESP:Y51A2B.6b
A;Map position: 5
A;Introns: 8/1; 33/1
C;Superfamily: Caenorhabditis elegans hypothetical protein Y116A8C.33

Query Match 46.6%; Score 41; DB 2; Length 717;
Best Local Similarity 52.9%; Pred. No. 36;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 ADHRQLQLSISSCLQQL 18
|| :||: |||||
Db 472 ADKVDNELSVIKLQQL 488

RESULT 9
JC1202
ribonuclease P (EC 3.1.26.5) protein component - Streptomyces bikiniensis
C;Species: Streptomyces bikiniensis
C;Date: 05-Mar-1993 #sequence_revision 05-Mar-1993 #text_change 24-Sep-1999
C;Accession: JC1202
R;Morse, D.P.; Schmidt, F.J.
Gene 117, 61-66, 1992
A;Title: Sequences encoding the protein and RNA components of ribonuclease P from Strept
A;Reference number: JC1202; MUID:92354937
A;Accession: JC1202
A;Molecule type: DNA
A;Residues: 1-123 <MOR>
A;Cross-references: GB:M83112; NID:g153425; PIDN:AAA26808.1; PID:g153427
A;Experimental source: strain zorbonensis
C;Comment: Ribonuclease P consists of the M1 RNA moiety and the protein component. Both
C;Comment: Ribonuclease P generates mature tRNA molecules by cleaving their 5' ends. It
C;Genetics:
A;Gene: rnpA
A;Start codon: GTG
C;Superfamily: Streptomyces ribonuclease P, protein component
C;Keywords: endonuclease; hydrolase; tRNA processing

Query Match 45.5%; Score 40; DB 2; Length 123;
Best Local Similarity 47.1%; Pred. No. 8.7;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 ADHRQLQLSISSCLQQL 18
||| || : : ||:|

Db 101 ADHAQLARDLDAALQRL 117

RESULT 10
D83751
hypothetical protein BH0812 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: D83751
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: D83751
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-170 <STO>
A;Cross-references: GB:AP001509; GB:BA000004; NID:gi0173176; PIDN:BAB04531.1; GSPDB:G
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH0812

Query Match 45.5%; Score 40; DB 2; Length 170;
Best Local Similarity 58.3%; Pred. No. 12;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 LQLSISSCLQQL 18
:|||: |||:|
Db 130 VQLSVDDCLQKL 141

RESULT 11
D83096
probable two-component response regulator PA4396 [imported] - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: D83096
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A;Reference number: A82950; MUID:20437337
A;Accession: D83096
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-366 <STO>
A;Cross-references: GB:AE004855; GB:AE004091; NID:g9950621; PIDN:AAG07784.1; GSPDB:GN
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA4396

Query Match 45.5%; Score 40; DB 2; Length 366;
Best Local Similarity 52.9%; Pred. No. 27;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 ADHRQLQLSISSCLQQL 18
| ||:| | : : ||||
Db 250 AFHRELLGVARRLQQL 266

RESULT 12
C82234
conserved hypothetical protein VC1163 [imported] - Vibrio cholerae (strain N16961 ser
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: C82234
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers
I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20406833

A;Accession: C82234

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-323 <HEI>

A;Cross-references: GB:AE004196; GB:AE003852; NID:g9655632; PIDN:AAF94322.1; GSPDB:GN001

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VC1163

A;Map position: 1.

C;Superfamily: conserved hypothetical protein HP0419; bioc homology

Query Match 44.3%; Score 39; DB 2; Length 323;
Best Local Similarity 52.9%; Pred. No. 36;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 ADHRQLQLSISSCLQQL 18

| | | | | : : : | | |

Db 12 AQHPQLQLWLNTLPQQL 28

RESULT 13

AB3499

miaB protein [imported] - Brucella melitensis (strain 16M)

C;Species: Brucella melitensis

C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002

C;Accession: AB3499

R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,

; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens

A;Reference number: AD3252; PMID:11756688

A;Accession: AB3499

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-467 <KUR>

A;Cross-references: GB:AE008917; PIDN:AAL53157.1; PID:g17984028; GSPDB:GN00190

A;Experimental source: strain 16M

C;Genetics:

A;Gene: BMEI1976

A;Map position: 1

C;Superfamily: conserved hypothetical protein b0835

Query Match 44.3%; Score 39; DB 2; Length 467;
Best Local Similarity 35.3%; Pred. No. 53;
Matches 6; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQ 17

| | | : | : : | |

Db 93 AADGKELTIGVAGCVAQ 109

RESULT 14

S49113

hypothetical protein 2 - Microcystis aeruginosa

C;Species: Microcystis aeruginosa

C;Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Mar-2001

C;Accession: S49113

R;Juerchott, K.; Boerner, T.

submitted to the EMBL Data Library, November 1993

A;Description: Sequence of the cyanobacterial plasmid pMA1 from Microcystis aeruginosa

A;Reference number: S49112

A;Accession: S49113

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-502 <JUE>

A;Cross-references: EMBL:Z28337; NID:g509352; PIDN:CAA82191.1; PID:g509354

C;Superfamily: Microcystis aeruginosa hypothetical protein 2

Query Match 44.3%; Score 39; DB 2; Length 502;
Best Local Similarity 50.0%; Pred. No. 57;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 RQLQLSISSCLQQL 18

| : | | : | | | |

Db 445 RESDLSVKECLQRL 458

RESULT 15

A35364

carcinoembryonic antigen-related protein (clone rnCGM1) - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 17-Aug-1990 #sequence_revision 17-Aug-1990 #text_change 23-Jul-1999

C;Accession: A35364

R;Rebstock, S.; Lucas, K.; Thompson, J.A.; Zimmermann, W.

J. Biol. Chem. 265, 7872-7879, 1990

A;Title: cDNA and gene analyses imply a novel structure for a rat carcinoembryonic an

A;Reference number: A35364; MUID:90243655

A;Accession: A35364

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-709 <REB>

A;Cross-references: GB:M32474; NID:g203430; PIDN:AAA66037.1; PID:g203431; GB:J05417

C;Superfamily: carcinoembryonic antigen-related protein rnCGM1; carcinoembryonic anti

F;1-137/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA1>

F;168-217/Domain: immunoglobulin homology <IMM1>

F;242-378/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA2>

F;480-612/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA3>

F;633-690/Domain: immunoglobulin homology <IMM2>

Query Match 44.3%; Score 39; DB 2; Length 709;
Best Local Similarity 53.3%; Pred. No. 82;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 HRQLQLSISSCLQQL 18

| | | | : | | | |

Db 375 HVQLQVNTSSCCDPL 389

Search completed: July 3, 2002, 11:10:53

Job time: 315 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:08:53 ; Search time 107.89 seconds
(without alignments)
28.862 Million cell updates/sec

Title: US-09-165-546A-8
Perfect score: 88
Sequence: 1 AADHRQLQLSISSCLQQL 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archheap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	100.0	180	4 Q9Y479	Q9Y479 homo sapien
2	46	52.3	262	4 Q96LM8	Q96LM8 homo sapien
3	43	48.9	140	2 Q9R9R5	Q9R9R5 aeromonas p
4	43	48.9	254	16 Q9HZ20	Q9HZ20 pseudomonas
5	43	48.9	263	16 Q9A907	Q9A907 caulobacter
6	43	48.9	323	13 Q9IBE4	Q9IBE4 fugu rubrip
7	43	48.9	323	13 Q9IBE3	Q9IBE3 fugu rubrip
8	43	48.9	323	13 Q9IBE2	Q9IBE2 fugu rubrip
9	43	48.9	323	13 Q9IBE1	Q9IBE1 fugu rubrip
10	43	48.9	323	13 Q9IBE0	Q9IBE0 fugu rubrip
11	43	48.9	971	12 O55768	O55768 chilo iride
12	42	47.7	867	5 Q95YD4	Q95YD4 caenorhabdi
13	41	46.6	339	16 Q9I586	Q9I586 pseudomonas
14	41	46.6	344	4 Q9UFC1	Q9UFC1 homo sapien
15	41	46.6	717	5 O45958	O45958 caenorhabdi
16	41	46.6	717	5 O45959	O45959 caenorhabdi

17	41	46.6	4083	3 Q9C1M7	Q9clm7 ashbya goss
18	40	45.5	170	16 Q9KEP0	Q9kep0 bacillus ha
19	40	45.5	171	10 Q946C2	Q946c2 theobroma c
20	40	45.5	255	5 Q9NDK1	Q9ndk1 leishmania
21	40	45.5	366	16 Q9HW10	Q9hw10 pseudomonas
22	40	45.5	2176	5 Q9W5R9	Q9w5r9 drosophila
23	39	44.3	92	12 Q86217	Q86217 rotavirus b
24	39	44.3	148	2 Q52372	Q52372 pseudomonas
25	39	44.3	323	16 Q9KSU3	Q9ksu3 vibrio chol
26	39	44.3	333	13 Q9PUJ9	Q9puj9 alligator m
27	39	44.3	466	13 Q90XC4	Q90xc4 poephila gu
28	39	44.3	468	13 Q9YI95	Q9yi95 rana rugosa
29	39	44.3	502	2 Q48904	Q48904 microcystis
30	39	44.3	607	10 Q9FG45	Q9fg45 arabidopsis
31	39	44.3	609	4 Q9NZN7	Q9nzn7 homo sapien
32	39	44.3	610	8 Q94T44	Q94t44 zu cristatu
33	39	44.3	617	11 Q63110	Q63110 rattus norv
34	39	44.3	709	11 Q63111	Q63111 rattus norv
35	39	44.3	743	5 Q9VCN9	Q9vcn9 drosophila
36	39	44.3	753	4 Q75175	Q75175 homo sapien
37	39	44.3	2354	5 Q24135	Q24135 drosophila
38	39	44.3	2354	5 Q9VXG8	Q9vxcg8 drosophila
39	38.5	43.8	208	4 Q9P119	Q9p119 homo sapien
40	38.5	43.8	278	10 Q9M9T0	Q9m9t0 arabidopsis
41	38.5	43.8	406	16 Q9ZDF4	Q9zdf4 rickettsia
42	38.5	43.8	1417	10 Q9C9M5	Q9c9m5 arabidopsis
43	38.5	43.8	2829	13 P70039	P70039 xenopus lae
44	38	43.2	83	16 Q97QV6	Q97qv6 streptococc
45	38	43.2	146	10 Q9LM42	Q9lm42 arabidopsis

ALIGNMENTS

RESULT 1
Q9Y479 ID Q9Y479 PRELIMINARY; PRT; 180 AA.
AC Q9Y479;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE LAGE-1S PROTEIN (CANCER/TESTIS ANTIGEN 2).
GN LAGE1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MELANOMA;
RX MEDLINE=99325550; PubMed=103999963;
RA Aarnoudse C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.;
RT "Interleukin-2-induced, melanoma-specific T cells recognize CAMEL, an
RT unexpected translation product of LAGE-1.";
RL Int. J. Cancer 82:442-448(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Aradhy S., Bardaro T., Galgoczy P., Yamagata T., Esposito T.,
RA Patlan H., Ciccodicola A., Kenwick S., Platzer M., D'Urso M.,
RA Nelson D.L.;
RT "Multiple pathogenic and benign genomic rearrangements occur at a 35-
RT kb duplication involving the NEMO and the LAGE2 genes.";
RL Hum. Mol. Genet. 0:0-0(2001).
DR EMBL; AJ012834; CAA10194.1; -
DR EMBL; AF277315; AAL27015.1; -
SQ SEQUENCE 180 AA; 18236 MW; 9077FAF953543A25 CRC64;

Query Match 100.0%; Score 88; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AADHRQLQLSISSCLQQL 18

Db 139 AADHRQLQLSISSCLQQL 156
|||||

RESULT 2
Q96LM8 PRELIMINARY; PRT; 262 AA.
AC Q96LM8;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE CDNA FLJ25361 FIS, CLONE TST01713.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
RA Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,
RA Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
RA Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA Kawakami B., Nagai K., Isogai T., Sugano S.;
RT "NEDO human cDNA sequencing project."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK058090; BAB71660.1; -.
SQ SEQUENCE 262 AA; 29006 MW; 5BED0EE9CEA87296 CRC64;

Query Match 52.3%; Score 46; DB 4; Length 262;
Best Local Similarity 53.3%; Pred. No. 2.9;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 ADHRQLQLSISSCLQ 16
:||| ||: ||||
Db 246 SEHRSFLLSLESLQ 260

RESULT 3
Q9R9R5 PRELIMINARY; PRT; 140 AA.
AC Q9R9R5;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE FLAJ.
GN FLAJ.
OS Aeromonas punctata (Aeromonas caviae).
OC Bacteria; Proteobacteria; gamma subdivision; Aeromonadaceae;
OC Aeromonas.
OX NCBI_TaxID=648;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SCH3N;
RX MEDLINE=21295073; PubMed=11401962;
RA Rabaan A.A., Gryllos I., Tomas J.M., Shaw J.G.;
RT "Motility and the Polar Flagellum Are Required for Aeromonas caviae
Adherence to Hep-2 Cells."
RL Infect. Immun. 69:4257-4267(2001).
DR EMBL; AF198617; AAF19183.1; -.
DR InterPro; IPR003713; Flis.
DR Pfam; PF02561; Flis; 1.
SQ SEQUENCE 140 AA; 15811 MW; 302613DD209C7DB0 CRC64;

Query Match 48.9%; Score 43; DB 2; Length 140;
Best Local Similarity 44.4%; Pred. No. 5.2;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1.AADHRQLQLSISSCLQQL 18
| ||: ||: ||::|

Db 21 ADPHRVIQLMMQGLERL 38
RESULT 4
Q9HZ20 PRELIMINARY; PRT; 254 AA.
AC Q9HZ20;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)
DE PROBABLE TRANSCRIPTIONAL REGULATOR.
GN PA3220.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
opportunistic pathogen."
RL Nature 406:959-964(2000).
CC -!- SIMILARITY: BELONGS TO THE ARAC/XYLS FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
DR EMBL; AF004745; AAG06608.1; -.
DR InterPro; IPR000005; HTHArac.
DR Pfam; PF00165; HTH_Arac; 1.
DR PRINTS; PR00032; HTHARAC.
DR SMART; SM00342; HTH_ARAC; 1.
DR PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.
KW Complete proteome; DNA-binding; Transcription regulation.
SQ SEQUENCE 254 AA; 27467 MW; 82911CF9122211F2 CRC64;

Query Match 48.9%; Score 43; DB 16; Length 254;
Best Local Similarity 61.5%; Pred. No. 9.7;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 DHRQLQLSISSCL 15
||| | | | | | | | | |
Db 20 DHAQLVLGLSGCL 32

RESULT 5
Q9A907 PRELIMINARY; PRT; 263 AA.
AC Q9A907;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE SPOU RNA METHYLASE FAMILY PROTEIN.
GN CC1187.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Caulobacter.
OX NCBI_TaxID=69394;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,

RA Salzberg S.L., Venter J.C., Shapiro L., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of *Caulobacter crescentus*.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AE005796; AAK23171.1; -.
DR TIGR; CC1187; -.
DR InterPro; IPR001537; SpoU_methylase.
DR ProDom; PD001243; SpoU_methylase; 1.
KW Methyltransferase; Complete proteome.
SQ SEQUENCE 263 AA; 27921 MW; DABC9817D73422CC CRC64;

Query Match 48.9%; Score 43; DB 16; Length 263;
Best Local Similarity 43.8%; Pred. No. 10;
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQ 16
||||| : : : : |||
Db 59 AADHPMLKKVAACLK 74

RESULT 6
Q9IBE4 PRELIMINARY; PRT; 323 AA.
ID Q9IBE4
AC Q9IBE4;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE OLFACTORY RECEPTOR 1-1.
GN FOR1-1.

OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.

OX NCBI_TaxID=31033;
RN [1]

RP SEQUENCE FROM N.A.

RA Asano-Miyoshi M., Suda T., Yasuoka A., Osima S., Yamashita S., Abe K.,
RA Emori Y.;
RT "Random expression of main and vomeronasal olfactory receptor genes in
RT immature and mature olfactory epithelia of *Fugu rubripes*.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AB031380; BAA92165.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCRRHODOPSN.

DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

KW Receptor.

SQ SEQUENCE 323 AA; 36580 MW; 16E780AA415FA3F6 CRC64;

Query Match 48.9%; Score 43; DB 13; Length 323;
Best Local Similarity 57.1%; Pred. No. 13;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 ADHRQLQLSISSCL 15
||||| : : : : |||
Db 276 ADQVLSLSLSCI 289

RESULT 7
Q9IBE3 PRELIMINARY; PRT; 323 AA.

ID Q9IBE3
AC Q9IBE3;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE OLFACTORY RECEPTOR 1-2.

GN FOR1-2.

OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RA Asano-Miyoshi M., Suda T., Yasuoka A., Osima S., Yamashita S., Abe K.,
RA Emori Y.;
RT "Random expression of main and vomeronasal olfactory receptor genes in
RT immature and mature olfactory epithelia of *Fugu rubripes*.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AB031381; BAA92166.1; -.

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCRRHODOPSN.

DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

KW Receptor.

SQ SEQUENCE 323 AA; 36715 MW; 9D1F76EF3B2EF69C CRC64;

Query Match 48.9%; Score 43; DB 13; Length 323;
Best Local Similarity 57.1%; Pred. No. 13;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 ADHRQLQLSISSCL 15
||||| : : : : |||
Db 276 ADQVLSLSLSCI 289

RESULT 8

Q9IBE2 PRELIMINARY; PRT; 323 AA.

ID Q9IBE2
AC Q9IBE2;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE OLFACTORY RECEPTOR 1-3.

GN FOR1-3.

OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

OC Tetraodontidae; Takifugu.

OX NCBI_TaxID=31033;

RN [1]

RP SEQUENCE FROM N.A.

RA Asano-Miyoshi M., Suda T., Yasuoka A., Osima S., Yamashita S., Abe K.,
RA Emori Y.;

RT "Random expression of main and vomeronasal olfactory receptor genes in
RT immature and mature olfactory epithelia of *Fugu rubripes*.";

RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AB031382; BAA92167.1; -.

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCRRHODOPSN.

DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

KW Receptor.

SQ SEQUENCE 323 AA; 36678 MW; 5B8DD6D52C9D20F8 CRC64;

Query Match 48.9%; Score 43; DB 13; Length 323;
Best Local Similarity 57.1%; Pred. No. 13;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 ADHRQLQLSISSCL 15
||||| : : : : |||
Db 276 ADQVLSLSLSCI 289

RESULT 9

Q9IBE1 PRELIMINARY; PRT; 323 AA.

ID Q9IBE1
AC Q9IBE1;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)


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Db 161 ADHLEDLDIEACIQSL 177
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RESULT 13
Q9I586
ID Q9I586 PRELIMINARY; PRT; 339 AA.
AC Q9I586;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE HYPOTHETICAL PROTEIN PA0855.
GN PA0855.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AE004520; AAG04244.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 339 AA; 37783 MW; 189184992E527C54 CRC64;

Query Match 46.6%; Score 41; DB 16; Length 339;
Best Local Similarity 75.0%; Pred. NO. 30;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 RQLQLSISSCLQ 16
||| | |||
Db 176 RQLGLPISGCLQ 187

RESULT 14
Q9UFC1
ID Q9UFC1 PRELIMINARY; PRT; 344 AA.
AC Q9UFC1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 38.0 KDA PROTEIN (FRAGMENT).
GN DKFZP434J1015.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Bloecker H., Boecher M., Brandt P., Mewes H.W., Gassenhuber J.,
RA Wiemann S.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL133055; CAB61381.1; -.
DR HSSP; P08047; 1SP2.
DR InterPro; IPR000822; Znf-C2H2.
DR Pfam; PF00096; zf-C2H2; 5.
DR SMART; SM00355; Znf.C2H2; 5.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 5.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 5.
KW DNA-binding; Hypothetical protein; Metal-binding; Zinc-finger.
FT NON_TER 1
SQ SEQUENCE 344 AA; 38040 MW; 7D53343FBB4DA733 CRC64;
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Query Match 46.6%; Score 41; DB 4; Length 344;
Best Local Similarity 56.2%; Pred. NO. 31;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 DHRQLQLSISSCLQQL 18
: ||||| : |||
Db 38 EQRQLQLKLQEELQQL 53

RESULT 15
O45958 PRELIMINARY; PRT; 717 AA.
ID O45958
AC O45958;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Y51A2B.6A PROTEIN.
GN Y51A2B.6A.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA McMurray A.A.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; Pubmed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; AL021493; CAA16394.1; -.
DR InterPro; IPR003125; WSN.
DR Pfam; PF02206; WSN; 1.
DR SMART; SM00453; WSN; 1.
SQ SEQUENCE 717 AA; 81475 MW; EA9C79E40E7FBD6E CRC64;

Query Match 46.6%; Score 41; DB 5; Length 717;
Best Local Similarity 52.9%; Pred. NO. 66;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
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QY 2 ADHRQLQLSISSCLQQL 18
||| :||| :|||
Db 472 ADKVDNELSVIKCLQQL 488

Search completed: July 3, 2002, 11:24:06
Job time: 913 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 13:00:27 ; Search time 30.16 Seconds
(without alignments)
66.291 Million cell updates/sec

Title: US-09-165-546A-8

Perfect score: 88

Sequence: 1 AADHRQLQLSISSCLQQL 18

Scoring table: BLOSUM62

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Searched: 747574 seqs, 111073796 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
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6:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
7:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
8:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
9:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
10:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
11:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
12:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
13:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
14:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
15:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
16:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
17:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
18:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
19:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	88	100.0	18	21	AA52435	Human tumour anti
2	88	100.0	18	22	AAE07770	Human NY ESO-1 HLA
3	88	100.0	18	22	AAU01539	HLA-DR53 recognisi
4	88	100.0	18	22	AAB69939	Human NY-ESO-1 HLA
5	88	100.0	180	19	AAW69664	Human LAGE-1 clone
6	88	100.0	180	19	AAW69665	Human NY-ESO-1 pro
7	88	100.0	180	19	AAW62584	Cancer associated
8	88	100.0	180	20	AA505965	Human cancer anti
9	88	100.0	180	21	AAB03154	Human oesophageal
10	88	100.0	180	21	AA570860	Human LAGE-1 splic
11	88	100.0	180	21	AA570862	Human tumour anti

12	88	100.0	180	21	AA52430	Human tumour anti
13	88	100.0	180	22	AAG67164	Amino acid sequenc
14	88	100.0	180	22	AAE07714	Human NY ESO-1 pro
15	88	100.0	180	22	AAU01535	Human NY-ESO-1 tum
16	88	100.0	180	22	AAB69946	Human NY-ESO-1 pro
17	88	100.0	397	22	AAE13122	NY-ESO-IC-HER-2 me
18	80	90.9	17	22	AAE07735	Human NY ESO-1 MHC
19	80	90.9	20	22	AAE07731	Human NY ESO-1 MHC
20	71	80.7	14	22	AAE07736	Human NY ESO-1 MHC
21	61	69.3	13	22	AAE07737	Human NY ESO-1 MHC
22	57	64.8	20	22	AAE07743	Human ESO p131-150
23	52	59.1	20	22	AAE07745	Human ESO p146-165
24	48	54.5	10	20	AA506011	Human cancer anti
25	47	53.4	10	20	AA506016	Human cancer anti
26	45	51.1	9	22	AAG67179	Cancer testis tumo
27	45	51.1	9	22	AAB69911	Human NY-ESO-1 HLA
28	45	51.1	10	22	AAG67202	Cancer testis tumo
29	45	51.1	10	22	AAB69934	Human NY-ESO-1 HLA
30	44.5	50.6	253	21	AAB03134	Pol fragment 2 enc
31	43	48.9	9	20	AA506035	Human cancer anti
32	43	48.9	9	21	AA579748	NY-ESO-1 derived p
33	42	47.7	9	20	AA506037	Human cancer anti
34	42	47.7	9	22	AAG67191	Cancer testis tumo
35	42	47.7	9	22	AAB69923	Human NY-ESO-1 HLA
36	41	46.6	125	22	AAO22203	Human polypeptide
37	41	46.6	198	22	AAU57005	Propionibacterium
38	40.5	46.0	914	18	AAW18030	Huntingtin interac
39	40.5	46.0	914	21	AA559269	Human huntingtin-i
40	40.5	46.0	1090	21	AA559270	Human huntingtin-i
41	40	45.5	2176	22	ABB66269	Drosophila melanog
42	39.5	44.9	756	21	AA559272	Mouse huntingtin-i
43	39	44.3	9	20	AA506042	Human cancer anti
44	39	44.3	9	22	AAG67173	Cancer testis tumo
45	39	44.3	9	22	AAB69905	Human NY-ESO-1 HLA

ALIGNMENTS

RESULT	1
AA52435	
ID	AA52435 standard; Protein; 18 AA.
XX	
AC	AA52435;
XX	
DT	15-FEB-2000 (first entry)
XX	
DE	Human tumour antigen NY-ESO-1 peptide #8.
XX	
KW	Cancer; tumour; antigen; MHC; major histocompatibility complex; Class II;
KW	T-cell; helper; stimulation; proliferation; treatment;
KW	diagnosis; prevention; melanoma; breast cancer; ovarian cancer;
KW	prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer;
KW	lymphoma.
XX	
OS	Synthetic.
XX	Homo sapiens.
PN	WO9953938-A1.
XX	
PD	28-OCT-1999.
XX	
PF	24-MAR-1999; 99WO-US06875.
XX	
PR	17-APR-1998; 98US-0062422.
PR	02-OCT-1998; 98US-0165546.
XX	
PA	(LUDW-) LUDWIG INST CANCER RES.
XX	
PI	Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
PI	Gure A, Ritter G;
XX	
DR	WPI; 2000-038483/03.

PT Novel peptides which bind to MHC class I and MHC class II molecules,
PT useful for therapeutic and diagnostic purposes -
XX Claim 4; Page 22; 49pp; English.
PS
XX Peptides #8-#13 (AAAY52435-Y52440) are peptides derived from the human
CC tumour antigen, NY-ESO-1 (AAAY52430) which can bind to MHC(major
CC histocompatibility Class II HLA-DR53 molecules, thereby stimulating
CC proliferation of helper T-cells. cDNA encoding NY-ESO-1 was initially
CC isolated from an oesophagus squamous cell cancer cDNA library. Tissue
CC localisation studies revealed it to be expressed at high levels
CC in normal ovary and testis but not in normal colon, kidney, liver,
CC brain, oesophagus and skin. It was expressed in certain tumours and
CC tumour cell lines with some degree of frequency - these included
CC melanoma specimens and cell lines, and breast and bladder cancer
CC specimens, with expression in other tumour types being sporadic.
CC These NY-ESO-1-derived peptides may be used in methods and
CC compositions used for the treatment, diagnosis and prevention of
CC cancers (such as melanoma, breast cancer, prostate cancer, lung
CC cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer,
CC or lymphoma) and to stimulate the proliferation of T cells.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 88; DB 21; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQQL 18
Db 1 aadhrqlqlsisssclqql 18

RESULT 2
AAE07770
ID AAE07770 standard; peptide; 18 AA.
XX
AC AAE07770;
XX
DT 06-NOV-2001 (first entry)
DE Human NY ESO-1 HLA DR restricted T cell cancer peptide #2.
XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.
XX Homo sapiens.
OS
XX WO200155393-A2.
PN
XX 02-AUG-2001.
PD
XX 26-JAN-2001; 2001WO-US02765.
PF
XX 28-JAN-2000; 2000US-0179004.
PR 29-SEP-2000; 2000US-0237107.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
XX Wang R, Rosenberg SA, Zeng G;
PI
XX WPI; 2001-496851/54.
DR
XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -
XX
PS Claim 84; Page 84; 134pp; English.

XX The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or hapten and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is human
CC NY ESO-1 HLA DR restricted T cell cancer peptide.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 88; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQQL 18
Db 1 aadhrqlqlsisssclqql 18

RESULT 3
AAU01539
ID AAU01539 standard; Peptide; 18 AA.
XX
AC AAU01539;
XX
DT 18-JUL-2001 (first entry)
XX
DE HLA-DR53 recognising NY-ESO-1 peptide #1.
XX
KW NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
KW human leukocyte antigen-determining region; disease progression;
KW disease regression; disease onset; body tissue; body fluid; enzyme label;
KW radioactive label; monoclonal antibody.
XX Homo sapiens.
OS
XX WO200123560-A2.
PN
XX
XX 05-APR-2001.
PD
XX 26-SEP-2000; 2000WO-US26411.
PF
XX 29-SEP-1999; 99US-0408036.
PR
XX (LUDW-) LUDWIG INST CANCER RES.
PA
XX Tureci O, Sahin U, Pfreundschuh M;
PI
XX WPI; 2001-266156/27.
DR
XX Polypeptides binding to major histocompatibility complex class II human
PT leukocyte antigen-determining region molecule having amino acid
PT sequence found in tumour rejection antigen precursor used for
PT stimulating proliferation of helper T cells -
XX
PS Example 13; Page 19; 62pp; English.
XX
CC The sequence represents a human NY-ESO-1 tumour rejection antigen
CC precursor fragment which recognises and binds to HLA-DR53. NY-ESO-1 and
CC SSX-2 polypeptides, or fragments of, bind to major histocompatibility

CC complex (MHC) Class II molecules such as human leukocyte
CC antigen-determining region (HLA-DR) molecules and stimulate proliferation
CC of helper T cells. The peptides can be administered to an HLA-DR positive
CC subject in order to stimulate the helper T cells. An MHC Class II
CC HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell or
CC present in free form is useful for this stimulation. The nucleic acid is
CC useful for screening for a cancerous condition, which involves contacting
CC a subject sample to a cell line transfected with the immunoreactive cell
CC (helper T cell), where interaction is indicative of cancer. In addition,
CC a sample from a patient (for example, a body fluid or tissue) can be
CC monitored for the amount of the complex present in the bloodstream. This
CC is useful for determining regression, progression or onset of a cancerous
CC condition. The method involves contacting the sample with a radioactive
CC labelled or enzyme labelled monoclonal antibody which specifically binds
CC with the complex.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 88; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. NO. 1.5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AADHRQLQLSISSCLOQL 18
| | | | | | | | | | | | | | | |
Db 1 aadhrqlqlsissclqql 18

RESULT 4
AAB69939
ID AAB69939 standard; Peptide; 18 AA.
XX
AC AAB69939;
XX

DT 27-APR-2001 (first entry)
XX

DE Human NY-ESO-1 HLA-DR53 binding motif #1.
XX

KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW non-small cell lung carcinoma; tumour status determination.
XX

OS Homo sapiens.
XX

PN WO200107917-A1.
XX

PD 01-FEB-2001.
XX

PF 14-JUL-2000; 2000WO-US19220.
XX

PR 23-JUL-1999; 99US-0359503.
XX

PA (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.

PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
XX

DR WPI; 2001-182822/18.
XX

PT Method useful for determining the status (e.g. progression, regression
PT or stability of the disease) of a cancerous condition, involves
PT determining the levels of NY-ESO-1 specific antibodies in a sample
PT taken from a patient -
XX

PS Example 16; Page 27; 50pp; English.
XX

CC The present sequence is given in a specification relating to a method
CC for determining the status of a cancerous condition in a patient
CC with a tumour that expresses NY-ESO-1. The method comprises assaying a
CC sample taken from the patient for antibodies that specifically bind to
CC the NY-ESO-1 and comparing the value obtained to a prior value obtained
CC from assay of a prior sample taken from the patient. Any difference

CC between the values is indicative of a change in status of the cancerous
CC condition. The method is useful for determining whether a cancerous
CC condition is progressing, regressing or remaining stable, in particular
CC in patients receiving treatment for a melanoma, adenocarcinoma,
CC non-small cell lung carcinoma or bladder carcinoma.
XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 88; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. NO. 1.5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AADHRQLQLSISSCLOQL 18
| | | | | | | | | | | | | | | |
Db 1 aadhrqlqlsissclqql 18

RESULT 5
AAW69664
ID AAW69664 standard; Protein; 180 AA.
XX

AC AAW69664;
XX

DT 27-OCT-1998 (first entry)
XX

DE Human LAGE-1 clone 4 protein sequence.
XX

KW Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour.
XX

OS Homo sapiens.
XX

PN WO9832855-A1.
XX

PD 30-JUL-1998.
XX

PF 27-JAN-1998; 98WO-US01445.
XX

PR 27-JAN-1997; 97US-0791495.
XX

PA (LUDW-) LUDWIG INST CANCER RES.
XX

PI Boon-Falleur T, De Smet C, Godelaine D, Lethe B;
PI Lucas S;
XX

DR WPI; 1998-427951/36.
DR N-PSDB; AAV50347.
XX

PT New isolated LAGE-1 tumour associated nucleic acids - used to
PT develop products for the diagnosis and treatment of LAGE-1
PT associated disorders, particularly tumours
XX

PS Claim 21; Page 55; 73pp; English.
XX

CC The present sequence represents LAGE-1 tumour associated protein (TAP).
CC The present invention also describes: (1) a method for treating a
CC subject with a disorder characterised by expression of a LAGE-1 nucleic
CC acid molecule or an expression product, comprising administering to the
CC subject autologous cytolytic T cells to ameliorate the disorder, where
CC the cytolytic T cells are specific for complexes of an HLA molecule and
CC a LAGE-1 TAP or an immunogenic fragment; (2) a method for treating a
CC subject with a disorder characterised by expression of a LAGE-1 nucleic
CC acid molecule or an expression product, comprising administering a
CC LAGE-1 TAP or an immunogenic fragment to ameliorate the disorder; and
CC (3) a method for selectively enriching a population of T cells with
CC cytolytic T cells specific for a LAGE-1 TAP comprising contacting an
CC isolated population of T cells with an agent presenting a complex of a
CC LAGE TAP or an immunogenic fragment and a HLA presenting molecule to
CC selectively enrich the isolated population of T cells with the cytolytic
CC T cells. The methods and products from the present invention can be used
CC for the diagnosis and treatment of LAGE-1 associated disorders,
CC particularly tumours.
XX

SQ Sequence 180 AA; Query Match 100.0%; Score 88; DB 19; Length 180; Best Local Similarity 100.0%; Pred. No. 2.1e-07; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQQL 18
Db 139 aadhrqlqlsisssclqql 156

RESULT 6
AAW69665
ID AAW69665 standard; Protein; 180 AA.
XX
AC AAW69665;
XX
DT 27-OCT-1998 (first entry)
XX
DE Human NY-ESO-1 protein sequence, formerly known as LL-1.2 clone.
XX
KW Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour.
XX
OS Homo sapiens.
XX
PN WO9832855-A1.
XX
PD 30-JUL-1998.
XX
PF 27-JAN-1998; 98WO-US01445.
XX
PR 27-JAN-1997; 97US-0791495.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Boon-Falleur T, De Smet C, Godelaine D, Lethe B;
PI Lucas S;
XX
DR WPI; 1998-427951/36.
DR N-PSDB; AAV50348.
XX
PT New isolated LAGE-1 tumour associated nucleic acids - used to develop products for the diagnosis and treatment of LAGE-1 associated disorders, particularly tumours
PT
XX
PS Example 2; Page 57-58; 73pp; English.
XX
CC The present sequence represents human NY-ESO-1, formerly known as LL-1.2 clone, which is used in an example from the present invention which describes LAGE-1 tumour associated protein (TAP). The present invention also describes: (1) a method for treating a subject with a disorder characterised by expression of a LAGE-1 nucleic acid molecule or an expression product, comprising administering to the subject autologous cytolytic T cells to ameliorate the disorder, where the cytolytic T cells are specific for complexes of an HLA molecule and a LAGE-1 TAP or an immunogenic fragment; (2) a method for treating a subject with a disorder characterised by expression of a LAGE-1 nucleic acid molecule or an expression product, comprising administering a LAGE-1 TAP or an immunogenic fragment to ameliorate the disorder; and (3) a method for selectively enriching a population of T cells with cytolytic T cells specific for a LAGE-1 TAP comprising contacting an isolated population of T cells with an agent presenting a complex of a LAGE TAP or an immunogenic fragment and a HLA presenting molecule to selectively enrich the isolated population of T cells with the cytolytic T cells. The methods and products from the present invention can be used for the diagnosis and treatment of LAGE-1 associated disorders, particularly tumours.
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 88; DB 19; Length 180;

Best Local Similarity 100.0%; Pred. No. 2.1e-07; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQQL 18
Db 139 aadhrqlqlsisssclqql 156

RESULT 7
AAW62584
ID AAW62584 standard; Protein; 180 AA.
XX
AC AAW62584;
XX
DT 17-SEP-1998 (first entry)
XX
DE Cancer associated antigen NY-ESO-1.
XX
KW Cancer associated antigen; NY-ESO-1; regression; progression; onset; cancer; treatment; diagnosis.
KW
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Misc-difference 7 /note= "potential myristoylation site"
FT Misc-difference 9 /note= "potential myristoylation site"
FT Misc-difference 11 /note= "potential phosphorylation site"
FT Misc-difference 98 /note= "potential phosphorylation site"
FT Misc-difference 134 /note= "potential phosphorylation site"
FT Misc-difference 138 /note= "potential phosphorylation site"
FT
XX WO9814464-A1.
XX
PD 09-APR-1998.
XX
PF 15-SEP-1997; 97WO-US16335.
XX
PR 03-OCT-1996; 96US-0725182.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Chen Y, Drijfhout JW, Gure A, Jager E, Knuth A;
PI Old LJ, Scanlan M;
XX
DR WPI; 1998-286417/25.
DR N-PSDB; AAV38566.
XX
PT New isolated cancer associated antigen - is used to develop products for the diagnosis and treatment of cancers and for monitoring cancer therapy
PT
XX Claim 8; Fig 3; 49pp; English.
XX
CC The present sequence represents a cancer associated antigen. The clone from which the DNA sequence is obtained is designated NY-ESO-1. The specification described a method for determining regression, progression of onset of a cancerous condition, comprising monitoring a sample from a patient with the cancerous condition for a parameter selected from NY-ESO-1 protein, a peptide derived from NY-ESO-1 protein and cytolytic T cells specific for the peptide and an MHC molecule with which it non-covalently complexes. Methods for the treatment of a cancerous condition are also described. The NY-ESO-1 protein and peptides derived from it can be used for diagnosis and treatment of cancers and to monitor the efficacy of a therapeutic regime.
XX
SQ Sequence 180 AA;

Query Match	100.0%;	Score 88;	DB 19;	Length 180;
Best Local Similarity	100.0%;	Pred. No. 2.1e-07;		
Matches 18;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 AADHRQLQLSISSCLOQL 18
| | | | | | | | | |
Db 139 aadhrqlqlsissclqql 156

RESULT 8
 AAY05965
 ID AAY05965 standard; Protein; 180 AA.

KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer antigen; human; leukaemia;
KW non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; ORF1.

OS	Homo sapiens.
XX	
PN	WO9918206-A2.
XX	
PD	15-APR-1999.
XX	
PF	21-SEP-1998; 98WO-US19609.
XX	
PR	08-OCT-1997; 97US-0061428.
XX	
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.

DR WPI; 1999-277270/23.
DR N-PSDB; AAX58599.

PT Cancer antigen NY ESO1/CAG-3
XX
PS Claim 4; Fig 3A; 88pp; English.

The present sequence represents the ORF1 protein encoded by open reading frame 1 of the human ESO-1/CAG-3 (or CAG-3) gene. CAG-3 is a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides comprising ORF1, ORF2 (see AAY05966), portions of these peptides and their variants (see AAY05965-87), are useful as cancer vaccines and protect the recipient from development of cancer. The invention provides: vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a transgenic animal; antisense oligonucleotides that inhibit expression of the cancer peptide or tumour antigen; antibodies reacting with the CAG-3 cancer peptide, useful in diagnostic and detection assays; and methods for preventing or inhibiting cancer by administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer-specific T cells in vitro for subsequent return to a patient.

Sequence	180 AA;
SQ	

```
Query Match      100.0%; Score 88; DB 20; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 AADHRQLQLSISSCLQQL 18
+++++
pb 139 aadhrqlqlsissclagl 156

RESULT	9	
AAB03154		
ID	AAB03154	standard; Protein; 180 AA.
XX		
AC	AAB03154;	
XX		
DT	23-OCT-2000	(first entry)
XX		
DE	Human oesophageal cancer-associated antigen NY-ESO-1.	
XX		
KW	Oesophageal cancer associated antigen; NY-ESO-1; human;	
KW	immunogen; oesophageal carcinoma; melanoma; ovary; testis	
KW	transmembrane domain; antibody; diagnostic marker; drug c	
XX		
OS	Homo sapiens.	
XX		
Key		Location/Qualifiers
Modified-site	7	
FT	/note=	"Potential N-myristoylation site"
FT	9	
Modified-site		
FT	/note=	"Potential N-myristoylation site"
FT	11	
Modified-site		
FT	/note=	"Potential O-phosphorylation site"
FT	98	
Modified-site		
FT	/note=	"Potential O-phosphorylation site"
FT	134	
Modified-site		
FT	/note=	"Potential O-phosphorylation site"
FT	138	
Modified-site		
FT	/note=	"Potential O-phosphorylation site"
FT	152..172	
Domain		
FT	/note=	"Potential transmembrane domain"
FT		

CC of the amino acid sequence of the protein indicates that the protein has
CC a transmembrane domain, several N-myristoylation sites and
CC O-phosphorylation sites and that it contains antigenic sequences in the
CC N-terminal half of the protein. The antigen is useful as an immunogen
CC when combined with an adjuvant, in both precursor and post-
CC translationally modified forms, and may be used to generate anti-NY-ESO-1
CC antibodies. It can also be used as a diagnostic marker for oesophageal
CC cancer, and can be utilised as a marker for the targetted delivery of
CC therapeutic agents to oesophageal cancer cells. It can also be used to
CC generate diagnostic or therapeutic agents.

SQ Sequence 180 AA;

Query Match 100.0%; Score 88; DB 21; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLOQL 18
Db 139 aadhrqlqlsissclqql 156
|||||

RESULT 10
AAY70860
ID AAY70860 standard; Protein; 180 AA.

XX AC AAY70860;

XX DT 31-JUL-2000 (first entry)

XX DE Human LAGE-1 splice variant, LAGE-1s protein.

XX KW LAGE-1s; splice variant; CAMEL; CTL-recognised Antigen on MELanoma; CTL;
KW cytotoxic T lymphocyte; tumour-associated antigen; NY-ESO-1; anticancer;
KW human; cancer; melanoma; immunotherapy; immune response.

XX OS Homo sapiens.

XX PN WO200023584-A1.

XX PD 27-APR-2000.

XX PF 15-OCT-1999; 99WO-EP07832.

XX PR 16-OCT-1998; 98EP-0119583.

XX PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
XX PA (UYHO-) UNIV HOSPITAL LEIDEN.

XX PI Schrier PI, Aarnoudse CA, Heider K, Klade C;

XX DR WPI; 2000-339685/29.

XX DR N-PSDB; AAD00150.

XX PT Tumor-associated antigen useful for cancer immunotherapy is encoded by
XX the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA -

XX PS Example 3; Page 57-58; 73pp; English.

XX CC The present sequence is the human LAGE-1 splice variant, LAGE-1s protein,
CC a tumour-specific antigen. The LAGE-1s protein is encoded by the open
CC reading frame-3 (ORF) and the CAMEL protein (Cytotoxic T lymphocytes
CC (CTL)-recognised Antigen on MELanoma) from ORF-1 of LAGE-1 cDNA. The
CC LAGE-1(s/l) protein derived from ORF-1 is identical to the CAMEL protein.
CC It is not expressed in healthy tissues except in testis and placenta.
CC It also shows homology with the NY-ESO-1, a tumour specific antigen. The
CC tumour-associated antigen displayed on melanoma cells is recognised by
CC cytotoxic T lymphocytes. This sequence has anticancer activity. CAMEL
CC tumour antigen and immunogenic peptides derived from it are useful for
CC cancer immunotherapy. They have the potential to induce an immune
CC response, by eliciting a CTL response. The DNA molecule is used for the
CC construction of recombinant or fusion proteins.

XX SQ Sequence 180 AA;

Query Match 100.0%; Score 88; DB 21; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLOQL 18
Db 139 aadhrqlqlsissclqql 156
|||||

RESULT 11
AAY70862
ID AAY70862 standard; Protein; 180 AA.

XX AC AAY70862;

XX DT 31-JUL-2000 (first entry)

XX DE Human tumour antigen, NY-ESO-1 protein.

XX KW NY-ESO-1; CAMEL; CTL-recognised Antigen on MELanoma; human; cancer; CTL;
KW cytotoxic T lymphocyte; tumour-associated antigen; LAGE-1; anticancer;
KW melanoma; immunotherapy; immune response.

XX OS Homo sapiens.

XX PN WO200023584-A1.

XX PD 27-APR-2000.

XX PF 15-OCT-1999; 99WO-EP07832.

XX PR 16-OCT-1998; 98EP-0119583.

XX PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
XX PA (UYHO-) UNIV HOSPITAL LEIDEN.

XX PI Schrier PI, Aarnoudse CA, Heider K, Klade C;

XX DR WPI; 2000-339685/29.

XX DR N-PSDB; AAD00152.

XX PT Tumor-associated antigen useful for cancer immunotherapy is encoded by
XX the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA -

XX PS Example 3; Page 62-63; 73pp; English.

XX CC The present sequence is the human NY-ESO-1 protein, a tumour antigen,
CC identified by screening an esophagus carcinoma cDNA library. This protein
CC is derived from open reading frame (ORF)-1 that contain epitopes of
CC tumour specific T-cells. NY-ESO-1 is expressed in different tumour types,
CC but not in healthy tissues except in testis. It also shows homology with
CC the CAMEL (Cytotoxic T lymphocytes (CTL)-recognised Antigen on MELanoma)
CC protein, a tumour-associated antigen. The tumour-associated antigen
CC displayed on melanoma cells is recognised by cytotoxic T lymphocytes.
CC This sequence has anticancer activity. CAMEL tumour antigen and
CC immunogenic peptides derived from it are useful for cancer immunotherapy.
CC They have the potential to induce an immune response, by eliciting a
CC CTL response. The DNA molecule is used for the construction of
CC recombinant or fusion proteins.

XX SQ Sequence 180 AA;

Query Match 100.0%; Score 88; DB 21; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLOQL 18
Db 139 aadhrqlqlsissclqql 156
|||||

RESULT 13
AAG67164
ID AAG67164 standard; Protein; 180 AA.
XX
AC AAG67164;
XX
DT 13-NOV-2001 (first entry)
XX
DE Amino acid sequence of cancer testis tumour antigen NY-ESO-1.
XX
KW Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;
KW HLA; HLA binding peptide; major histocompatibility complex; MHC;
KW tumour; cancer; testis tumour.
XX
OS Homo sapiens.
XX
PN WO200162917-A1.
XX
PD 30-AUG-2001.
XX
PF 22-JAN-2001; 2001WO-US02126.
XX
PR 22-FEB-2000; 2000US-0510635.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Lethe B, Boon-Falleur T;
XX
DR WPI; 2001-550091/61.
DR N-PSDB; AAH75118.
XX
PT Genomic sequences of tumour associated antigen EY-ESO-1 (LAGE-2) useful
PT for diagnosing testicular tumours -
XX
PS Example 5; Fig 3; 50pp; English.
XX
CC The present sequence represents cancer testis tumour antigen NY-ESO-1
CC (also called LAGE-2). NY-ESO-1 is a molecule that is processed to at
CC least one human leukocyte antigen (HLA) binding peptide, which binds
CC to Class I and Class II major histocompatibility complex (MHC).
CC NY-ESO-1 is expressed in tumour mRNA and in testis, but not normal
CC colon, kidney, liver or brain tissue. The presence or level of expression
CC of NY-ESO-1 may be assayed for the diagnosis of cancer, especially
CC testis tumours.
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 88; DB 22; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQQL 18
| | | | | | | | | | | | | | | | | | | | | |
Db 139 aadhrqlqlsissclqql 156

RESULT 14
AAE07714
ID AAE07714 standard; Protein; 180 AA.
XX
AC AAE07714;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human NY ESO-1 protein.
XX
KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leukocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.
XX

OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 45..47
FT /note= "Encoded by CCGGGGGC"
XX
PN WO200155393-A2.
XX
PD 02-AUG-2001.
XX
PF 26-JAN-2001; 2001WO-US02765.
XX
PR 28-JAN-2000; 2000US-0179004.
PR 29-SEP-2000; 2000US-0237107.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang R, Rosenberg SA, Zeng G;
XX
DR WPI; 2001-496851/54.
DR N-PSDB; AAD14179, AAD14180.
XX
PT New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -
XX
PS Example 1; Fig 1; 134pp; English.
XX
CC The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY-ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or hapten and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is
CC human NY ESO-1 protein.
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 88; DB 22; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQQL 18
| | | | | | | | | | | | | | | | | | | | | |
Db 139 aadhrqlqlsissclqql 156

RESULT 15
AAU01535
ID AAU01535 standard; Protein; 180 AA.
XX
AC AAU01535;
XX
DT 18-JUL-2001 (first entry)
XX
DE Human NY-ESO-1 tumour rejection antigen precursor protein.
XX
KW NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
KW human leukocyte antigen-determining region; disease progression;
KW disease regression; disease onset; body tissue; body fluid; enzyme label;
KW radioactive label; monoclonal antibody.

XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Modified-site 7 /note= "Myristoylated"
FT Modified-site 9 /note= "Myristoylated"
FT Modified-site 11 /note= "Phosphorylated"
FT Modified-site 98 /note= "Phosphorylated"
FT Modified-site 134 /note= "Phosphorylated"
FT Modified-site 138 /note= "Phosphorylated"
FT Modified-site /note= "Phosphorylated"
XX WO200123560-A2.
PN 05-APR-2001.
PD 26-SEP-2000; 2000WO-US26411.
XX 29-SEP-1999; 99US-0408036.
XX (LUDW-) LUDWIG INST CANCER RES.
PA Tureci O, Sahin U, Pfreundschuh M;
XX WPI; 2001-266156/27.
DR N-PSDB; AAS02254.
XX Polypeptides binding to major histocompatibility complex class II human
PT leukocyte antigen-determining region molecule having amino acid
PT sequence found in tumour rejection antigen precursor used for
PT stimulating proliferation of helper T cells -
XX 'Claim 4; Fig 3; 62pp; English.
PS The sequence represents a human NY-ESO-1 tumour rejection antigen
XX precursor. NY-ESO-1 and SSX-2 polypeptides, or fragments of, bind to
CC major histocompatibility complex (MHC) Class II molecules such as human
CC leukocyte antigen-determining region (HLA-DR) molecules and stimulate
CC proliferation of helper T cells. The peptides can be administered to an
CC HLA-DR positive subject in order to stimulate the helper T cells. An MHC
CC Class II HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell
CC or present in free form is useful for this stimulation. The nucleic acid
CC is useful for screening for a cancerous condition, which involves
CC contacting a subject sample to a cell line transfected with the
CC immunoreactive cell (helper T cell), where interaction is indicative of
CC cancer. In addition, a sample from a patient (for example, a body fluid
CC or tissue) can be monitored for the amount of the complex present in the
CC bloodstream. This is useful for determining regression, progression or
CC onset of a cancerous condition. The method involves contacting the sample
CC with a radioactive labelled or enzyme labelled monoclonal antibody which
CC specifically binds with the complex.
XX SQ Sequence 180 AA;

Query Match 100.0%; Score 88; DB 22; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQQL 18
Db 139 aadhrqlqlsissclql 156

RESULT 16
AAB69946
ID AAB69946 standard; Protein; 180 AA.
XX

AC AAB69946;
XX 27-APR-2001 (first entry)
XX DE Human NY-ESO-1 protein.
XX KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW non-small cell lung carcinoma; tumour status determination.
XX OS Homo sapiens.
XX WO200107917-A1.
PN 01-FEB-2001.
PD 14-JUL-2000; 2000WO-US19220.
XX 23-JUL-1999; 99US-0359503.
XX (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.
XX Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
PI WPI; 2001-182822/18.
XX N-PSDB; AAF58634.
DR Method useful for determining the status (e.g. progression, regression
XX or stability of the disease) of a cancerous condition, involves
PT determining the levels of NY-ESO-1 specific antibodies in a sample
PT taken from a patient -
XX Example 5; Fig 3; 50pp; English.
PS The present sequence is human NY-ESO-1 protein. It is provided in a
XX specification relating to a method for determining the status of a
CC cancerous condition in a patient with a tumour that expresses NY-ESO-1.
CC The method comprises assaying a sample taken from the patient for
CC antibodies that specifically bind to the NY-ESO-1 and comparing the
CC value obtained to a prior value obtained from assay of a prior sample
CC taken from the patient. Any difference between the values is indicative
CC of a change in status of the cancerous condition. The method is useful
CC for determining whether a cancerous condition is progressing, regressing
CC or remaining stable, in particular in patients receiving treatment for a
CC melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder
CC carcinoma.
XX SQ Sequence 180 AA;

Query Match 100.0%; Score 88; DB 22; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQQL 18
Db 139 aadhrqlqlsissclql 156

RESULT 17
AAE13122
ID AAE13122 standard; Protein; 397 AA.
XX
AC AAE13122;
XX 28-JAN-2002 (first entry)
DT NY-ESO-IC-HER-2 membrane distal intracellular domain fusion protein.
XX DE Immunostimulatory fusion protein; IFP; antigen component; therapy;
XX KW Immunostimulatory component; T-cell mediated immune response; DC;
KW

KW dendritic cell; colon cancer; breast carcinoma; ovarian cancer;
KW human; HER-2 membrane distal intracellular domain; NY-ESO-IC;
KW autoimmunogenic cancer/testis antigen.

XX OS Homo sapiens.

XX PN WO200174855-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US10515.

XX PR 30-MAR-2000; 2000US-193504P.

XX PA (DEND-) DENDREON CORP.

XX PI Laus R, Vidovic D, Graddis T;

XX DR WPI; 2001-662965/76.

DR N-PSDB; AAD21573.

XX
PT An immunostimulatory fusion protein comprising the intracellular domain
PT of HER-2 and an antigen elicits an immune response to the antigen and
PT is useful for the treatment of associated cancer associated -

XX PS Disclosure; Page 54-55; 59pp; English.

XX
CC The invention relates to immunostimulatory fusion proteins (IFP) and
CC nucleic acid molecules encoding such proteins. The IFPs comprise a
CC polypeptide antigen component and an immunostimulatory component derived
CC from the intracellular domain of HER-2 protein which is effective to
CC elicit a protective dendritic cell (DC)-induced T-cell mediated cellular
CC immune response to the antigen. IFP or superactivated dendritic cells
CC are used to treat cancer e.g. breast carcinoma, ovarian and colon cancer
CC associated with a particularly antigen. The present sequence is a
CC fusion protein which comprises human autoimmunogenic
CC cancer/testis antigen, NY-ESO-IC and mature human HER-2 membrane distal
CC intracellular domain.

XX SQ Sequence 397 AA;

Query Match 100.0%; Score 88; DB 22; Length 397;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISCLQQL 18

Db 139 aadhrqlqlsissclqql 156

Search completed: July 3, 2002, 13:01:06
Job time: 39 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:06:13 ; Search time 599.92 Seconds
(without alignments)
10.561 Million cell updates/sec

Title: US-09-165-546A-8

Perfect score: 88

Sequence: 1 AADHRQLQLSISSCLQQL 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US08_COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US081_COMB.pep.*
- 6: /cgn2_6/ptodata/2/paa/US082_COMB.pep.*
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- 26: /cgn2_6/ptodata/2/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	88	100.0	18	15 US-09-165-546A-8	Sequence 8, Appli
2	88	100.0	18	18 US-09-408-036B-7	Sequence 7, Appli
3	88	100.0	180	11 US-08-791-495-7	Sequence 7, Appli
4	88	100.0	180	11 US-08-791-495-9	Sequence 9, Appli
5	88	100.0	180	17 US-09-341-829A-7	Sequence 7, Appli
6	88	100.0	180	17 US-09-341-829A-9	Sequence 9, Appli
7	88	100.0	180	17 US-09-392-714-25	Sequence 25, Appli

8	88	100.0	180	19 US-09-529-206-4	Sequence 4, Appli
9	88	100.0	180	19 US-09-529-206A-3	Sequence 3, Appli
10	88	100.0	180	19 US-09-529-206B-3	Sequence 3, Appli
11	88	100.0	180	19 US-09-561-571-3	Sequence 3, Appli
12	88	100.0	180	21 US-09-751-798-8	Sequence 8, Appli
13	88	100.0	180	24 US-10-005-905-3	Sequence 3, Appli
14	88	100.0	180	24 US-10-023-182-8	Sequence 8, Appli
15	88	100.0	180	24 US-10-026-066-3	Sequence 3, Appli
16	88	100.0	180	26 US-60-336-968-11	Sequence 11, Appl
17	88	100.0	397	22 US-09-821-883-27	Sequence 27, Appl
18	76	86.4	122	26 US-60-336-968-17	Sequence 17, Appl
19	48	54.5	10	19 US-09-529-206-99	Sequence 99, Appl
20	48	54.5	10	19 US-09-529-206A-99	Sequence 99, Appl
21	48	54.5	10	19 US-09-529-206B-99	Sequence 99, Appl
22	47	53.4	10	19 US-09-529-206-103	Sequence 103, App
23	47	53.4	10	19 US-09-529-206A-103	Sequence 103, App
24	47	53.4	10	19 US-09-529-206B-103	Sequence 103, App
25	44.5	50.6	73	16 US-09-248-796-25545	Sequence 25545, A
26	44.5	50.6	73	26 US-60-096-409-25545	Sequence 25545, A
27	44.5	50.6	253	18 US-09-430-590-48	Sequence 48, Appl
28	44.5	50.6	253	18 US-09-430-590C-115	Sequence 115, Appl
29	44.5	50.6	253	18 US-09-430-590E-115	Sequence 115, Appl
30	44.5	50.6	253	22 US-09-830-868-50	Sequence 50, Appl
31	44.5	50.6	1122	16 US-09-248-796-16374	Sequence 16374, A
32	44.5	50.6	1122	26 US-60-096-409-16374	Sequence 16374, A
33	44	50.0	166	18 US-09-417-507-34734	Sequence 34734, A
34	44	50.0	261	17 US-09-328-352-6554	Sequence 6554, Ap
35	43	48.9	9	18 US-09-409-455A-115	Sequence 115, App
36	43	48.9	9	19 US-09-529-206-74	Sequence 74, Appl
37	43	48.9	9	19 US-09-529-206A-74	Sequence 74, Appl
38	43	48.9	9	19 US-09-529-206B-74	Sequence 74, Appl
39	43	48.9	9	22 US-09-833-039-115	Sequence 115, App
40	43	48.9	276	16 US-09-252-991A-21623	Sequence 21623, A
41	42	47.7	9	19 US-09-529-206-75	Sequence 75, Appl
42	42	47.7	9	19 US-09-529-206A-75	Sequence 75, Appl
43	42	47.7	9	19 US-09-529-206B-75	Sequence 75, Appl
44	42	47.7	61	16 US-09-270-767-37415	Sequence 37415, A
45	42	47.7	61	16 US-09-270-767-52632	Sequence 52632, A

ALIGNMENTS

RESULT 1

US-09-165-546A-8

; Sequence 8, Application US/09165546A

; GENERAL INFORMATION:

; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao,

; Canlan, Matt; Gure, Ali, Old, Lloyd, Ritter, Gerd

; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO

; AMINO ACID SEQUENCES OF NY-ESO-1, WHICH BIND TO

; MHC CLASS I AND MHC CLASS II MOLECULES, AND

; USES THEREOF

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FULBRIGHT & JAWORSKI LLP

; STREET: 666 Fifth Avenue

; CITY: New York City

; STATE: New York

; COUNTRY: USA

; ZIP: 10158

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage

; COMPUTER: IBM

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: WordPerfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/165,546A

; FILING DATE: 02-Oct-1998

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/062,422

; FILING DATE: April 17, 1998

;
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-165-546A-8

Query Match 100.0%; Score 88; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQQL 18
| | | | | | | | | | | | | | | |
Db 1 AADHRQLQLSISSCLQQL 18

RESULT 2
US-09-408-036B-7
; Sequence 7, Application US/09408036B
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Isolated Peptides Which Bind to MHC Class II Molecules and Uses T
; FILE REFERENCE: LUD 5624
; CURRENT APPLICATION NUMBER: US/09/408,036B
; CURRENT FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/165,546
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 7
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-408-036B-7

Query Match 100.0%; Score 88; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQQL 18
| | | | | | | | | | | | | | | |
Db 1 AADHRQLQLSISSCLQQL 18

RESULT 3
US-08-791-495-7
; Sequence 7, Application US/08791495
; GENERAL INFORMATION:
; APPLICANT: Leth , Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:

;
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-7

Query Match 100.0%; Score 88; DB 11; Length 180;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQQL 18
| | | | | | | | | | | | | | | |
Db 139 AADHRQLQLSISSCLQQL 156

RESULT 4
US-08-791-495-9
; Sequence 9, Application US/08791495
; GENERAL INFORMATION:
; APPLICANT: Leth , Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500

```

; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 180 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-791-495-9

Query Match      100.0%; Score 88; DB 11; Length 180;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQQL 18
Db 139 AADHRQLQLSISSCLQQL 156

RESULT 5
US-09-341-829A-7
; Sequence 7, Application US/09341829A
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-341-829A-7

Query Match      100.0%; Score 88; DB 17; Length 180;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQQL 18
Db 139 AADHRQLQLSISSCLQQL 156

RESULT 6
US-09-341-829A-9
; Sequence 9, Application US/09341829A
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-341-829A-9

Query Match      100.0%; Score 88; DB 17; Length 180;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQQL 18
Db 139 AADHRQLQLSISSCLQQL 156

RESULT 7
US-09-392-714-25
; Sequence 25, Application US/09392714A
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Gure, Ali O.
; APPLICANT: Williamson, Barbara
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Cancer Associated Antigens and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: L0461/7062
; CURRENT APPLICATION NUMBER: US/09/392,714A
; CURRENT FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: PCT/US98/14679
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-392-714-25

Query Match      100.0%; Score 88; DB 17; Length 180;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQQL 18
Db 139 AADHRQLQLSISSCLQQL 156

RESULT 8
US-09-529-206-4
; Sequence 4, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-4

Query Match      100.0%; Score 88; DB 19; Length 180;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQQL 18
Db 139 AADHRQLQLSISSCLQQL 156
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Db 139 AADHRQLQLSISSCLQQL 156

RESULT 9
US-09-529-206A-3
; Sequence 3, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206A-3

Query Match 100.0%; Score 88; DB 19; Length 180;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQQL 18
|||||
Db 139 AADHRQLQLSISSCLQQL 156

RESULT 10
US-09-529-206B-3
; Sequence 3, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-3

Query Match 100.0%; Score 88; DB 19; Length 180;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQQL 18
|||||
Db 139 AADHRQLQLSISSCLQQL 156

RESULT 11
US-09-561-571-3
; Sequence 3, Application US/09561571
; GENERAL INFORMATION:
```

```
; APPLICANT: CTL ImmunoTherapies Corp.
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; TITLE OF INVENTION: EPITOPE CLUSTERS
; FILE REFERENCE: CTLIMM.010A
; CURRENT APPLICATION NUMBER: US/09/561,571
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-561-571-3

Query Match 100.0%; Score 88; DB 19; Length 180;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQQL 18
|||||
Db 139 AADHRQLQLSISSCLQQL 156

RESULT 12
US-09-751-798-8
; Sequence 8, Application US/09751798
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
; APPLICANT: Knuth, Alexander; Old, Lloyd J.
; TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
; TITLE OF INVENTION: Associated Proteins, Uses Thereof,
; TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
; TITLE OF INVENTION: Binding Peptides Derived Therefrom
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/751,798
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
US-09-751-798-8
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Query Match      100.0%; Score 88; DB 21; Length 180;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AADHRQLQLSISSCLOQL 18
db 139 AADHRQLQLSISSCLOQL 156

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RESULT 13
US-10-005-905-3
; Sequence 3, Application US/10005905
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; TITLE OF INVENTION: EPTOPE SYNCHRONIZATION IN ANTIGEN
; TITLE OF INVENTION: PRESENTING CELLS
; FILE REFERENCE: CTLM.021CP1
; CURRENT APPLICATION NUMBER: US/10/005,905
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 09/561,074
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/560,465
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,572
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,571
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US01/13806
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-005-905-3

```

```
Query Match      100.0%; Score 88; DB 24; Length 180;
Best Local Similarity 100.0%; Pred. NO. 3e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AADHRQLQLSISSCLQQL 18
 |||||
 Db 139 AADHROQLSISSCLOOL 156

```

RESULT 14
US-10-023-182-8
; Sequence 8, Application US/10023182
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; Chen, Yao-tseng; Scanlan, Matthew;
; Knuth, Alexander; Old, Lloyd J.
; TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
; Associated Proteins, Uses Thereof,
; Truncated Forms of NY-ESO-1, and HLA
; Binding Peptides Derived Therefrom
;
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/10/023,182
FILING DATE: 17-Dec-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/751,798
FILING DATE: December 29, 2000
APPLICATION NUMBER: 09/062,422
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, Norman D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 180
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-023-182-8

Query Match	100.0%;	Score 88;	DB 24;	Length 180;
Best Local Similarity	100.0%;	Pred. NO. 3e-06;		
Matches 18; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	AADHRQLQLSISSCLQQL	18
Db	139	AADHRQLQLSISSCLQQL	156

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RESULT 15
US-10-026-066-3
; Sequence 3, Application US/10026066
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; TITLE OF INVENTION: EPITOPE SYNCHRONIZATION IN ANTIGEN
; TITLE OF INVENTION: PRESENTING CELLS
; FILE REFERENCE: CTLIMM.21CPIC
; CURRENT APPLICATION NUMBER: US/10/026,066
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 09/561,074
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/560,465
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,572
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,571
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US01/13806
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-026-066-3

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Query Match      100.0%; Score 88; DB 24; Length 180;
Best Local Similarity 100.0%; Pred. NO. 3e-06;
Matches 18: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AADHRQLQLSISCLQQL 18
 |||||
 Db 139 AADHRQLQLSISCLQQL 156

Search completed: July 3, 2002, 11:21:00
Job time: 887 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:06:28 ; Search time 64.42 Seconds
(without alignments)
28.270 Million cell updates/sec

Title: US-09-165-546A-8
Perfect score: 88
Sequence: 1 AADHRQLQLSISSCLQQL 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 308740 seqs, 101176262 residues

Total number of hits satisfying chosen parameters: 308740

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	100.0	28	6 US-10-117-937-254	Sequence 254, App
2	88	100.0	180	1 PCT-US02-13994-30	Sequence 30, Appl
3	88	100.0	180	5 US-09-807-512-4	Sequence 4, Appli
4	88	100.0	180	5 US-09-807-512-8	Sequence 8, Appli
5	88	100.0	180	6 US-10-117-937-74	Sequence 74, Appl
6	88	100.0	180	6 US-10-117-937-75	Sequence 75, Appl
7	88	100.0	180	6 US-10-146-473-69	Sequence 69, Appl
8	47	53.4	10	6 US-10-117-937-194	Sequence 194, App
9	45	51.1	9	6 US-10-117-937-192	Sequence 192, App
10	45	51.1	10	6 US-10-117-937-195	Sequence 195, App
11	43	48.9	9	5 US-09-344-040C-115	Sequence 115, App
12	43	48.9	9	6 US-10-117-937-193	Sequence 193, App
13	41	46.6	317	6 US-10-155-881-10846	Sequence 10846, A
14	39	44.3	134	6 US-10-144-860-201	Sequence 201, App
15	39	44.3	142	5 US-09-937-060A-12	Sequence 12, Appl
16	39	44.3	210	6 US-10-144-860-247	Sequence 247, App
17	39	44.3	419	6 US-10-155-881-25684	Sequence 25684, A
18	39	44.3	1715	6 US-10-155-881-30675	Sequence 30675, A
19	38.5	43.8	767	5 US-09-987-482-3	Sequence 3, Appli
20	38.5	43.8	2842	5 US-09-442-489B-7	Sequence 7, Appli
21	38.5	43.8	2843	5 US-09-987-482-1	Sequence 1, Appli
22	38.5	43.8	2843	5 US-09-442-489B-2	Sequence 2, Appli
23	38	43.2	540	7 US-60-360-039-21289	Sequence 21289, A
24	38	43.2	585	6 US-10-119-480-242	Sequence 242, App
25	38	43.2	585	6 US-10-104-047-2739	Sequence 2739, Ap
26	38	43.2	615	5 US-09-609-360D-49	Sequence 49, Appl

27	38	43.2	678	7 US-60-360-039-5301	Sequence 5301, Ap
28	38	43.2	879	5 US-09-573-655B-30	Sequence 30, Appl
29	38	43.2	1067	7 US-60-360-039-2079	Sequence 2079, Ap
30	37	42.0	280	6 US-10-155-881-11348	Sequence 11348, A
31	37	42.0	298	6 US-10-155-881-11360	Sequence 11360, A
32	37	42.0	346	6 US-10-155-881-25851	Sequence 25851, A
33	37	42.0	346	6 US-10-155-881-28609	Sequence 28609, A
34	37	42.0	721	5 US-09-937-060A-7	Sequence 7, Appli
35	37	42.0	992	6 US-10-104-047-2473	Sequence 2473, Ap
36	37	42.0	997	6 US-10-155-881-26623	Sequence 26623, A
37	37	42.0	1140	6 US-10-155-881-30314	Sequence 30314, A
38	36.5	41.5	791	1 PCT-US02-12063-366	Sequence 366, App
39	36.5	41.5	791	6 US-10-126-022-366	Sequence 366, App
40	36	40.9	9	5 US-09-344-040C-121	Sequence 121, App
41	36	40.9	229	5 US-09-573-655B-1389	Sequence 1389, Ap
42	36	40.9	441	6 US-10-115-406-4	Sequence 4, Appli
43	36	40.9	454	6 US-10-115-406-26	Sequence 26, Appl
44	36	40.9	1289	5 US-09-573-655B-758	Sequence 758, App
45	35	39.8	9	6 US-10-117-937-198	Sequence 198, App

ALIGNMENTS

RESULT 1
US-10-117-937-254
; Sequence 254, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 254
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-254

Query Match 100.0%; Score 88; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQQL 18
Db 4 AADHRQLQLSISSCLQQL 21

RESULT 2
PCT-US02-13994-30
; Sequence 30, Application PC/TUS0213994
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research
; APPLICANT: Cornell Research Foundation, Inc.
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd
; APPLICANT: Scanlan, Matthew
; APPLICANT: Stockert, Elisabeth
; TITLE OF INVENTION: COLON CANCER ANTIGEN PANEL
; FILE REFERENCE: L00461/70105WO(JRV)


```
; CURRENT APPLICATION NUMBER: PCT/US02/13994
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US 09/849,602
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-13994-30
```

```
Query Match      100.0%; Score 88; DB 1; Length 180;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 AADHRQLQLSISSCLQQL 18
      |||||||
Db      139 AADHRQLQLSISSCLQQL 156
```

RESULT 3

US-09-807-512-4

; Sequence 4, Application US/09807512

; GENERAL INFORMATION:

; APPLICANT: Schrier, Peter I.

; APPLICANT: Aarnoudse, Corlien

; APPLICANT: Heider, Karl-Heinz

; APPLICANT: Klade, Christoph

; TITLE OF INVENTION: Camel, An Alternative Translation Product of the Tumor

; TITLE OF INVENTION: Antigen-Lage 1

; FILE REFERENCE: 0652.2200000

; CURRENT APPLICATION NUMBER: US/09/807,512

; CURRENT FILING DATE: 2001-04-16

; PRIOR APPLICATION NUMBER: PCT/EP99/07832

; PRIOR FILING DATE: 1999-10-15

; PRIOR APPLICATION NUMBER: EP 98119583.7

; PRIOR FILING DATE: 1998-10-16

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 180

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-807-512-4

```
Query Match      100.0%; Score 88; DB 5; Length 180;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 AADHRQLQLSISSCLQQL 18
      |||||||
Db      139 AADHRQLQLSISSCLQQL 156
```

RESULT 4

US-09-807-512-8

; Sequence 8, Application US/09807512

; GENERAL INFORMATION:

; APPLICANT: Schrier, Peter I.

; APPLICANT: Aarnoudse, Corlien

; APPLICANT: Heider, Karl-Heinz

; APPLICANT: Klade, Christoph

; TITLE OF INVENTION: Camel, An Alternative Translation Product of the Tumor

; TITLE OF INVENTION: Antigen-Lage 1

; FILE REFERENCE: 0652.2200000

; CURRENT APPLICATION NUMBER: US/09/807,512

; CURRENT FILING DATE: 2001-04-16

; PRIOR APPLICATION NUMBER: PCT/EP99/07832

; PRIOR FILING DATE: 1999-10-15

; PRIOR APPLICATION NUMBER: EP 98119583.7

```
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-807-512-8
```

```
Query Match      100.0%; Score 88; DB 5; Length 180;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 AADHRQLQLSISSCLQQL 18
      |||||||
Db      139 AADHRQLQLSISSCLQQL 156
```

RESULT 5

US-10-117-937-74

; Sequence 74, Application US/10117937

; GENERAL INFORMATION:

; APPLICANT: CTL IMMUNO THERAPIES CORP.

; APPLICANT: SIMARD, John, J.L.

; APPLICANT: DIAMOND, David, C.

; APPLICANT: LIU, Liping

; APPLICANT: XIE, Zhidong

; TITLE OF INVENTION: EPITOPE SEQUENCES

; FILE REFERENCE: CTIMM.027A

; CURRENT APPLICATION NUMBER: US/10/117,937

; CURRENT FILING DATE: 2002-04-04

; PRIOR APPLICATION NUMBER: US 60/282,211

; PRIOR FILING DATE: 2001-04-06

; PRIOR APPLICATION NUMBER: US 60/337,017

; PRIOR FILING DATE: 2001-11-07

; PRIOR APPLICATION NUMBER: US 60/363,210

; PRIOR FILING DATE: 2002-03-07

; NUMBER OF SEQ ID NOS: 602

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 74

; LENGTH: 180

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-117-937-74

```
Query Match      100.0%; Score 88; DB 6; Length 180;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 AADHRQLQLSISSCLQQL 18
      |||||||
Db      139 AADHRQLQLSISSCLQQL 156
```

RESULT 6

US-10-117-937-75

; Sequence 75, Application US/10117937

; GENERAL INFORMATION:

; APPLICANT: CTL IMMUNO THERAPIES CORP.

; APPLICANT: SIMARD, John, J.L.

; APPLICANT: DIAMOND, David, C.

; APPLICANT: LIU, Liping

; APPLICANT: XIE, Zhidong

; TITLE OF INVENTION: EPITOPE SEQUENCES

; FILE REFERENCE: CTIMM.027A

; CURRENT APPLICATION NUMBER: US/10/117,937

; CURRENT FILING DATE: 2002-04-04

; PRIOR APPLICATION NUMBER: US 60/282,211

; PRIOR FILING DATE: 2001-04-06

; PRIOR APPLICATION NUMBER: US 60/337,017

; PRIOR FILING DATE: 2001-11-07

; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-75

Query Match 100.0%; Score 88; DB 6; Length 180;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLOQL 18
| | | | | | | | | | | | | | | | | |
Db 139 AADHRQLQLSISSCLOQL 156

RESULT 7
US-10-146-473-69
; Sequence 69, Application US/10146473
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Gout, Ivan
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Gure, Ali
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd
; TITLE OF INVENTION: Breast Cancer Antigens
; FILE REFERENCE: L00461/70130(JRV)
; CURRENT APPLICATION NUMBER: US/10/146,473
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/291,150
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 69
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-473-69

Query Match 100.0%; Score 88; DB 6; Length 180;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLOQL 18
| | | | | | | | | | | | | | | | | |
Db 139 AADHRQLQLSISSCLOQL 156

RESULT 8
US-10-117-937-194
; Sequence 194, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07

; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 194
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-194

Query Match 53.4%; Score 47; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LSISSCLOQL 18
| | | | | | | | | | | | | | | | | |
Db 1 LSISSCLOQL 10

RESULT 9
US-10-117-937-192
; Sequence 192, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 192
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-192

Query Match 51.1%; Score 45; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQL 9
| | | | | | | | | | | | | | | | | |
Db 1 AADHRQLQL 9

RESULT 10
US-10-117-937-195
; Sequence 195, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210

; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 195
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-195

Query Match 51.1%; Score 45; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQL 9
| | | | | | | |
Db 2 AADHRQLQL 10

RESULT 11
US-09-344-040C-115
; Sequence 115, Application US/09344040C
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determining Presence of an SSX Gene, Peptides Derived From Said SSX Gene and Uses Thereof
; TITLE OF INVENTION: Expression of an SSX Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 115
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-115

Query Match 48.9%; Score 43; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 SSSCLQQL 18
| | | | | | | |
Db 1 SSSCLQQL 9

RESULT 12
US-10-117-937-193
; Sequence 193, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210

; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 193
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-193

Query Match 48.9%; Score 43; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 SSSCLQQL 18
| | | | | | | |
Db 1 SSSCLQQL 9

RESULT 13
US-10-155-881-10846
; Sequence 10846, Application US/10155881
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lutfiyya, Linda L.
; APPLICANT: McIninch, James
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH TRANSCRIPTION IN PLANTS
; TITLE OF INVENTION: TRANSCRIPTION IN PLANTS
; FILE REFERENCE: 38-21(15300)J
; CURRENT APPLICATION NUMBER: US/10/155,881
; CURRENT FILING DATE: 2002-05-22
; NUMBER OF SEQ ID NOS: 37595
; SEQ ID NO 10846
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Zea mays
US-10-155-881-10846

Query Match 46.6%; Score 41; DB 6; Length 317;
Best Local Similarity 72.7%; Pred. No. 26;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 LQLSISSCLOQ 17
| | | | | | | |
Db 13 LSLSLSSCLRQ 23

RESULT 14
US-10-144-860-201
; Sequence 201, Application US/10144860
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PM021C1N
; CURRENT APPLICATION NUMBER: US/10/144,860
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 09/758,456
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 201
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-860-201

Query Match 44.3%; Score 39; DB 6; Length 134;
Best Local Similarity 43.8%; Pred. No. 23;
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 3 DHRQLQLSISSCLQQL 18
::| |::| |::| |
Db 105 ENRTLRLAQSQCVEQL 120

RESULT 15
US-09-937-060A-12
; Sequence 12, Application US/09937060A
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: BANDMAN, Olga
; APPLICANT: TANG, Y. Tom
; APPLICANT: YUE, Henry
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: AU-YOUNG, Janice
; TITLE OF INVENTION: REGULATORS OF INTRACELLULAR PHOSPHORYLATION
; FILE REFERENCE: PF-0683 PCT
; CURRENT APPLICATION NUMBER: US/09/937,060A
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 60/125,593; 60/135,049; 60/143,188
; PRIOR FILING DATE: 1999-03-18; 1999-05-20; 1999-07-09
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PERL Program
; SEQ ID NO 12
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 1877133CD1
US-09-937-060A-12

Query Match 44.3%; Score 39; DB 5; Length 142;
Best Local Similarity 43.8%; Pred. No. 25;
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 3 DHRQLQLSISSCLQQL 18
::| |::| |::| |
Db 113 ENRTLRLAQSQCVEQL 128

Search completed: July 3, 2002, 11:22:11
Job time: 943 sec

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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:05:18 ; Search time 49.27 Seconds
(without alignments)
8.923 Million cell updates/sec

Title: US-09-165-546A-8
Perfect score: 88
Sequence: 1 AADHRQLQLSISSCLQL 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	100.0	18	4 US-09-359-503-8	Sequence 8, Appli
2	88	100.0	180	2 US-08-791-495-7	Sequence 7, Appli
3	88	100.0	180	2 US-08-791-495-9	Sequence 9, Appli
4	88	100.0	180	4 US-08-937-263B-8	Sequence 8, Appli
5	40.5	46.0	914	4 US-09-085-199B-4	Sequence 4, Appli
6	40.5	46.0	1090	4 US-09-085-199B-5	Sequence 5, Appli
7	39.5	44.9	756	4 US-09-085-199B-9	Sequence 9, Appli
8	38.5	43.8	2842	1 US-07-741-940-7	Sequence 7, Appli
9	38.5	43.8	2842	1 US-08-289-548A-7	Sequence 7, Appli
10	38.5	43.8	2842	1 US-08-452-654-7	Sequence 7, Appli
11	38.5	43.8	2843	1 US-07-741-940-2	Sequence 2, Appli
12	38.5	43.8	2843	1 US-08-289-548A-2	Sequence 2, Appli
13	38.5	43.8	2843	1 US-08-452-654-2	Sequence 2, Appli
14	38.5	43.8	2843	1 US-08-452-655B-2	Sequence 2, Appli
15	38.5	43.8	2843	1 US-08-452-655B-7	Sequence 7, Appli
16	38.5	43.8	2843	2 US-08-370-235A-2	Sequence 2, Appli
17	38.5	43.8	2843	3 US-08-450-582-2	Sequence 2, Appli
18	38.5	43.8	2843	3 US-08-450-582-7	Sequence 7, Appli
19	38.5	43.8	2973	2 US-08-821-355A-7	Sequence 7, Appli
20	38.5	43.8	2973	2 US-09-003-687A-7	Sequence 7, Appli
21	38.5	43.8	2973	4 US-09-136-605-7	Sequence 7, Appli
22	37	42.0	2930	4 US-09-417-822-2	Sequence 2, Appli
23	36.5	41.5	171	2 US-08-853-659A-54	Sequence 54, Appl
24	36.5	41.5	501	2 US-08-660-963-13	Sequence 13, Appl
25	36	40.9	441	2 US-08-491-835-4	Sequence 4, Appli
26	36	40.9	441	3 US-08-946-092A-4	Sequence 4, Appli
27	36	40.9	441	4 US-09-172-062-4	Sequence 4, Appli

28	36	40.9	441	5	PCT-US94-00685-4	Sequence 4, Appli
29	36	40.9	454	2	US-08-491-835-26	Sequence 26, Appl
30	36	40.9	454	3	US-08-946-092A-26	Sequence 26, Appl
31	36	40.9	454	4	US-09-172-062-26	Sequence 26, Appl
32	36	40.9	454	5	PCT-US94-00685-26	Sequence 26, Appl
33	36	40.9	620	3	US-09-126-646-2	Sequence 2, Appli
34	36	40.9	732	1	US-08-317-522A-5	Sequence 5, Appli
35	36	40.9	778	1	US-08-439-818A-5	Sequence 5, Appli
36	36	40.9	778	2	US-08-751-965-5	Sequence 5, Appli
37	36	40.9	778	2	US-08-738-975-5	Sequence 5, Appli
38	36	40.9	778	2	US-08-728-626-5	Sequence 5, Appli
39	36	40.9	778	3	US-08-808-599A-5	Sequence 5, Appli
40	36	40.9	824	1	US-08-221-750A-3	Sequence 3, Appli
41	35	39.8	21	1	US-07-861-962-1	Sequence 1, Appli
42	35	39.8	23	1	US-08-447-411-69	Sequence 69, Appl
43	35	39.8	23	2	US-08-662-227-27	Sequence 27, Appl
44	35	39.8	23	4	US-09-017-947-27	Sequence 27, Appl
45	35	39.8	849	1	US-08-405-392-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-09-359-503-8
; Sequence 8, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS: 18 amino acids
; LENGTH: 18 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
US-09-359-503-8

Query Match 100.0%; Score 88; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.1e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQQL 18
|||||
Db 1 AADHRQLQLSISSCLQQL 18

RESULT 2

US-08-791-495-7
; Sequence 7, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-7

Query Match 100.0%; Score 88; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQQL 18
|||||
Db 139 AADHRQLQLSISSCLQQL 156

RESULT 3

US-08-791-495-9
; Sequence 9, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie

; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-9

Query Match 100.0%; Score 88; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQQL 18
|||||
Db 139 AADHRQLQLSISSCLQQL 156

RESULT 4

US-08-937-263B-8
; Sequence 8, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
; APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
; APPLICANT: Alexander, Knuth; Drifhout, Jan W.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
; TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,263B
; FILING DATE: September 15, 1997


```
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sinn, Eric, Patent Agent
; REGISTRATION NUMBER: 40,177
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
US-08-937-263B-8

Query Match 100.0%; Score 88; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQQL 18
| | | | | | | | | | | | | | | | | | | | | |
Db 139 AADHRQLQLSISSCLQQL 156

RESULT 5
US-09-085-199B-4
; Sequence 4, Application US/09085199B
; Patent No. 6235879
; GENERAL INFORMATION:
; APPLICANT: Hayden. Michael R.
; APPLICANT: Hackam, Abigail
; APPLICANT: Huq, A.H.M. Mahbubul
; APPLICANT: Chopra, Vikramjit Singh
; APPLICANT: Kalchman, Michael
; TITLE OF INVENTION: Apoptosis Modulators That Interact with the
; TITLE OF INVENTION: Huntington's Disease Gene
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: PO Box 5270
; CITY: Frisco
; STATE: CO
; COUNTRY: USA
; ZIP: 80443-5270
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Kb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS DOS 5.0
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/085,199B
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Larson, Marina T.
; REGISTRATION NUMBER: 32038
; REFERENCE/DOCKET NUMBER: UBC.P-013US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (970) 668-2050
; TELEFAX: (970) 668-2052
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 914
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: no
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE: Huntington-interacting protein

US-09-085-199B-9
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US-09-085-199B-4

Query Match 46.0%; Score 40.5; DB 4; Length 914;
Best Local Similarity 52.6%; Pred. No. 38;
Matches 10; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 1 AADH-RQLQLSISSCLQQL 18
: | | | | | | | | | | | | | | | | | | | | | |
Db 530 SADHLLSTVTSISSCIEQL 548

RESULT 6
US-09-085-199B-5
; Sequence 5, Application US/09085199B
; Patent No. 6235879
; GENERAL INFORMATION:
; APPLICANT: Hayden. Michael R.
; APPLICANT: Hackam, Abigail
; APPLICANT: Huq, A.H.M. Mahbubul
; APPLICANT: Chopra, Vikramjit Singh
; APPLICANT: Kalchman, Michael
; TITLE OF INVENTION: Apoptosis Modulators That Interact with the
; TITLE OF INVENTION: Huntington's Disease Gene
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: PO Box 5270
; CITY: Frisco
; STATE: CO
; COUNTRY: USA
; ZIP: 80443-5270
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Kb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS DOS 5.0
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/085,199B
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Larson, Marina T.
; REGISTRATION NUMBER: 32038
; REFERENCE/DOCKET NUMBER: UBC.P-013US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (970) 668-2050
; TELEFAX: (970) 668-2052
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1090
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: no
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; OTHER INFORMATION: Huntington-interacting protein

US-09-085-199B-5
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Query Match 46.0%; Score 40.5; DB 4; Length 1090;
Best Local Similarity 52.6%; Pred. No. 47;
Matches 10; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 1 AADH-RQLQLSISSCLQQL 18
: | | | | | | | | | | | | | | | | | | | | | |
Db 706 SADHLLSTVTSISSCIEQL 724

RESULT 7
US-09-085-199B-9
```

; Sequence 9, Application US/09085199B
; Patent No. 6235879
; GENERAL INFORMATION:
; APPLICANT: Hayden, Michael R.
; APPLICANT: Hackam, Abigail
; APPLICANT: Huq, A.H.M. Mahbubul
; APPLICANT: Chopra, Vikramjit Singh
; APPLICANT: Kalchman, Michael
; TITLE OF INVENTION: Apoptosis Modulators That Interact with the
; TITLE OF INVENTION: Huntington's Disease Gene
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: PO Box 5270
; CITY: Frisco
; STATE: CO
; COUNTRY: USA
; ZIP: 80443-5270
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Kb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS DOS 5.0
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/085,199B
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Larson, Marina T.
; REGISTRATION NUMBER: 32038
; REFERENCE/DOCKET NUMBER: UBC.P-013US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (970) 668-2050
; TELEFAX: (970) 668-2052
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: no
; ORIGINAL SOURCE:
; ORGANISM: mouse
; FEATURE:
; OTHER INFORMATION: Huntington-interacting protein
; US-09-085-199B-9

Query Match 44.9%; Score 39.5; DB 4; Length 756;
Best Local Similarity 47.4%; Pred. No. 46;
Matches 9; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

QY 1 AADHRQLQL-SISSCLQQL 18
: || :|:|||||
Db 372 STDHLLSKVSSVSSCLEQL 390

RESULT 8
US-07-741-940-7
; Sequence 7, Application US/07741940
; Patent No. 5352775
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, HANS
; APPLICANT: ANAND, RAKESH
; APPLICANT: CARLSON, MARY
; APPLICANT: GRODEN, JOANNA
; APPLICANT: HEDGE, PHILIP J.
; APPLICANT: JOSLYN, GEOFF
; APPLICANT: KINZLER, KENNETH
; APPLICANT: MAKHAM, ALEXANDER F.
; APPLICANT: NAKAMURA, YUSUKE
; APPLICANT: THLIVERIS, ANDREW
; TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC

; TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4598
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/741,940
; FILING DATE: 19920109
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 1107.035574
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2842 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: APC
; US-07-741-940-7

Query Match 43.8%; Score 38.5; DB 1; Length 2842;
Best Local Similarity 56.2%; Pred. No. 3.4e+02;
Matches 9; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 3 DHRQLQLSISSCLQQL 18
||||:|:|||||
Db 650 DHRQI-LRENNCLQTL 664

RESULT 9
US-08-289-548A-7
; Sequence 7, Application US/08289548A
; Patent No. 5648212
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, HANS
; APPLICANT: ANAND, RAKESH
; APPLICANT: CARLSON, MARY
; APPLICANT: GRODEN, JOANNA
; APPLICANT: HEDGE, PHILIP J.
; APPLICANT: JOSLYN, GEOFF
; APPLICANT: KINZLER, KENNETH
; APPLICANT: MARKHAM, ALEXANDER F.
; APPLICANT: NAKAMURA, YUSUKE
; APPLICANT: THLIVERIS, ANDREW
; TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, LTD
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4598

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/289,548A
; FILING DATE: 12-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 1107.46943
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2842 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: APC
; US-08-289-548A-7

Query Match 43.8%; Score 38.5; DB 1; Length 2842;
Best Local Similarity 56.2%; Pred. No. 3.4e+02;
Matches 9; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 3 DHRQLQLSISSCLOQL 18
||||:|:|||||
Db 650 DHRQI-LRENNCLQTL 664

RESULT 10
US-08-452-654-7
; Sequence 7, Application US/08452654
; Patent No. 5691454
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, HANS
; APPLICANT: ANAND, RAKESH
; APPLICANT: CARLSON, MARY
; APPLICANT: GRODEN, JOANNA
; APPLICANT: HEDGE, PHILIP J.
; APPLICANT: JOSLYN, GEOFF
; APPLICANT: KINZLER, KENNETH
; APPLICANT: MARKHAM, ALEXANDER F.
; APPLICANT: NAKAMURA, YUSUKE
; APPLICANT: THLIVERIS, ANDREW
; TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4598
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,654
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 536

;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/741,940
; FILING DATE: 08-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 1107.035574
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2842 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: APC
; US-08-452-654-7

Query Match 43.8%; Score 38.5; DB 1; Length 2842;
Best Local Similarity 56.2%; Pred. No. 3.4e+02;
Matches 9; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 3 DHRQLQLSISSCLOQL 18
||||:|:|||||
Db 650 DHRQI-LRENNCLQTL 664

RESULT 11
US-07-741-940-2
; Sequence 2, Application US/07741940
; Patent No. 5352775
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, HANS
; APPLICANT: ANAND, RAKESH
; APPLICANT: CARLSON, MARY
; APPLICANT: GRODEN, JOANNA
; APPLICANT: HEDGE, PHILIP J.
; APPLICANT: JOSLYN, GEOFF
; APPLICANT: KINZLER, KENNETH
; APPLICANT: MARKHAM, ALEXANDER F.
; APPLICANT: NAKAMURA, YUSUKE
; APPLICANT: THLIVERIS, ANDREW
; TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4598
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/741,940
; FILING DATE: 19920109
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 1107.035574
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100

- ; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2843 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-741-940-2

Query Match 43.8%; Score 38.5; DB 1; Length 2843;
Best Local Similarity 56.2%; Pred. No. 3.4e+02;
Matches 9; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 3 DHRQLQLSISSCLQQL 18
| | | | : | | | |
Db 651 DHRQI-LRENNCLQTL 665

RESULT 12

US-08-289-548A-2
; Sequence 2, Application US/08289548A
; Patent No. 5648212

; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, HANS
; APPLICANT: ANAND, RAKESH
; APPLICANT: CARLSON, MARY
; APPLICANT: GRODEN, JOANNA
; APPLICANT: HEDGE, PHILIP J.
; APPLICANT: JOSLYN, GEOFF
; APPLICANT: KINZLER, KENNETH
; APPLICANT: MARKHAM, ALEXANDER F.
; APPLICANT: NAKAMURA, YUSUKE
; APPLICANT: THLIVERIS, ANDREW
; TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
; TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Banner & Allegretti, LTD
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4598

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/289,548A
; FILING DATE: 12-AUG-1994
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 1107.46943

; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2843 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-289-548A-2

Query Match 43.8%; Score 38.5; DB 1; Length 2843;
Best Local Similarity 56.2%; Pred. No. 3.4e+02;
Matches 9; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 3 DHRQLQLSISSCLQQL 18
| | | | : | | | |
Db 651 DHRQI-LRENNCLQTL 665

RESULT 13

US-08-452-654-2
; Sequence 2, Application US/08452654
; Patent No. 5691454

; GENERAL INFORMATION:

; APPLICANT: ALBERTSEN, HANS

; APPLICANT: ANAND, RAKESH

; APPLICANT: CARLSON, MARY

; APPLICANT: GRODEN, JOANNA

; APPLICANT: HEDGE, PHILIP J.

; APPLICANT: JOSLYN, GEOFF

; APPLICANT: KINZLER, KENNETH

; APPLICANT: MARKHAM, ALEXANDER F.

; APPLICANT: NAKAMURA, YUSUKE

; APPLICANT: THLIVERIS, ANDREW

; TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC

; TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS

; NUMBER OF SEQUENCES: 94

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Banner, Birch, McKie & Beckett

; STREET: 1001 G Street, NW

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20001-4598

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/452,654

; FILING DATE: 25-MAY-1995

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/741,940

; FILING DATE: 08-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Kagan, Sarah A.

; REGISTRATION NUMBER: 32,141

; REFERENCE/DOCKET NUMBER: 1107.035574

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-508-9100

; TELEFAX: 202-508-9299

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2843 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-452-654-2

Query Match 43.8%; Score 38.5; DB 1; Length 2843;
Best Local Similarity 56.2%; Pred. No. 3.4e+02;
Matches 9; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 3 DHRQLQLSISSCLQQL 18
| | | | : | | | |
Db 651 DHRQI-LRENNCLQTL 665

RESULT 14

US-08-452-655B-2

; Sequence 2, Application US/08452655B

; Patent No. 5783666

; GENERAL INFORMATION:

; APPLICANT: ALBERTSEN, HANS

APPLICANT: ANAND, RAKESH
APPLICANT: CARLSON, MARY
APPLICANT: GRODEN, JOANNA
APPLICANT: HEDGE, PHILIP J.
APPLICANT: JOSLYN, GEOFF
APPLICANT: KINZLER, KENNETH
APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: THLIVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1001 G Street, NW
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20001-4598
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,655B
FILING DATE: 25-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,548
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/741,940
FILING DATE: 08-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107.49964
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2843 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-452-655B-2

Query Match 43.8%; Score 38.5; DB 1; Length 2843;
Best Local Similarity 56.2%; Pred. No. 3.4e+02;
Matches 9; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Qy 3 DHRQLQLSISSCLQQL 18
| | | | : | : | | |
Db 651 DHRQI-LRENNCLQTL 665

RESULT 15
US-08-452-655B-7
; Sequence 7, Application US/08452655B
; Patent No. 5783666
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, HANS
; APPLICANT: ANAND, RAKESH
; APPLICANT: CARLSON, MARY
; APPLICANT: GRODEN, JOANNA
; APPLICANT: HEDGE, PHILIP J.
; APPLICANT: JOSLYN, GEOFF
; APPLICANT: KINZLER, KENNETH
; APPLICANT: MARKHAM, ALEXANDER F.
; APPLICANT: NAKAMURA, YUSUKE

APPLICANT: THLIVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1001 G Street, NW
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20001-4598
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,655B
FILING DATE: 25-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,548
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/741,940
FILING DATE: 08-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107.49964
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2843 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
US-08-452-655B-7

Query Match 43.8%; Score 38.5; DB 1; Length 2843;
Best Local Similarity 56.2%; Pred. No. 3.4e+02;
Matches 9; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Qy 3 DHRQLQLSISSCLQQL 18
| | | | : | : | | |
Db 651 DHRQI-LRENNCLQTL 665

Search completed: July 3, 2002, 11:09:45
Job time: 267 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:10:53 ; Search time 61.47 Seconds
(without alignments)
28.137 Million cell updates/sec

Title: US-09-165-546A-9
Perfect score: 84
Sequence: 1 VLLKEFTVSGNLTIRLT 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	45	53.6	1524	2	S68553	surface layer prot
2	44	52.4	614	2	A69845	Na+/H+ antiporter
3	43	51.2	289	2	C87158	probable oxidoredu
4	43	51.2	788	2	A72330	phenylalanine--trn
5	41	48.8	338	2	AE3079	hypothetical prote
6	41	48.8	382	2	D98207	oligopeptide ABC t
7	41	48.8	585	2	F90460	AAA family ATPase
8	40	47.6	104	2	I48151	adrenergic alpha2
9	40	47.6	134	2	AH1877	hypothetical prote
10	40	47.6	162	2	B90402	hypothetical prote
11	40	47.6	298	2	F69502	hypothetical prote
12	40	47.6	450	2	A38316	alpha-2-adrenergic
13	40	47.6	450	2	B40392	alpha-2-adrenergic
14	40	47.6	450	2	JH0190	alpha-2-adrenergic
15	40	47.6	450	2	I49481	alpha-2 adrenergic
16	40	47.6	623	2	I64034	hypothetical prote
17	40	47.6	1019	2	F70342	cation efflux syst
18	40	47.6	1048	2	H64459	hypothetical prote
19	40	47.6	1208	2	C82779	hemolysin-type cal
20	40	47.6	1212	2	T00332	hypothetical prote
21	40	47.6	1401	2	T02255	probable ubiquitou
22	39	46.4	234	2	H75390	hypothetical prote
23	39	46.4	265	2	F70315	pyrroline carboxyl
24	39	46.4	314	2	G86835	hypothetical prote
25	39	46.4	323	2	A82747	polar amino acid t
26	39	46.4	445	2	B40590	flagellar distal c
27	39	46.4	513	2	AI2555	hypothetical prote
28	39	46.4	563	2	S78224	virulence-associat
29	39	46.4	591	1	S09498	virulence-associat

30	39	46.4	591	1	S22664	virulence-associat
31	39	46.4	593	2	S15215	virulence-associat
32	39	46.4	646	2	T26427	hypothetical prote
33	39	46.4	653	2	T32328	hypothetical prote
34	39	46.4	659	2	T20753	hypothetical prote
35	39	46.4	788	2	AG0786	secreted effector
36	39	46.4	802	2	G96640	hypothetical prote
37	39	46.4	809	2	T16448	hypothetical prote
38	39	46.4	999	2	S72267	Ca2+-transporting
39	39	46.4	3066	1	JQ1662	genome polypeptid
40	38.5	45.8	977	2	E86349	hypothetical prote
41	38	45.2	94	2	G72682	hypothetical prote
42	38	45.2	120	2	D89910	large-conductance
43	38	45.2	121	2	B81972	probable integral
44	38	45.2	135	2	D81029	conserved hypothet
45	38	45.2	142	2	T28386	hypothetical prote

ALIGNMENTS

RESULT 1
S68553
surface layer protein tetrabrachion precursor - Staphylothermus marinus
C:Species: Staphylothermus marinus
C:Date: 27-Nov-1997 #sequence_revision 12-Dec-1997 #text_change 17-Mar-1999
C:Accession: S68553; S78081
R:Peters, J.; Baumeister, W.; Lupas, A.
J. Mol. Biol. 257, 1031-1041, 1996
A:Title: Hyperthermostable surface layer protein tetrabrachion from the archaeobacteri
ture.
A:Reference number: S68553; MUID:96192087
A:Accession: S68553
A:Molecule type: DNA
A:Residues: 1-1524 <PET1>
A:Cross-references: EMBL:U57967
A:Experimental source: strain F1
A:Accession: S78081
A:Molecule type: protein
A:Residues: 40-45;91-95;151-158;327-331;445-449;490-497;499-505;596-614;617-624;638-6
5-1451 <PET2>
A:Experimental source: strain F1
C:Complex: heterotetramer; two alpha chains and two beta chains
C:Keywords: blocked amino end; glycoprotein; membrane bound
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-700/Product: surface layer protein tetrabrachion alpha chain #status predicted <
F:701-1524/Product: surface layer protein tetrabrachion beta chain #status experiment
F:1019-1029/Region: hinge
F:1495-1519/Domain: membrane anchor #status predicted <MBN>
F:44,605,641,685,708,1279,1402/Binding site: carbohydrate (Asn) (covalent) #status ex

Query Match 53.6%; Score 45; DB 2; Length 1524;
Best Local Similarity 60.0%; Pred. NO. 36;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 KEFTVSGNLTIRLT 18
|||:|:|:|
Db 661 KEFNLSFNLTLSLT 675

RESULT 2
A69845
Na+/H+ antiporter homolog yjbQ - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C:Accession: A69845
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M

Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
 A.;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
 Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
 A.;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
 A.;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
 A;Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
 A;Reference number: A69580; MUID:98044033
 A;Accession: A69845
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-614 <KUN>
 A;Cross-references: GB:Z99110; GB:AL009126; NID:g2633472; PIDN:CAB13021.1; PID:e1183184;
 A;Experimental source: strain 168
 C;Genetics:
 A;Gene: yjbQ

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Query Match      52.4%; Score 44; DB 2; Length 614;
Best Local Similarity 35.3%; Pred. No. 20;
Matches 6; Conservative 9; Mismatches 2; Indels 0; Gaps 0;
```

RESULT 3
C87158
probable oxidoreductase ML1992 [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: C87158
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: C87158
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-289 <STO>
A;Cross-references: GB:AL450380; NID:gl3093634; PIDN:CAC30947.1; GSPDB:GN00147
C;Genetics:
A;Gene: ML1992

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Query Match          51.2%;   Score 43;   DB 2;   Length 289;
Best Local Similarity 60.0%;   Pred. No. 13;
Matches          9;   Conservative      2;   Mismatches      4;   Indels      0;   Gaps      0;

QY      4  KEFTVSGNLTIRLT 18
      |  |||| :| |||
Db      263 KHGTVSGTLITYRLT 277

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RESULT 4
A72330
phenylalanine--trna ligase (EC 6.1.1.20) beta chain - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: A72330
C:Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316
A:Accession: A72330

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-788 <ARN>
A;Cross-references: GB:AE001749; GB:AE000512; NID:g4981346; PIDN:AAD35904.1; PID:g498
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM0822
C;Superfamily: phenylalanine--trRNA ligase beta chain
C;Keywords: aminoacyl-trRNA synthetase; ligase; protein biosynthesis

Query Match 51.2%; Score 43; DB 2; Length 788;
Best Local Similarity 50.0%; Pred. No. 38;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

RESULT 5
AE3079
hypothetical protein Atu4257 [imported] - Agrobacterium tumefaciens (strain C58, Dupo
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C;Accession: AE3079
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyaev, T.; Levy, R.; Li, M.; McCl
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
A;Accession: AE3079
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-338 <KUR>
A;Cross-references: GB:AE008689; PIDN:AAL45051.1; PID:gl7742715; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu4257
A;Map position: linear chromosome

Query Match 48.8%; Score 41; DB 2; Length 338;
Best Local Similarity 50.0%; Pred. NO. 34;
Matches 9: Conservative 2; Mismatches 7; Indels 0; Gaps 0;

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RESULT      6
D98207
oligopeptide ABC transporter, permease protein (oppC-1) homolog [imported] - Agrobact
C/Species: Agrobacterium tumefaciens
C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C/Accession: D98207
R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm
  A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz,
  Science 294, 2323-2328, 2001
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
A/Reference number: A97359; PMID:11743194
A/Accession: D98207
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-382 <KUR>
A/Cross-references: GB:AE007870; PIDN:AAK89182.1; PID:gl5158998; GSPDB:GN00170
C/Genetics:
A/Gene: AGR_L_1208
A/Map position: linear chromosome

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A;Accession: F69502
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-298 <KLE>
A;Cross-references: GB:AE000963; GB:AE000782; NID:g2689286; PIDN:AAB89240.1; PID:g264852

Query Match 47.6%; Score 40; DB 2; Length 298;
Best Local Similarity 46.7%; Pred. No. 44;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 LLKEFTVSGNLTIR 16
||: ||: ||: : |
Db 250 LLQFTISGDVGEVR 264

RESULT 12
A38316
alpha-2-adrenergic receptor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
C;Accession: A38316
R;Guyer, C.A.; Horstman, D.A.; Wilson, A.L.; Clark, J.D.; Cragoe Jr., E.J.; Limbird, L.E
J. Biol. Chem. 265, 17307-17317, 1990
A;Title: Cloning, sequencing, and expression of the gene encoding the porcine alpha-2-ad
A;Reference number: A38316; MUID:91009167
A;Accession: A38316
A;Molecule type: DNA
A;Residues: 1-450 <GUY>
A;Cross-references: GB:J05652; NID:g164303; PIDN:AAA30984.1; PID:g164304
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match 47.6%; Score 40; DB 2; Length 450;
Best Local Similarity 64.3%; Pred. No. 68;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 LLKEFTVSGNLTIR 15
|| ||| ||: |
Db 42 LLMFTVFGNVLVI 55

RESULT 13
B40392
alpha-2-adrenergic receptor (clone RG10) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Dec-1991 #sequence_revision 03-Apr-1992 #text_change 13-Aug-1999
C;Accession: B40392
R;Lanier, S.M.; Downing, S.; Duzic, E.; Homcy, C.J.
J. Biol. Chem. 266, 10470-10478, 1991
A;Title: Isolation of rat genomic clones encoding subtypes of the alpha-2-adrenergic re
A;Reference number: A40392; MUID:91244823
A;Accession: B40392
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-450 <LAN>
A;Cross-references: GB:M62372; NID:g206615; PIDN:AAA42034.1; PID:g206616
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 47.6%; Score 40; DB 2; Length 450;
Best Local Similarity 64.3%; Pred. No. 68;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 LLKEFTVSGNLTIR 15
|| ||| ||: |
Db 42 LLMFTVFGNVLVI 55

RESULT 14
JH019

alpha-2-adrenergic receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Feb-1997
C;Accession: JH0190
R;Chalberg, S.C.; Duda, T.; Rhine, J.A.; Sharma, R.K.
Mol. Cell. Biochem. 97, 161-172, 1990
A;Title: Molecular cloning, sequencing and expression of an alpha2-adrenergic recepto
A;Reference number: JH0190; MUID:91125329
A;Accession: JH0190
A;Molecule type: mRNA
A;Residues: 1-450 <CHA>
A;Experimental source: brain
C;Comment: Alpha-2-adrenergic receptor is a predominant catecholamine receptor. It me
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
F;34-59/Domain: hydrophobic <HDI>
F;71-96/Domain: hydrophobic <HII>
F;106-131/Domain: hydrophobic <III>
F;150-175/Domain: hydrophobic <HIV>
F;193-218/Domain: hydrophobic <HDV>
F;375-400/Domain: hydrophobic <HVI>
F;405-430/Domain: hydrophobic <VII>

Query Match 47.6%; Score 40; DB 2; Length 450;
Best Local Similarity 64.3%; Pred. No. 68;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 LLKEFTVSGNLTIR 15
|| ||| ||: |
Db 42 LLMFTVFGNVLVI 55

RESULT 15
I49481
alpha-2 adrenergic receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C;Accession: I49481
R;Link, R.; Daunt, D.; Barsh, G.S.; Chruscinski, A.; Kobilka, B.
Mol. Pharmacol. 42, 16-27, 1992
A;Title: Cloning of two mouse genes encoding alpha-2 adrenergic receptor subtypes and
in antagonist binding.
A;Reference number: I49480; MUID:92342131
A;Accession: I49481
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-450 <RES>
A;Cross-references: GB:M99377; NID:g191882; PIDN:AAA37213.1; PID:g191883
C;Superfamily: vertebrate rhodopsin
C;Keywords: neurotransmitter receptor

Query Match 47.6%; Score 40; DB 2; Length 450;
Best Local Similarity 64.3%; Pred. No. 68;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 LLKEFTVSGNLTIR 15
|| ||| ||: |
Db 42 LLMFTVFGNVLVI 55

Search completed: July 3, 2002, 11:10:54
Job time: 316 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:24:42 ; Search time 29.65 Seconds
(without alignments)
23.506 Million cell updates/sec

Title: US-09-165-546A-9
Perfect score: 84
Sequence: 1 VLLKEFTVSGNLTIRLT 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100.0	180	1 CTAG_HUMAN	P78358 homo sapien
2	49	58.3	210	1 LAG1_HUMAN	O75638 homo sapien
3	43	51.2	788	1 SYFB_THEMEA	Q9wzs9 thermotoga
4	40	47.6	298	1 YK23_ARCFU	O28256 archaeoglob
5	40	47.6	450	1 A2AA_MOUSE	Q01338 mus musculu
6	40	47.6	450	1 A2AA_PIG	P18871 sus scrofa
7	40	47.6	450	1 A2AA_RAT	P22909 rattus norv
8	40	47.6	452	1 A2AA_BOVIN	Q28838 bos taurus
9	40	47.6	623	1 VPS_HAEIN	P44242 haemophilus
10	40	47.6	1401	1 UTX_HUMAN	O15550 homo sapien
11	39	46.4	265	1 PROC_AQUAE	O66553 aquifex aeo
12	39	46.4	445	1 FLDL_VIBPA	Q03475 vibrio para
13	39	46.4	591	1 VRP2_SALCH	P17450 salmonella
14	39	46.4	591	1 VRP2_SALEN	P55220 salmonella
15	39	46.4	593	1 VRP2_SALDU	P24419 salmonella
16	39	46.4	1043	1 ATA3_HUMAN	Q93084 homo sapien
17	38	45.2	120	1 MSCL_STAAM	O68285 staphylococ
18	38	45.2	199	1 HIS5_HAEIN	P44340 haemophilus
19	38	45.2	221	1 Y700_RICPR	Q9zcm4 rickettsia
20	38	45.2	322	1 LIPA_RHIET	O05941 rhizobium e
21	38	45.2	364	1 MRP_AQUAE	O66946 aquifex aeo
22	38	45.2	425	1 RAFB_ECOLI	P16552 escherichia
23	38	45.2	462	1 VSII_REOVJ	P04507 reovirus (t
24	38	45.2	533	1 THAS_MOUSE	P36423 mus musculu
25	38	45.2	533	1 THAS_RAT	P49430 rattus norv
26	38	45.2	768	1 YDBD_ECOLI	P25907 escherichia
27	38	45.2	942	1 PKL1_HUMAN	Q16512 homo sapien
28	38	45.2	1502	1 N170_YEAST	P38181 saccharomyc
29	37	44.0	127	1 RL21_SYNP7	Q9z3h5 synechococc
30	37	44.0	130	1 YQJF_ECOLI	P42619 escherichia
31	37	44.0	367	1 Y205_MYCTU	O53656 mycobacteri
32	37	44.0	408	1 ODPK_KLULA	Q13366 kluyveromyc
33	37	44.0	464	1 FLID_AERPU	Q9r9r6 aeromonas p

34	37	44.0	488	1 SYK_MYCHO	P46191 mycoplasma
35	37	44.0	490	1 CPCK_MACFA	P33262 macaca fasc
36	37	44.0	541	1 TRPE_VIBPA	P22099 vibrio para
37	37	44.0	542	1 ESTS_DROVI	Q05487 drosophila
38	37	44.0	543	1 TLMD_MYCPN	P75436 mycoplasma
39	37	44.0	917	1 IL6B_MOUSE	Q00560 mus musculu
40	37	44.0	946	1 PKL1_RAT	Q63433 rattus norv
41	37	44.0	956	1 GLK4_HUMAN	Q16099 homo sapien
42	37	44.0	956	1 GLK4_RAT	Q01812 rattus norv
43	37	44.0	2481	1 FINC_XENLA	Q91740 xenopus lae
44	37	44.0	3066	1 POLG_SBMVG	Q90069 s genome po
45	37	44.0	4725	1 DYHC_DICDI	P34036 dictyostell

ALIGNMENTS

RESULT 1	CTAG_HUMAN	STANDARD;	PRT;	180 AA.
ID	CTAG_HUMAN			
AC	P78358;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Autoimmunogenic cancer/testis antigen NY-ESO-1.			
GN	CTAG.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97203161; PubMed=9050879;			
RA	Chen Y.-T., Scanlan M.J., Sahin U., Tuereci O., Gure A.O., Tsang S.,			
RA	Williamson B., Stockert E., Pfreundschuh M., Old L.J.;			
RT	"A testicular antigen aberrantly expressed in human cancers detected			
RT	by autologous antibody screening."			
RL	Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Melanoma;			
RX	MEDLINE=98289662; PubMed=9626360;			
RA	Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,			
RA	de Plaen E., Boon T.;			
RT	"LAGE-1 a new gene with tumor specificity."			
RL	Int. J. Cancer 76:903-908(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98430682; PubMed=9759882;			
RA	Wang R.-F., Johnston S.L., Zeng G., Topalian S.L.,			
RA	Schwartzentruber D.J., Rosenberg S.A.;			
RT	"A breast and melanoma-shared tumor antigen: T cell responses to			
RT	antigenic peptides translated from different open reading frames.";			
RL	J. Immunol. 161:3596-3606(1998).			
CC	-!- TISSUE SPECIFICITY: EXPRESSED IN TESTIS AND OVARY AND IN A WIDE			
CC	VARIETY OF CANCERS. DETECTED IN UTERINE MYOMETRIUM.			
CC	-!- SIMILARITY: STRONG, TO LAGE-1.			
CC	-----			
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CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; U87459; AAB49693.1; -.			
DR	EMBL; AJ003149; CAA05908.1; -.			
DR	EMBL; AF038567; AAD05202.1; -.			
DR	MIM; 300156; -.			
KW	Transmembrane; Antigen.			
FT	DOMAIN 5 82			GLY-RICH.
FT	TRANSMEM 156 172			POTENTIAL.

DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein AF2023 precursor.
GN AF2023.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
OC Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).
CC -----
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CC -----
CC EMBL; AE00963; AAB89240.1; -.
DR TIGR; AF2023; -.
DR Hypothetical protein; Signal; Complete proteome.
KW SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 298 HYPOTHETICAL PROTEIN AF2023.
FT SEQUENCE 298 AA; 33532 MW; 2C6B60CFC8175C0C CRC64;
SQ
Query Match 47.6%; Score 40; DB 1; Length 298;
Best Local Similarity 46.7%; Pred. No. 13;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY 2 LLKEFTVSGNLTIR 16
II: ||:|::: |
Db 250 LLQNFTISGDVGEVR 264 .
RESULT 5
A2AA_MOUSE STANDARD; PRT; 450 AA.
ID A2AA_MOUSE
AC Q01338;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-2A adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2AAR).
GN ADRA2A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92342131; PubMed=1353249;
RA Link R.E., Daunt D.A., Barsh G., Chruscinski A.J., Kobilka B.K.;
RT "Cloning of two mouse genes encoding alpha 2-adrenergic receptor
RT subtypes and identification of a single amino acid in the mouse alpha
RT 2-C10 homolog responsible for an interspecies variation in
RT antagonist binding.";
RL Mol. Pharmacol. 42:16-27(1992).

CC -!- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M99377; AAA37213.1; -.
DR HSSP; P29274; 1MMH.
DR GCRDB; GCR_0439; -.
DR MGD; MGI:87934; Adra2a.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHRDOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 59 1 (POTENTIAL).
FT DOMAIN 60 70 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 71 96 2 (POTENTIAL).
FT DOMAIN 97 106 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 107 129 3 (POTENTIAL).
FT DOMAIN 130 149 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 150 173 4 (POTENTIAL).
FT DOMAIN 174 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 217 5 (POTENTIAL).
FT DOMAIN 218 374 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 375 399 6 (POTENTIAL).
FT DOMAIN 400 409 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 410 430 7 (POTENTIAL).
FT DOMAIN 431 450 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 106 188 BY SIMILARITY.
FT LIPID 442 442 PALMITATE (BY SIMILARITY).
FT SITE 113 113 IMPLICATED IN LIGAND BINDING (BY
FT SIMILARITY).
FT SITE 200 200 IMPLICATED IN CATECHOL AGONIST BINDING
FT SITE 204 204 (BY SIMILARITY).
FT SITE 204 204 IMPLICATED IN CATECHOL AGONIST BINDING
FT (BY SIMILARITY).
SQ SEQUENCE 450 AA; 48865 MW; F07E225393AFA93B CRC64;
Query Match 47.6%; Score 40; DB 1; Length 450;
Best Local Similarity 64.3%; Pred. No. 20;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 2 LLKEFTVSGNLTIR 15
II: ||:|::: |
Db 42 LLMLFTVFGNVLVI 55
RESULT 6
A2AA_PIG STANDARD; PRT; 450 AA.
ID A2AA_PIG
AC P18871;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Alpha-2A adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2AAR).
GN ADRA2A OR A2AR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 212-232.
RC TISSUE=Liver;
RX MEDLINE=91009167; PubMed=2170371;
RA Guyer C.A., Horstman D.A., Wilson A.L., Clark J.D., Kragoe E.J. Jr.,
RA Limbird L.E.;
RT "Cloning, sequencing, and expression of the gene encoding the porcine
RT 'alpha 2-adrenergic receptor. Allosteric modulation by Na⁺, H⁺, and
RT amiloride analogs.";
RL J. Biol. Chem. 265:17307-17317(1990).
RN [2]
RP MUTAGENESIS OF CYS-442.
RX MEDLINE=93216775; PubMed=8385131;
RA Kennedy M.E., Limbird L.E.;
RT "Mutations of the alpha 2A-adrenergic receptor that eliminate
RT detectable palmitoylation do not perturb receptor-G-protein
RT coupling.";
RL J. Biol. Chem. 268:8003-8011(1993).
RN [2]
RP FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC -!- INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- MISCELLANEOUS: ALPHA2-ADRENERGIC RECEPTOR SHOWS AN ALLOSTERIC
CC MODULATION BY NA⁺, H⁺, AND AMILORIDE ANALOGS.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; J05652; AAA30984.1; -.
DR PIR; A38316; A38316.
DR HSSP; P29274; 1MMH.
DR GCRDb; GCR_0101; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 59 1 (POTENTIAL).
FT DOMAIN 60 70 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 71 96 2 (POTENTIAL).
FT DOMAIN 97 106 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 107 129 3 (POTENTIAL).
FT DOMAIN 130 149 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 150 173 4 (POTENTIAL).
FT DOMAIN 174 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 217 5 (POTENTIAL).
FT DOMAIN 218 374 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 375 399 6 (POTENTIAL).
FT DOMAIN 400 409 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 410 430 7 (POTENTIAL).
FT DOMAIN 431 450 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 106 188 BY SIMILARITY.
FT LIPID 442 442 PALMITATE.
FT SITE 113 113 IMPLICATED IN LIGAND BINDING (BY
FT SIMILARITY).
FT SITE 200 200 IMPLICATED IN CATECHOL AGONIST BINDING
FT (BY SIMILARITY).
FT SITE 204 204 IMPLICATED IN CATECHOL AGONIST BINDING
FT (BY SIMILARITY).
FT MUTAGEN 442 442 C->A,S: LOSS OF PALMITOYLATION.

SQ SEQUENCE 450 AA; 48975 MW; 79D7D5B47372074E CRC64;

Query Match 47.6%; Score 40; DB 1; Length 450;
Best Local Similarity 64.3%; Pred. No. 20;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 LLKEFTVSGNILTI 15
|| ||| ||:| |
Db 42 LLMLFTVFGNVLVI 55

RESULT 7
A2AA_RAT STANDARD; PRT; 450 AA.
ID A2AA_RAT
AC P22909;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-2A adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2AAR)
DE (CA2-47) (Alpha-2D adrenergic receptor).
GN ADRA2A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91244823; PubMed=1645350;
RA Lanier S.M., Downing S., Duzic E., Homcy C.J.;
RT "Isolation of rat genomic clones encoding subtypes of the alpha 2-
RT adrenergic receptor. Identification of a unique receptor subtype.";
RL J. Biol. Chem. 266:10470-10478(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91125329; PubMed=2177834;
RA Chalberg S.C., Duda T., Rhine J.A., Sharma R.K.;
RT "Molecular cloning, sequencing and expression of an alpha 2-adrenergic
RT receptor complementary DNA from rat brain.";
RL Mol. Cell. Biochem. 97:161-172(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95349560; PubMed=7623790;
RA Wypijewski K., Duda T., Sharma R.K.;
RT "Structural, genetic and pharmacological identity of the rat alpha
RT 2-adrenergic receptor subtype CA2-47 and its molecular
RT characterization in rat adrenal, adrenocortical carcinoma and bovine
RT retina.";
RL Mol. Cell. Biochem. 144:181-190(1995).
CC -!- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
CC EMBL; M62372; AAA42034.1; -.
DR EMBL; U79031; AAC24959.1; -.
DR PIR; B40392; B40392.
DR PIR; JH0190; JH0190.
DR HSSP; P29274; 1MMH.
DR GCRDb; GCR_0154; -.
DR GCRDb; GCR_0200; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 59 1 (POTENTIAL).
FT DOMAIN 60 70 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 71 96 2 (POTENTIAL).
FT DOMAIN 97 106 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 107 129 3 (POTENTIAL).
FT DOMAIN 130 149 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 150 173 4 (POTENTIAL).
FT DOMAIN 174 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 217 5 (POTENTIAL).
FT DOMAIN 218 374 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 375 399 6 (POTENTIAL).
FT DOMAIN 400 409 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 410 430 7 (POTENTIAL).
FT DOMAIN 431 450 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 106 188 BY SIMILARITY.
FT LIPID 442 442 PALMITATE (BY SIMILARITY).
FT SITE 113 113 IMPLICATED IN LIGAND BINDING (BY SIMILARITY).
FT SITE 200 200 IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
FT SITE 204 204 IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
FT CONFLICT 147 147 P -> R (IN REF. 2).
FT CONFLICT 154 158 IVTVW -> HCHCV (IN REF. 2).
FT CONFLICT 252 253 GL -> AV (IN REF. 1).
FT CONFLICT 264 264 A -> G (IN REF. 2).
FT CONFLICT 304 305 RP -> PR (IN REF. 1).
FT CONFLICT 333 333 P -> R (IN REF. 1).
FT CONFLICT 445 445 D -> N (IN REF. 2).
SQ SEQUENCE 450 AA; 48939 MW; AFA078DCA3D612AC CRC64;

Query Match 47.6%; Score 40; DB 1; Length 450;
Best Local Similarity 64.3%; Pred. No. 20;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 LLKEFTVSGNIIITI 15
|| ||| ||:| |
Db 42 LLMLFTVFGNVLVI 55

RESULT 8
A2AA_BOVIN STANDARD; PRT; 452 AA.
AC Q28838;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-2A adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2AAR)
DE (Alpha-2D adrenergic receptor).
GN ADRA2A.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98111113; PubMed=9450652;
RA Venkataraman V., Duda T., Sharma R.K.;
RT "The bovine alpha 2D-adrenergic receptor gene: structure, expression in retina, and pharmacological characterization of the encoded receptor.";
RT Mol. Cell. Biochem. 177:113-123(1997).
RN [2]
RP SEQUENCE OF 171-210 FROM N.A.

RX MEDLINE=94018366; PubMed=8412494;
RA Blaxall H.S., Heck D.A., Bylund D.B.;
RT "Molecular determinants of the alpha-2D adrenergic receptor subtype.";
RL Life Sci. 53:9-9(1993).
CC -!- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G PROTEINS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: RETINA, BRAIN AND OLFACTORY LOBE.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
CC EMBL; U79030; AAC24958.1; -.
DR EMBL; S66295; AAB28450.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 59 1 (POTENTIAL).
FT DOMAIN 60 70 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 71 96 2 (POTENTIAL).
FT DOMAIN 97 106 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 107 129 3 (POTENTIAL).
FT DOMAIN 130 149 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 150 173 4 (POTENTIAL).
FT DOMAIN 174 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 217 5 (POTENTIAL).
FT DOMAIN 218 376 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 377 401 6 (POTENTIAL).
FT DOMAIN 402 411 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 412 432 7 (POTENTIAL).
FT DOMAIN 433 452 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 106 188 BY SIMILARITY.
FT LIPID 444 444 PALMITATE (BY SIMILARITY).
SQ SEQUENCE 452 AA; 49252 MW; F10C1DD2860CD6F9 CRC64;

Query Match 47.6%; Score 40; DB 1; Length 452;
Best Local Similarity 64.3%; Pred. No. 20;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 LLKEFTVSGNIIITI 15
|| ||| ||:| |
Db 42 LLMLFTVFGNVLVI 55

RESULT 9
VPS_HAEIN STANDARD; PRT; 623 AA.
ID VPS_HAEIN
AC P44242;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Mu-like prophage FluMu defective tail fiber protein.
GN HI1522.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]

QY 2 LLKEFTVSGNLTIRLT 18
||||| :| :| :|
Db 213 LLKEFQVNPNELIAKVT 229

RESULT 12
FLDL_VIBPA STANDARD; PRT; 445 AA.
AC Q03475;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lateral flagellar hook-associated protein 2 (HAP2) (Filament CAP protein) (Flagellar cap protein).
GN FLIDL OR LAFB.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BB22;
RX MEDLINE=93273702; PubMed=8501040;
RA McCarter L.L., Wright M.E.;
RT "Identification of genes encoding components of the swarmer cell flagellar motor and propeller and a sigma factor controlling differentiation of Vibrio parahaemolyticus.";
RL J. Bacteriol. 175:3361-3371(1993).
CC -!- FUNCTION: REQUIRED FOR THE MORPHOGENESIS AND FOR THE ELONGATION OF THE FLAGELLAR FILAMENT BY FACILITATING POLYMERIZATION OF THE FLAGELLIN MONOMERS AT THE TIP OF GROWING FILAMENT. FORMS A CAPPING STRUCTURE, WHICH PREVENTS FLAGELLIN SUBUNITS (TRANSPORTED THROUGH THE CENTRAL CHANNEL OF THE FLAGELLUM) FROM LEAKING OUT WITHOUT POLYMERIZATION AT THE DISTAL END. ESSENTIAL FOR SWARMING MOTILITY.
CC -!- SUBUNIT: HOMOPENTAMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: FLAGELLAR.
CC -!- MISCELLANEOUS: V.PARAHAEVOLYTICUS POSSESSES TWO FLAGELLAR SYSTEMS: A SINGLE POLAR FLAGELLUM PROPELS THE BACTERIUM IN LIQUID (SWIMMING), WHILE MULTIPLE LATERAL (PERITRICHOUS) FLAGELLA MOVE THE BACTERIUM OVER SURFACES (SWARMING). THE POLAR FLAGELLUM IS SYNTHESIZED CONSTITUTIVELY BUT LATERAL FLAGELLA ARE PRODUCED ONLY UNDER CONDITIONS IN WHICH THE POLAR FLAGELLUM IS NOT FUNCTIONAL.
CC -!- SIMILARITY: BELONGS TO THE FLID FAMILY.

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EMBL; L06176; AAA27530.1; -.
EMBL; U52957; AAB07351.1; -.
PIR; B40590; B40590.
DR InterPro; IPR003481; Flid.
DR Pfam; PF02465; Flid; 1.
KW Flagella; Coiled coil.
FT DOMAIN 388 423 COILED COIL (POTENTIAL).
SQ SEQUENCE 445 AA; 48264 MW; 0F7F7089A525852A CRC64;

Query Match 46.4%; Score 39; DB 1; Length 445;
Best Local Similarity 50.0%; Pred. No. 29;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 5 EFTVSGNLTIRLT 18
||||| :| :| :|
Db 123 EFTNGKTMIDLS 136

RESULT 13
VRP2_SALCH

ID VRP2_SALCH STANDARD; PRT; 591 AA.
AC P17450;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 65 kDa virulence protein (Protein M2 in mba region).
OS Salmonella cholerae-suis (Salmonella enterica).
OG Plasmid pKDS50.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=591;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RF-1;
RX MEDLINE=90245675; PubMed=2336400;
RA Matsui H.;
RT "Nucleotide sequences of genes encoding 32 kDa and 70 kDa polypeptides in mba region of the virulence plasmid, pKDS50, of Salmonella cholerae-suis.";
RL Nucleic Acids Res. 18:2181-2181(1990).
CC -!- FUNCTION: NOT KNOWN. THIS PROTEIN IS INVOLVED IN THE VIRULENCE OF SALMONELLAS.
CC -!- SIMILARITY: TO SIMILAR PROTEIN IN OTHER SALMONELLA VIRULENCE PLASMIDS.

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EMBL; X52035; CAA36278.1; -.
PIR; S09498; S09498.
DR InterPro; IPR003284; Sal_SpvB.
DR PRINTS; PR01341; SALSPVBPROT.
KW Plasmid; Virulence.
FT DOMAIN 367 373 POLY-PRO.
SQ SEQUENCE 591 AA; 65341 MW; 836EFC15BC151F1 CRC64;

Query Match 46.4%; Score 39; DB 1; Length 591;
Best Local Similarity 58.3%; Pred. No. 40;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 LLKEFTVSGNIL 13
:||||| :| :| :|
Db 483 VLKEYTTIGNII 494

RESULT 14
VRP2_SALEN STANDARD; PRT; 591 AA.
AC P55220;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE 65 kDa virulence protein.
GN SPVB.
OS Salmonella enteritidis.
OG Plasmid pNL2001.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=592;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AL1190;
RX MEDLINE=94362897; PubMed=8081495;
RA Suzuki S., Komase K., Matsui H., Abe A., Kawahara K., Tamura Y., Kijima M., Danbara H., Nakamura M., Sato S.;
RT "Virulence region of plasmid pNL2001 of Salmonella enteritidis.";
RL Microbiology 140:1307-1318(1994).

```
CC -!- FUNCTION: NOT KNOWN. THIS PROTEIN IS INVOLVED IN THE VIRULENCE
CC OF SALMONELLAS.
CC -!- SIMILARITY: TO SIMILAR PROTEIN IN OTHER SALMONELLA VIRULENCE
CC PLASMIDS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D14490; BAA03383.1; -.
CC InterPro; IPR003284; Sal_SpvB.
CC PRINTS; PR01341; SALSPVBPROT.
CC KW Plasmid; Virulence.
CC FT DOMAIN 367 373 POLY-PRO.
CC SEQUENCE 591 AA; 65350 MW; F83F33E02915D58F CRC64;

Query Match 46.4%; Score 39; DB 1; Length 591;
Best Local Similarity 58.3%; Pred. No. 40;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 LLKEFTVSGNIL 13
:||||:| |||:
Db 483 VLKEYTTIGNII 494

RESULT 15
VRP2_SALDU
ID VRP2_SALDU STANDARD; PRT; 593 AA.
AC P24419;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 65 kDa virulence protein.
GN VSDC.
OS Salmonella dublin.
OG Plasmid pSDL2.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=98360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LANE;
RX MEDLINE=91251759; PubMed=2041471;
RA Krause M., Roudier C., Fierer J., Harwood J., Guiney D.;
RT "Molecular analysis of the virulence locus of the Salmonella dublin
RT plasmid pSDL2.";
RL Mol. Microbiol. 5:307-316(1991).
CC -!- FUNCTION: NOT KNOWN. THIS PROTEIN IS INVOLVED IN THE VIRULENCE
CC OF SALMONELLAS.
CC -!- SIMILARITY: TO SIMILAR PROTEIN IN OTHER SALMONELLA VIRULENCE
CC PLASMIDS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X56727; CAA40049.1; -.
CC PIR; S15215; S15215.
CC InterPro; IPR003284; Sal_SpvB.
CC PRINTS; PR01341; SALSPVBPROT.
CC KW Plasmid; Virulence.
CC FT DOMAIN 367 375 POLY-PRO.
CC SEQUENCE 593 AA; 65613 MW; ECD C218FC41D6567 CRC64;
```

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Query Match 46.4%; Score 39; DB 1; Length 593;
Best Local Similarity 58.3%; Pred. No. 40;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 LLKEFTVSGNIL 13
:||||:| |||:
Db 485 VLKEYTTIGNII 496

Search completed: July 3, 2002, 11:24:43
Job time: 890 sec
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DE LAGE-1S PROTEIN (CANCER/TESTIS ANTIGEN 2).
GN LAGEL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MELANOMA;
RX MEDLINE=99325550; PubMed=10399963;
RA Aarnoudse C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.;
RT "Interleukin-2-induced, melanoma-specific T cells recognize CAMEL, an
RT unexpected translation product of LAGE-1.";
RL Int. J. Cancer 82:442-448(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Aradhya S., Bardaro T., Galgoczy P., Yamagata T., Esposito T.,
RA Patlan H., Ciccodicola A., Kenwrick S., Platzner M., D'Urso M.,
RA Nelson D.L.;
RT "Multiple pathogenic and benign genomic rearrangements occur at a 35-
RT kb duplication involving the NEMO and the LAGE2 genes.";
RL Hum. Mol. Genet. 0:0-0(2001).
DR EMBL; AJ012834; CAA10194.1; -.
DR EMBL; AF277315; AAL27015.1; -.
SQ SEQUENCE 180 AA; 18236 MW; 9077FAF953543A25 CRC64;

Query Match 77.4%; Score 65; DB 4; Length 180;
Best Local Similarity 76.5%; Pred. No. 0.0016;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LLKEFTVSGNLTIRLT.18
:|||||:|
Db 122 VLKDFTVSGNLLFIRLT 138

RESULT 3
Q9BU80
ID Q9BU80 PRELIMINARY; PRT; 210 AA.
AC Q9BU80;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CANCER/TESTIS ANTIGEN 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA, CHORIOCARCINOMA;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002833; AAH02833.1; -.
SQ SEQUENCE 210 AA; 21089 MW; 8FB5BF04FB04E8BE CRC64;

Query Match 58.3%; Score 49; DB 4; Length 210;
Best Local Similarity 75.0%; Pred. No. 1.3;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLKEFTVSGNIL 13
:|||||:|
Db 122 VLKDFTVSGNLL 133

RESULT 4
Q9UJ89
ID Q9UJ89 PRELIMINARY; PRT; 210 AA.
AC Q9UJ89;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

DE LAGE-1L PROTEIN.
GN LAGE-1L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MELANOMA;
RX MEDLINE=99325550; PubMed=10399963;
RA Aarnoudse C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.;
RT "Interleukin-2-induced, melanoma-specific T cells recognize CAMEL, an
RT unexpected translation product of LAGE-1.";
RL Int. J. Cancer 82:442-448(1999).
DR EMBL; AJ012835; CAA10196.1; -.
SQ SEQUENCE 210 AA; 21060 MW; 1DD0B1829735B60A CRC64;

Query Match 58.3%; Score 49; DB 4; Length 210;
Best Local Similarity 75.0%; Pred. No. 1.3;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLKEFTVSGNIL 13
:|||||:|
Db 122 VLKDFTVSGNLL 133

RESULT 5
Q9D9S4
ID Q9D9S4 PRELIMINARY; PRT; 219 AA.
AC Q9D9S4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE 1700030B21RIK PROTEIN.
GN 1700030B21RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK006526; BAB24635.1; -.
DR MGD; MGI:1917312; 1700030B21Rik.
SQ SEQUENCE 219 AA; 23670 MW; FB9B7B5A11FA2C37 CRC64;

Query Match 53.6%; Score 45; DB 11; Length 219;
Best Local Similarity 60.0%; Pred. No. 6.8;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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QY      4 KEFTVSGNLTIRLT 18
      :||||: |||:| |
Db      163 QEFTVNDTILTVRWT 177

RESULT      6
Q54436      PRELIMINARY;      PRT;      1524 AA.
AC      Q54436;
DT      01-NOV-1996 (TREMBLrel. 01, Created)
DT      01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT      01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE      TETRABRACHION PRECURSOR.
OS      Staphylothermus marinus.
OC      Archaea; Crenarchaeota; Desulfurococcaceae; Desulfurococcaceae;
OC      Staphylothermus.
OX      NCBI_TaxID=2280;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=F1;
RX      MEDLINE=95139068; PubMed=7837271;
RA      Peters J., Nitsch M., Kuhlmoegen B., Golbik R., Lupas A.,
RA      Kellermann J., Engelhardt H., Pfander J.P., Muller S., Goldie K.,
RA      Engel A., Stetter K.O., Baumeister W.;
RT      "Tetrabrachion: a filamentous archaeobacterial surface protein assembly
RT      of unusual structure and extreme stability.";
RL      J. Mol. Biol. 245:385-401(1995).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=F1;
RX      MEDLINE=96192087; PubMed=8632466;
RA      Peters J., Baumeister W., Lupas A.;
RT      "Hyperthermostable surface layer protein tetraabrachion from the
RT      archaeobacterium Staphylothermus marinus: Evidence for the presence of
RT      a right-handed coiled coil derived from the primary structure.";
RL      J. Mol. Biol. 257:1031-1041(1996).
DR      EMBL; U57967; AAC44118.1; -.
DR      InterPro; IPR001150; Gly_radical.
DR      PROSITE; PS00850; GLY_RADICAL; UNKNOWN_1..
KW      Signal.
FT      SIGNAL
SQ      SEQUENCE      1 26      POTENTIAL.
      1524 AA; 166278 MW; 970F9499F7A5AF87 CRC64;

Query Match      53.6%; Score 45; DB 1; Length 1524;
Best Local Similarity 60.0%; Pred. No. 54;
Matches      9; Conservative      3; Mismatches      3; Indels      0; Gaps      0;

QY      4 KEFTVSGNLTIRLT 18
      :|||:| |:||:| |
Db      661 KEFNLSFNLTLSLT 675 .

RESULT      7
Q9D6H8      PRELIMINARY;      PRT;      197 AA.
AC      Q9D6H8;
DT      01-JUN-2001 (TREMBLrel. 17, Created)
DT      01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT      01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE      290002802IRIK PROTEIN.
GN      290002802IRIK.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=HIPPOCAMPUS;
RX      MEDLINE=21085660; PubMed=11217851;
RA      Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA      Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA      Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
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RA      Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA      Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA      Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA      Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA      Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA      Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA      Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA      Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA      Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA      Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA      Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA      Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA      Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA      Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA      Hayashizaki Y.;
RT      "Functional annotation of a full-length mouse cDNA collection.";
RL      Nature 409:685-690(2001).
DR      EMBL; AK013605; BAB28925.1; -.
DR      MGD; MGI:1914505; 290002802IRik.
SQ      SEQUENCE      197 AA; 22360 MW; 0A431F65371890A3 CRC64;

Query Match      52.4%; Score 44; DB 11; Length 197;
Best Local Similarity 46.7%; Pred. No. 9.1;
Matches      7; Conservative      4; Mismatches      4; Indels      0; Gaps      0;

QY      3 LKEFTVSGNLTIRLT 17
      :||||| | | : :
Db      1 MKEFTVKGFMHVNI 15

RESULT      8
O31615      PRELIMINARY;      PRT;      614 AA.
AC      O31615;
DT      01-JAN-1998 (TREMBLrel. 05, Created)
DT      01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT      01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE      YJBQ PROTEIN.
GN      YJBQ.
OS      Bacillus subtilis.
OC      Bacteria; Firmicutes; Bacillus/Clostridium group;
OC      Bacillus/Staphylococcus group; Bacillus.
OX      NCBI_TaxID=1423;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=168;
RX      MEDLINE=98044033; PubMed=9384377;
RA      Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA      Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA      Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA      Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA      Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA      Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA      Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA      Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA      Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA      Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA      Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA      Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA      Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA      Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA      Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
RA      Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA      Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA      Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA      Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA      Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA      Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA      Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA      Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA      Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA      Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
```


RESULT 12
Q9AP67
ID Q9AP67 PRELIMINARY; PRT; 211 AA.
AC Q9AP67;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE NITROUS OXIDE REDUCTASE (FRAGMENT).
GN NOSZ.
OS uncultured temperate forest soil bacterium CZ0X09.
OC Bacteria; environmental samples.
OX NCBI_TaxID=151486;
RN [1]
RP SEQUENCE FROM N.A.
RA Roesch C., Mergel A., Bothe H.;
RT "Distribution and diversity of nitrogen fixing and denitrifying
RT bacteria in temperate forest soils.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF315439; AAK06544.1; -.
DR InterPro; IPR001505; COX2.
DR ProDom; PD000131; COX2; 1.
FT NON_TER 1
FT NON_TER 211
SQ SEQUENCE 211 AA; 23738 MW; 0A187EB51CF50363 CRC64;

Query Match 50.6%; Score 42.5; DB 2; Length 211;
Best Local Similarity 58.8%; Pred. No. 18;
Matches 10; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 3 LKEFTV-SGNILTIRLT 18
:||||| |:|:|
Db 148 MREFTVKKGDIVTITLT 164

RESULT 13
Q943R7
ID Q943R7 PRELIMINARY; PRT; 697 AA.
AC Q943R7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PUTATIVE RECEPTOR KINASE.
GN OSJNBA0083M16.19.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
RT clone:OSJNba0083M16.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003214; BAB64619.1; -.
KW Receptor; Kinase.
SQ SEQUENCE 697 AA; 72292 MW; CD1028488D051FB0 CRC64;

Query Match 50.0%; Score 42; DB 10; Length 697;
Best Local Similarity 50.0%; Pred. No. 80;
Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 LKEFTVSGNILTIRLT 17
:|:| | | | | | |
Db 200 VLQDFNVSNLLTGRI 215

RESULT 14
Q9C0G6

ID Q9C0G6 PRELIMINARY; PRT; 1354 AA.
AC Q9C0G6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE KIAA1697 PROTEIN (FRAGMENT).
GN KIAA1697.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082932; PubMed=11214970;
RA Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XIX.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 7:347-355(2000).
DR EMBL; AB051484; BAB21788.1; -.
FT NON_TER 1
FT NON_TER 1354
SQ SEQUENCE 1354 AA; 154878 MW; 56787A7EFF321A1D CRC64;

Query Match 50.0%; Score 42; DB 4; Length 1354;
Best Local Similarity 52.9%; Pred. No. 1.6e+02;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNILTIRLT 17
:||||| |:|:|
Db 334 ILLKQIFISGGRLLIRL 350

RESULT 15
Q97AQ0
ID Q97AQ0 PRELIMINARY; PRT; 280 AA.
AC Q97AQ0;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL PROTEIN TVG0764458.
GN TVG0764458.
OS Thermoplasma volcanium.
OC Archaea; Euryarchaeota; Thermoplasmales; Thermoplasmaceae;
OC Thermoplasma.
OX NCBI_TaxID=50339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GSS1 / DSM 4299 / JCM 9571;
RX MEDLINE=20570466; PubMed=11121031;
RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
RA Kawashima Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
RA Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
RT "Archaeal adaptation to higher temperatures revealed by genomic
RT sequence of Thermoplasma volcanium.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
DR EMBL; AP000993; BAB59901.1; -.
DR InterPro; IPR000620; DUF6.
DR InterPro; IPR003015; HLH_Myc.
DR Pfam; PF00892; DUF6; 2.
DR PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 280 AA; 30856 MW; 1E49FA2E48A15F94 CRC64;

Query Match 48.8%; Score 41; DB 17; Length 280;
Best Local Similarity 57.1%; Pred. No. 45;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 LLKEFTVSGNILTIRLT 15
:|:| | | | | | |
Db 129 LMKGFTIFGAVLTI 142

Search completed: July 3, 2002, 11:24:07
Job time: 914 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:08:49 ; Search time 136.43 Seconds
(without alignments)
14.655 Million cell updates/sec

Title: US-09-165-546A-9
Perfect score: 84
Sequence: 1 VLLKEFTVSGNLTIRLT 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802: *
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2: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT: *
3: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT: *
4: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT: *
5: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1984.DAT: *
6: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT: *
7: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT: *
8: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1987.DAT: *
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20: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT: *
21: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT: *
22: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84	100.0	18	AAE07769	Human NY ESO-1 HLA
2	84	100.0	18	AAU01540	HLA-DR53 recognisi
3	84	100.0	18	AAB69940	Human NY-ESO-1 HLA
4	84	100.0	180	AAW69665	Human NY-ESO-1 pro
5	84	100.0	180	AAW62584	Cancer associated
6	84	100.0	180	AAW05965	Human cancer antig
7	84	100.0	180	AAW03154	Human oesophageal
8	84	100.0	180	AAW70862	Human tumour antig
9	84	100.0	180	AAW52430	Human tumour antig
10	84	100.0	180	AAG67164	Amino acid sequenc
11	84	100.0	180	AAE07714	Human NY ESO-1 pro

12	84	100.0	180	22	AAU01535	Human NY-ESO-1 tum
13	84	100.0	180	22	AAB69946	Human NY-ESO-1 pro
14	84	100.0	397	22	AAE13122	NY-ESO-IC-HER-2 me
15	79	94.0	25	22	AAE07718	Human NY ESO-1 MHC
16	79	94.0	27	22	AAE07717	Human NY ESO-1 MHC
17	71	84.5	15	22	AAE07726	Human NY ESO-1 MHC
18	71	84.5	15	22	AAE07727	Human NY ESO-1 MHC
19	71	84.5	15	22	AAE07786	Human NY ESO-1 pep
20	71	84.5	15	22	AAE07787	Human NY ESO-1 pep
21	70	83.3	20	22	AAE07729	Human NY ESO-1 MHC
22	68.5	81.5	17	21	AAW52436	Human tumour antig
23	67	79.8	14	22	AAE07728	Human NY ESO-1 MHC
24	67	79.8	14	22	AAE07788	Human NY ESO-1 pep
25	65	77.4	180	19	AAW69664	Human LAGE-1 clone
26	65	77.4	180	21	AAW70860	Human LAGE-1 splic
27	62	73.8	20	22	AAE07742	Human ESO p126-145
28	57	67.9	18	22	AAU01541	HLA-DR53 recognisi
29	57	67.9	18	22	AAB69941	Human NY-ESO-1 HLA
30	56	66.7	18	21	AAW52440	Human tumour antig
31	56	66.7	18	22	AAU01544	HLA-DR53 recognisi
32	56	66.7	18	22	AAB69944	Human NY-ESO-1 HLA
33	49	58.3	210	19	AAW69663	Human LAGE-1 clone
34	49	58.3	210	21	AAW70861	Human LAGE-1 unspl
35	48	57.1	10	20	AAW06001	Human cancer antig
36	48	57.1	19	21	AAW52437	Human tumour antig
37	47	56.0	10	20	AAW05988	Human cancer antig
38	47	56.0	10	20	AAW05980	Human cancer antig
39	47	56.0	10	22	AAE07730	Human NY ESO-1 MHC
40	47	56.0	10	22	AAE07785	Human NY ESO-1 pep
41	47	56.0	11	22	AAE07725	Human NY ESO-1 MHC
42	47	56.0	11	22	AAE07784	Human NY ESO-1 pep
43	47	56.0	12	22	AAE07716	Human NY ESO-1 MHC
44	47	56.0	12	22	AAE07724	Human NY ESO-1 MHC
45	47	56.0	12	22	AAE07783	Human NY ESO-1 pep

ALIGNMENTS

RESULT 1
AAE07769
ID AAE07769 standard; peptide; 18 AA.
XX
AC AAE07769;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human NY ESO-1 HLA DR restricted T cell cancer peptide #1.
XX
KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.
XX
OS Homo sapiens.
XX
PN WO200155393-A2.
XX
PD 02-AUG-2001.
XX
PF 26-JAN-2001; 2001WO-US02765.
XX
PR 28-JAN-2000; 2000US-0179004.
PR 29-SEP-2000; 2000US-0237107.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang R, Rosenberg SA, Zeng G;
XX
DR WPI; 2001-496851/54.
XX
PT New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,

PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -
XX
PS Claim 84; Page 84; 134pp; English.
XX
CC The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or haptan and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is human
CC NY ESO-1 HLA DR restricted T cell cancer peptide.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 84; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNILTIRLT 18
Db | | | | | | | | | | | | | | | |
1 vllkeftvsgniltirt 18

RESULT 2
AAU01540
ID AAU01540 standard; Peptide; 18 AA.
XX
AC AAU01540;
XX
DT 18-JUL-2001 (first entry)
XX
DE HLA-DR53 recognising NY-ESO-1 peptide #2.
XX
KW NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
KW human leukocyte antigen-determining region; disease progression;
KW disease regression; disease onset; body tissue; body fluid; enzyme label;
KW radioactive label; monoclonal antibody.
XX
OS Homo sapiens.
XX
PN WO200123560-A2.
XX
PD 05-APR-2001.
XX
PF 26-SEP-2000; 2000WO-US26411.
XX
PR 29-SEP-1999; 99US-0408036.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Tureci O, Sahin U, Pfreundschuh M;
XX
DR WPI; 2001-266156/27.
XX
PT Polypeptides binding to major histocompatibility complex class II human
PT leukocyte antigen-determining region molecule having amino acid
PT sequence found in tumour rejection antigen precursor used for
PT stimulating proliferation of helper T cells -
XX
PS Example 13; Page 19; 62pp; English.

XX The sequence represents a human NY-ESO-1 tumour rejection antigen
CC precursor fragment which recognises and binds to HLA-DR53. NY-ESO-1 and
CC SSX-2 polypeptides, or fragments of, bind to major histocompatibility
CC complex (MHC) Class II molecules such as human leukocyte
CC antigen-determining region (HLA-DR) molecules and stimulate proliferation
CC of helper T cells. The peptides can be administered to an HLA-DR positive
CC subject in order to stimulate the helper T cells. An MHC Class II
CC HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell or
CC present in free form is useful for this stimulation. The nucleic acid is
CC useful for screening for a cancerous condition, which involves contacting
CC a subject sample to a cell line transfected with the immunoreactive cell
CC (helper T cell), where interaction is indicative of cancer. In addition,
CC a sample from a patient (for example, a body fluid or tissue) can be
CC monitored for the amount of the complex present in the bloodstream. This
CC is useful for determining regression, progression or onset of a cancerous
CC condition. The method involves contacting the sample with a radioactive
CC labelled or enzyme labelled monoclonal antibody which specifically binds
CC with the complex.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 84; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNILTIRLT 18
Db | | | | | | | | | | | | | | | |
1 vllkeftvsgniltirt 18

RESULT 3
AAB69940
ID AAB69940 standard; Peptide; 18 AA.
XX
AC AAB69940;
XX
DT 27-APR-2001 (first entry)
XX
DE Human NY-ESO-1 HLA-DR53 binding motif #2.
XX
KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW non-small cell lung carcinoma; tumour status determination.
XX
OS Homo sapiens.
XX
PN WO200107917-A1.
XX
PD 01-FEB-2001.
XX
PF 14-JUL-2000; 2000WO-US19220.
XX
PR 23-JUL-1999; 99US-0359503.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.
XX
PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
XX
DR WPI; 2001-182822/18.
XX
PT Method useful for determining the status (e.g. progression, regression
PT or stability of the disease) of a cancerous condition, involves
PT determining the levels of NY-ESO-1 specific antibodies in a sample
PT taken from a patient -
XX
PS Example 16; Page 27; 50pp; English.
XX
CC The present sequence is given in a specification relating to a method
CC for determining the status of a cancerous condition in a patient

CC with a tumour that expresses NY-ESO-1. The method comprises assaying a
CC sample taken from the patient for antibodies that specifically bind to
CC the NY-ESO-1 and comparing the value obtained to a prior value obtained
CC from assay of a prior sample taken from the patient. Any difference
CC between the values is indicative of a change in status of the cancerous
CC condition. The method is useful for determining whether a cancerous
CC condition is progressing, regressing or remaining stable, in particular
CC in patients receiving treatment for a melanoma, adenocarcinoma,
CC non-small cell lung carcinoma or bladder carcinoma.

XX Sequence 18 AA;

SQ

Query Match 100.0%; Score 84; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNILTIRLT 18
|||||
Db 1 vllkeftvsgniltirtl 18

RESULT 4
AAW69665
ID AAW69665 standard; Protein; 180 AA.
XX
AC AAW69665;
XX
DT 27-OCT-1998 (first entry)
XX
DE Human NY-ESO-1 protein sequence, formerly known as LL-1.2 clone.
XX
KW Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour.
XX
OS Homo sapiens.
XX
PN WO9832855-A1.
XX
PD 30-JUL-1998.
XX
PF 27-JAN-1998; 98WO-US01445.
XX
PR 27-JAN-1997; 97US-0791495.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Boon-Falleur T, De Smet C, Godelaine D, Lethe B;
PI Lucas S;
XX
DR WPI; 1998-427951/36.
DR N-PSDB; AAV50348.
XX
PT New isolated LAGE-1 tumour associated nucleic acids - used to
PT develop products for the diagnosis and treatment of LAGE-1
PT associated disorders, particularly tumours
XX
PS Example 2; Page 57-58; 73pp; English.

XX The present sequence represents human NY-ESO-1, formerly known as LL-1.2
CC clone, which is used in an example from the present invention which
CC describes LAGE-1 tumour associated protein (TAP). The present invention
CC also describes: (1) a method for treating a subject with a disorder
CC characterised by expression of a LAGE-1 nucleic acid molecule or an
CC expression product, comprising administering to the subject autologous
CC cytolytic T cells to ameliorate the disorder, where the cytolytic T
CC cells are specific for complexes of an HLA molecule and a LAGE-1 TAP or
CC an immunogenic fragment; (2) a method for treating a subject with a
CC disorder characterised by expression of a LAGE-1 nucleic acid molecule
CC or an expression product, comprising administering a LAGE-1 TAP or an
CC immunogenic fragment to ameliorate the disorder; and (3) a method for
CC selectively enriching a population of T cells with cytolytic T cells
CC specific for a LAGE-1 TAP comprising contacting an isolated population
CC of T cells with an agent presenting a complex of a LAGE TAP or an

CC immunogenic fragment and a HLA presenting molecule to selectively
CC enrich the isolated population of T cells with the cytolytic T cells.
CC The methods and products from the present invention can be used for the
CC diagnosis and treatment of LAGE-1 associated disorders, particularly
CC tumours.

XX Sequence 180 AA;

SQ

Query Match 100.0%; Score 84; DB 19; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNILTIRLT 18
|||||
Db 121 vllkeftvsgniltirtl 138

RESULT 5
AAW62584
ID AAW62584 standard; Protein; 180 AA.
XX
AC AAW62584;
XX
DT 17-SEP-1998 (first entry)
XX
DE Cancer associated antigen NY-ESO-1.
XX
KW Cancer associated antigen; NY-ESO-1; regression; progression; onset;
KW cancer; treatment; diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 7 /note= "potential myristoylation site"
FT Misc-difference 9 /note= "potential myristoylation site"
FT Misc-difference 11 /note= "potential phosphorylation site"
FT Misc-difference 98 /note= "potential phosphorylation site"
FT Misc-difference 134 /note= "potential phosphorylation site"
FT Misc-difference 138 /note= "potential phosphorylation site"
FT
XX WO9814464-A1.
XX
PD 09-APR-1998.
XX
PF 15-SEP-1997; 97WO-US16335.
XX
PR 03-OCT-1996; 96US-0725182.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Chen Y, Drijfhout JW, Gure A, Jager E, Knuth A;
PI Old LJ, Scanlan M;
XX
DR WPI; 1998-286417/25.
DR N-PSDB; AAV38566.
XX
PT New isolated cancer associated antigen - is used to develop products
PT for the diagnosis and treatment of cancers and for monitoring cancer
PT therapy
XX
PS Claim 8; Fig 3; 49pp; English.

XX The present sequence represents a cancer associated antigen. The clone
CC from which the DNA sequence is obtained is designated NY-ESO-1. The
CC specification described a method for determining regression, progression
CC of onset of a cancerous condition, comprising monitoring a sample from a

CC patient with the cancerous condition for a parameter selected from
CC NY-ESO-1 protein, a peptide derived from NY-ESO-1 protein and cytolytic
CC T cells specific for the peptide and an MHC molecule with which it
CC non-covalently complexes. Methods for the treatment of a cancerous
CC condition are also described. The NY-ESO-1 protein and peptides derived
CC from it can be used for diagnosis and treatment of cancers and to monitor
CC the efficacy of a therapeutic regime.

XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 84; DB 19; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNLTIRLT 18
|
Db 121 vllkeftvsgnltirtl 138

RESULT 6
AAY05965
ID AAY05965 standard; Protein; 180 AA.
XX
AC AAY05965;

DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 ORF1 protein.

XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer antigen; human; leukaemia;
KW non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; ORF1.

XX Homo sapiens.
XX WO9182206-A2.
PN

XX 15-APR-1999.

PF 21-SEP-1998; 98WO-US19609.

XX 08-OCT-1997; 97US-0061428.

PR (USSH) US DEPT HEALTH & HUMAN SERVICES.

PA Rosenberg SA, Wang RF;

XX WPI; 1999-277270/23.

DR N-PSDB; AAX58599.

XX Cancer antigen NY ESOL/CAG-3

PS Claim 4; Fig 3A; 88pp; English.

XX The present sequence represents the ORF1 protein encoded by
CC open reading frame 1 of the human ESO-1/CAG-3 (or CAG-3) gene.
CC CAG-3 is a new and potent tumour antigen capable of eliciting an
CC antigen specific immune response by T cells. Cancer peptides
CC comprising ORF1, ORF2 (see AAY05966), portions of these peptides and
CC their variants (see AAY05965-87), are useful as cancer vaccines that
CC protect the recipient from development of cancer. The invention
CC provides vectors and host cells (also useful as vaccines); a
CC method of diagnosis of cancer or precancer; a transgenic animal;
CC antisense oligonucleotides that inhibit expression of the cancer
CC peptide or tumour antigen; antibodies reacting with the CAG-3
CC cancer peptide, useful in diagnostic and detection assays; and
CC methods for preventing or inhibiting cancer by administering a
CC cancer peptide, with or without an HLA molecule. The cancer

CC peptides form part of, or are derived from, cancers such as primary
CC or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer,
CC liver cancer, leukaemia, uterine cancer, cervical cancer, bladder
CC cancer, kidney cancer and adenocarcinomas such as breast, prostate,
CC ovarian, pancreatic and thyroid cancers. Melanoma is treated by
CC inducing cancer-specific T cells in vitro for subsequent return to
CC a patient.

XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 84; DB 20; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNLTIRLT 18
|
Db 121 vllkeftvsgnltirtl 138

RESULT 7
AAB03154
ID AAB03154 standard; Protein; 180 AA.
XX
AC AAB03154;

DT 23-OCT-2000 (first entry)
XX
DE Human oesophageal cancer-associated antigen NY-ESO-1.

XX Oesophageal cancer associated antigen; NY-ESO-1; human;
KW immunogen; oesophageal carcinoma; melanoma; ovary; testis;
KW transmembrane domain; antibody; diagnostic marker; drug delivery target.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 7 /note= "Potential N-myristoylation site"

FT Modified-site 9 /note= "Potential N-myristoylation site"

FT Modified-site 11 /note= "Potential O-phosphorylation site"

FT Modified-site 98 /note= "Potential O-phosphorylation site"

FT Modified-site 134 /note= "Potential O-phosphorylation site"

FT Modified-site 138 /note= "Potential O-phosphorylation site"

FT Domain 152..172 /note= "Potential transmembrane domain"

FT US6069233-A.

XX 30-MAY-2000.

XX 26-JAN-1998; 98US-0013150.

XX 03-OCT-1996; 96US-0725381.

XX (SLOK) SLOAN KETTERING INST CANCER RES.

PA (CORR) CORNELL RES FOUND INC.

PA (LUDW-) LUDWIG INST CANCER RES.

XX Scanlan M, Gure AO, Chen Y, Tureci O, Sahin U, Pfreundschuh M;

PI Old LJ;

XX WPI; 2000-410880/35.

DR N-PSDB; AAA61483.

XX New isolated esophageal cancer-associated antigen useful as markers for
PT producing antibodies and as targets for identifying abnormal
PT conditions, e.g. infections and cancer -

FT Peptide /note= "Peptide presented by MHC Class I HLA-B44"
FT 107..116
FT Peptide /note= "Peptide presented by MHC Class I HLA-A24"
FT 110..118
FT Peptide /note= "Peptide presented by MHC Class I HLA-B52"
FT 113..121
FT Peptide /note= "Peptide presented by MHC Class I HLA-B7"
FT 113..122
FT Peptide /note= "Peptide presented by MHC Class I HLA-B7 and
FT HLA-B52"
FT 115..124
FT Peptide /note= "Peptide presented by MHC Class I HLA-A3"
FT 118..126
FT Peptide /note= "Peptide presented by MHC Class I HLA-B35"
FT 124..133
FT Peptide /note= "Peptide presented by MHC Class I HLA-B52"
FT 125..133
FT Peptide /note= "Peptide presented by MHC Class I HLA-A24"
FT 138..147
FT Peptide /note= "Peptide presented by MHC Class I HLA-B8"
FT 139..147
FT Peptide /note= "Peptide presented by MHC Class I HLA-B7"
FT 145..153
FT Peptide /note= "Peptide presented by MHC Class I HLA-A24 and
FT HLA-B52"
FT 153..162
FT Peptide /note= "Peptide presented by MHC Class I HLA-B52"
FT 154..162
FT Peptide /note= "Peptide presented by MHC Class I HLA-B52"
FT 154..163
FT Peptide /note= "Peptide presented by MHC Class I HLA-B52"
FT 156..167
FT Peptide /note= "Peptide (AAY52434) presented by MHC Class I
FT HLA-A2" Peptide 158..166
FT Peptide /note= "Peptide presented by MHC Class I HLA-A3"
FT 159..167
FT Peptide /note= "Peptide presented by MHC Class I HLA-A3"
FT 162..170
FT Peptide /note= "Peptide presented by MHC Class I HLA-B52"
FT XX
PN WO9953938-A1.
XX
PD 28-OCT-1999.
XX
PF 24-MAR-1999; 99WO-US06875.
XX
PR 17-APR-1998; 98US-0062422.
PR 02-OCT-1998; 98US-0165546.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
PI Gure A, Ritter G;
XX
DR WPI; 2000-038483/03.
DR N-PSDB; AAZ38380.
XX
PT Novel peptides which bind to MHC class I and MHC class II molecules,
PT useful for therapeutic and diagnostic purposes -
XX
PS Claim 30; Fig 3; 49pp; English.
XX
CC This sequence represents a human tumour antigen, NY-ESO-1, the cDNA
CC encoding which was isolated from an oesophagus squamous cell cancer
CC library. Tissue localisation studies revealed it to be expressed at
CC high levels in normal ovary and testis but not in normal colon, kidney,
CC liver, brain, oesophagus and skin. It was expressed in certain tumours
CC and tumour cell lines with some degree of frequency - these included
CC melanoma specimens and cell lines, and breast and bladder cancer
CC specimens, with expression in other tumour types being sporadic.
CC Peptides derived from NY-ESO-1 are bound by both MHC (major
CC histocompatibility complex) Class I and Class II molecules for
CC presentation to T-cells. Peptides AAY52431-Y52434 bind to Class I HLA-A2

CC molecules, thereby stimulating proliferation of cytotoxic T-cells, while
CC peptides AAY52435-Y52440 bind to Class II HLA-DR53 molecules, stimulating
CC helper T-cell proliferation. The peptides derived from NY-ESO-1 may be
CC used in methods and compositions used for the treatment, diagnosis and
CC prevention of cancers (such as melanoma, breast cancer, prostate cancer,
CC lung cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer,
CC or lymphoma) and to stimulate the proliferation of T cells.
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 84; DB 21; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNILTIRLT 18
Db 121 vllkeftvsgniltirt 138
|||||

RESULT 10
AAG67164
ID AAG67164 standard; Protein; 180 AA.
XX AAG67164;
AC
XX 13-NOV-2001 (first entry)
DT
DE Amino acid sequence of cancer testis tumour antigen NY-ESO-1.
XX
KW Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;
KW HLA binding peptide; major histocompatibility complex; MHC;
KW tumour; cancer; testis tumour.
XX
OS Homo sapiens.
XX
PN WO200162917-A1.
PD 30-AUG-2001.
XX
PF 22-JAN-2001; 2001WO-US02126.
XX
PR 22-FEB-2000; 2000US-0510635.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Lethe B, Boon-Falleur T;
XX
DR WPI; 2001-550091/61.
DR N-PSDB; AAH75118.
XX
PT Genomic sequences of tumour associated antigen EY-ESO-1 (LAGE-2) useful
PT for diagnosing testicular tumours -
XX
PS Example 5; Fig 3; 50pp; English.
XX
CC The present sequence represents cancer testis tumour antigen NY-ESO-1
CC (also called LAGE-2). NY-ESO-1 is a molecule that is processed to at
CC least one human leukocyte antigen (HLA) binding peptide, which binds
CC to Class I and Class II major histocompatibility complex (MHC).
CC NY-ESO-1 is expressed in tumour mRNA and in testis, but not normal
CC colon, kidney, liver or brain tissue. The presence or level of expression
CC of NY-ESO-1 may be assayed for the diagnosis of cancer, especially
CC testis tumours.
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 84; DB 22; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNILTIRLT 18

Db121vllkeftvsgniltirtl138

|||||

AAE07714standard; Protein; 180 AA.

AAE07714;

06-NOV-2001 (first entry)

Human NY ESO-1 protein.

Human; major histocompatibility complex; MHC; vaccine; metastasis; class II restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

Homo sapiens.

KeyLocation/Qualifiers

Misc-difference 45..47/note= "Encoded by CCGGGGGC"

WO200155393-A2.

02-AUG-2001.

26-JAN-2001; 2001WO-US02765.

28-JAN-2000; 2000US-0179004.

29-SEP-2000; 2000US-0237107.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Wang R, Rosenberg SA, Zeng G;

WPI; 2001-496851/54.

N-PSDB; AAD14179, AAD14180.

New NY-ESO cancer peptide or MHC class II restricted T cell epitopes, useful as immunogen and vaccine for inhibiting cancer in a mammal or as protection from metastasis

Example 1; Fig 1; 134pp; English.

The invention relates to the identification and isolation of major histocompatibility (MHC) class II restricted T cell epitope (MHC-II epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP restricted. The products of the gene are promising candidates for immunotherapeutic strategies for the prevention, treatment and diagnosis of patients with cancer. The cancer epitopes are useful as immunogen and vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T lymphocytes resulting in protection of the recipient from development of cancer and protection from metastasis, or by inhibiting the growth of cells expressing the NY-ESO-1 gene product. The cancer peptides are also useful as diagnostic agent to detect the presence of cancer, to enhance the generation of antibody and/or CD8+ T cell responses against any given target antigen and/or hapten and to induce tumour-specific humoral-mediated immunity against cancer. The present sequence is human NY ESO-1 protein.

Sequence180 AA;

Query Match100.0%; Score 84; DB 22; Length 180;

Best Local Similarity100.0%; Pred. No. 1.4e-07;

Matches18; Conservative0; Mismatches0; Indels0; Gaps0;

OY1VLLKEFTVSGNILTIRLT18

|||||

Db121vllkeftvsgniltirtl138

RESULT 12

AAU01535

IDAAU01535 standard; Protein; 180 AA.

XXACAAU01535;

XXDT18-JUL-2001 (first entry)

XXHuman NY-ESO-1 tumour rejection antigen precursor protein.

DEHuman NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II; major histocompatibility complex; helper T cell; HLA-DR; cancer;

KWhuman leucocyte antigen-determining region; disease progression;

KWdisease regression; disease onset; body tissue; body fluid; enzyme label;

KWradiolactive label; monoclonal antibody.

XXHomo sapiens.

OS

XX

FHKeyLocation/Qualifiers

FTModified-site7/note= "Myristoylated"

FTModified-site9/note= "Myristoylated"

FTModified-site11/note= "Phosphorylated"

FTModified-site98/note= "Phosphorylated"

FTModified-site134/note= "Phosphorylated"

FTModified-site138/note= "Phosphorylated"

XXWO200123560-A2.

XX05-APR-2001.

XX26-SEP-2000; 2000WO-US26411.

XX29-SEP-1999; 99US-0408036.

XX(LUDW-) LUDWIG INST CANCER RES.

XXTureci O, Sahin U, Pfreundschuh M;

XXWPI; 2001-266156/27.

XXN-PSDB; AAS02254.

XXPolypeptides binding to major histocompatibility complex class II human leukocyte antigen-determining region molecule having amino acid sequence found in tumour rejection antigen precursor used for stimulating proliferation of helper T cells -

XXClaim 4; Fig 3; 62pp; English.

XXThe sequence represents a human NY-ESO-1 tumour rejection antigen precursor. NY-ESO-1 and SSX-2 polypeptides, or fragments of, bind to major histocompatibility complex (MHC) Class II molecules such as human leukocyte antigen-determining region (HLA-DR) molecules and stimulate proliferation of helper T cells. The peptides can be administered to an HLA-DR positive subject in order to stimulate the helper T cells. An MHC Class II HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell or present in free form is useful for this stimulation. The nucleic acid is useful for screening for a cancerous condition, which involves contacting a subject sample to a cell line transfected with the immunoreactive cell (helper T cell), where interaction is indicative of cancer. In addition, a sample from a patient (for example, a body fluid or tissue) can be monitored for the amount of the complex present in the bloodstream. This is useful for determining regression, progression or

CC onset of a cancerous condition. The method involves contacting the sample
CC with a radioactive labelled or enzyme labelled monoclonal antibody which
CC specifically binds with the complex.

XX Sequence 180 AA;

Query Match 100.0%; Score 84; DB 22; Length 180;

Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNILTIRLT 18
| | | | | | | | | | | | | | | |
Db 121 vlleftvsgniltirtl 138

RESULT 13
AAB69946

ID AAB69946 standard; Protein; 180 AA.

XX AAB69946;

DT 27-APR-2001 (first entry)

XX Human NY-ESO-1 protein.

KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW non-small cell lung carcinoma; tumour status determination.

XX Homo sapiens.

PN WO200107917-A1.

PD 01-FEB-2001.

PF 14-JUL-2000; 2000WO-US19220.

PR 23-JUL-1999; 99US-0359503.

PA (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.

PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;

XX WPI; 2001-182822/18.
DR N-PSDB; AAF58634.

XX Method useful for determining the status (e.g. progression, regression
PT or stability of the disease) of a cancerous condition, involves
PT determining the levels of NY-ESO-1 specific antibodies in a sample
PT taken from a patient -

XX Example 5; Fig 3; 50pp; English.

XX The present sequence is human NY-ESO-1 protein. It is provided in a
CC specification relating to a method for determining the status of a
CC cancerous condition in a patient with a tumour that expresses NY-ESO-1.
CC The method comprises assaying a sample taken from the patient for
CC antibodies that specifically bind to the NY-ESO-1 and comparing the
CC value obtained to a prior value obtained from assay of a prior sample
CC taken from the patient. Any difference between the values is indicative
CC of a change in status of the cancerous condition. The method is useful
CC for determining whether a cancerous condition is progressing, regressing
CC or remaining stable, in particular in patients receiving treatment for a
CC melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder
CC carcinoma.

XX Sequence 180 AA;

Query Match 100.0%; Score 84; DB 22; Length 180;

Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNILTIRLT 18
| | | | | | | | | | | | | | | |
Db 121 vlleftvsgniltirtl 138

RESULT 14

ID AAE13122 standard; Protein; 397 AA.

XX AAE13122;

DT 28-JAN-2002 (first entry)

XX NY-ESO-IC-HER-2 membrane distal intracellular domain fusion protein.
DE Immunostimulatory fusion protein; IFP; antigen component; therapy;
XX Immunostimulatory component; T-cell mediated immune response; DC;
KW dendritic cell; colon cancer; breast carcinoma; ovarian cancer;
KW human; HER-2 membrane distal intracellular domain; NY-ESO-IC;
KW autoimmunogenic cancer/testis antigen.

XX Homo sapiens.

PN WO200174855-A2.

PD 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10515.

PR 30-MAR-2000; 2000US-193504P.

XX (DEND-) DENDREON CORP.

PI Laus R, Vidovic D, Graddis T;

XX WPI; 2001-662965/76.
DR N-PSDB; AAD21573.

XX An immunostimulatory fusion protein comprising the intracellular domain
PT of HER-2 and an antigen elicits an immune response to the antigen and
PT is useful for the treatment of associated cancer associated -

XX Disclosure; Page 54-55; 59pp; English.

XX The invention relates to immunostimulatory fusion proteins (IFP) and
CC nucleic acid molecules encoding such proteins. The IFPs comprise a
CC polypeptide antigen component and an immunostimulatory component derived
CC from the intracellular domain of HER-2 protein which is effective to
CC elicit a protective dendritic cell (DC)-induced T-cell mediated cellular
CC immune response to the antigen. IFP or superactivated dendritic cells
CC are used to treat cancer e.g. breast carcinoma, ovarian and colon cancer
CC associated with a particularly antigen. The present sequence is a
CC fusion protein which comprises human autoimmunogenic
CC cancer/testis antigen, NY-ESO-IC and mature human HER-2 membrane distal
CC intracellular domain.

XX Sequence 397 AA;

Query Match 100.0%; Score 84; DB 22; Length 397;

Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNILTIRLT 18
| | | | | | | | | | | | | | | |
Db 121 vlleftvsgniltirtl 138

RESULT 15

AAE07718

ID AAE07718 standard; peptide; 25 AA.
XX
AC AAE07718;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human NY ESO-1 MHC class II restricted T cell epitope #4.
XX
KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.
XX
OS Homo sapiens.
XX
PN WO200155393-A2.
XX
PD 02-AUG-2001.
XX
PF 26-JAN-2001; 2001WO-US02765.
XX
PR 28-JAN-2000; 2000US-0179004.
PR 29-SEP-2000; 2000US-0237107.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang R, Rosenberg SA, Zeng G;
XX
DR WPI; 2001-496851/54.
XX
PT New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -
XX
PS Claim 4; Page 16; 134pp; English.
XX
CC The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or hapten and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is MHC
CC class II restricted T cell epitope of human NY ESO-1 protein.
XX
SQ Sequence 25 AA;

Query Match 94.0%; Score 79; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.5e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNLTIRL 17
| | | | | | | | | | | | | | | | | | | | |
Db 9 vllkeftvsgnltirl 25

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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:21:00 ; Search time 599.92 Seconds
(without alignments)
10.561 Million cell updates/sec

Title: US-09-165-546A-9
Perfect score: 84
Sequence: 1 VLLKEFTVSGNLTIRLT 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2:	/cgn2_6/ptodata/2/paa/US06_COMB.pep:*				
3:	/cgn2_6/ptodata/2/paa/US07_COMB.pep:*				
4:	/cgn2_6/ptodata/2/paa/US08_COMB.pep:*				
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10:	/cgn2_6/ptodata/2/paa/US086_COMB.pep:*				
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13:	/cgn2_6/ptodata/2/paa/US089_COMB.pep:*				
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21:	/cgn2_6/ptodata/2/paa/US097_COMB.pep:*				
22:	/cgn2_6/ptodata/2/paa/US098_COMB.pep:*				
23:	/cgn2_6/ptodata/2/paa/US099_COMB.pep:*				
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query		Match Length DB ID		Description	
No.	Score	Match	Length	DB	ID		
1	84	100.0	18	15	US-09-165-546A-9		Sequence 9, Appli
2	84	100.0	18	18	US-09-408-036B-8		Sequence 8, Appli
3	84	100.0	122	26	US-60-336-968-17		Sequence 17, Appli
4	84	100.0	180	11	US-08-791-495-9		Sequence 9, Appli
5	84	100.0	180	17	US-09-341-829A-9		Sequence 9, Appli
6	84	100.0	180	17	US-09-392-714-25		Sequence 25, Appli
7	84	100.0	180	19	US-09-529-206-4		Sequence 4, Appli

8	84	100.0	180	19	US-09-529-206A-3	Sequence 3, Appli
9	84	100.0	180	19	US-09-529-206B-3	Sequence 3, Appli
10	84	100.0	180	19	US-09-561-571-3	Sequence 3, Appli
11	84	100.0	180	21	US-09-751-798-8	Sequence 8, Appli
12	84	100.0	180	24	US-10-005-905-3	Sequence 3, Appli
13	84	100.0	180	24	US-10-023-182-8	Sequence 8, Appli
14	84	100.0	180	24	US-10-026-066-3	Sequence 3, Appli
15	84	100.0	180	26	US-60-336-968-11	Sequence 11, Appli
16	84	100.0	397	22	US-09-821-883-27	Sequence 27, Appli
17	79	94.0	61	19	US-09-529-206-55	Sequence 55, Appli
18	79	94.0	61	19	US-09-529-206B-55	Sequence 55, Appli
19	79	94.0	61	19	US-09-529-206B-55	Sequence 55, Appli
20	65	77.4	180	11	US-08-791-495-7	Sequence 7, Appli
21	65	77.4	180	17	US-09-341-829A-7	Sequence 7, Appli
22	57	67.9	18	15	US-09-165-546A-10	Sequence 10, Appli
23	57	67.9	18	18	US-09-408-036B-9	Sequence 9, Appli
24	56	66.7	18	15	US-09-165-546A-13	Sequence 13, Appli
25	56	66.7	18	18	US-09-408-036B-12	Sequence 12, Appli
26	49	58.3	210	11	US-08-791-495-5	Sequence 5, Appli
27	49	58.3	210	17	US-09-341-829A-5	Sequence 5, Appli
28	48	57.1	10	19	US-09-529-206-91	Sequence 91, Appli
29	48	57.1	10	19	US-09-529-206A-91	Sequence 91, Appli
30	48	57.1	10	19	US-09-529-206B-91	Sequence 91, Appli
31	47	56.0	10	19	US-09-529-206-15	Sequence 15, Appli
32	47	56.0	10	19	US-09-529-206-84	Sequence 84, Appli
33	47	56.0	10	19	US-09-529-206A-15	Sequence 15, Appli
34	47	56.0	10	19	US-09-529-206A-84	Sequence 84, Appli
35	47	56.0	10	19	US-09-529-206B-15	Sequence 15, Appli
36	47	56.0	10	19	US-09-529-206B-84	Sequence 84, Appli
37	44	52.4	9	18	US-09-409-455A-120	Sequence 120, App
38	44	52.4	9	22	US-09-833-039-120	Sequence 120, App
39	43	51.2	86	26	US-60-242-679-1108	Sequence 1108, Ap
40	43	51.2	130	21	US-09-757-026-247	Sequence 247, App
41	42	50.0	9	18	US-09-409-455A-125	Sequence 125, App
42	42	50.0	9	19	US-09-529-206-12	Sequence 12, Appli
43	42	50.0	9	19	US-09-529-206-69	Sequence 69, Appli
44	42	50.0	9	19	US-09-529-206A-12	Sequence 12, Appli
45	42	50.0	9	19	US-09-529-206A-69	Sequence 69, Appli

ALIGNMENTS

RESULT 1
US-09-165-546A-9
; Sequence 9, Application US/09165546A
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao,
; Canlan, Matt; Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO
; AMINO ACID SEQUENCES OF NY-ESO-1, WHICH BIND TO
; MHC CLASS I AND MHC CLASS II MOLECULES, AND
; USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,546A
; FILING DATE: 02-Oct-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998

; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-165-546A-9

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Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNLTIRLT 18
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Db 1 VLLKEFTVSGNLTIRLT 18

RESULT 2
US-09-408-036B-8
; Sequence 8, Application US/09408036B
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Isolated Peptides Which Bind to MHC Class II Molecules and Uses T
; FILE REFERENCE: LUD 5624
; CURRENT APPLICATION NUMBER: US/09/408,036B
; CURRENT FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/165,546
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-408-036B-8

Query Match 100.0%; Score 84; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNLTIRLT 18
| | | | | | | | | | | | | | | |
Db 1 VLLKEFTVSGNLTIRLT 18

RESULT 3
US-60-336-968-17
; Sequence 17, Application US/60336968
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: CTLLMM.022PR
; CURRENT APPLICATION NUMBER: US/60/336,968

; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-336-968-17

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Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNLTIRLT 18
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Db 64 VLLKEFTVSGNLTIRLT 81

RESULT 4
US-08-791-495-9
; Sequence 9, Application US/08791495
; GENERAL INFORMATION:
; APPLICANT: Leth , Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-9

Query Match 100.0%; Score 84; DB 11; Length 180;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNLTIRLT 18
| | | | | | | | | | | | | | | |
Db 121 VLLKEFTVSGNLTIRLT 138

RESULT 5
US-09-341-829A-9

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; Sequence 19, Application US/09341829A
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495 <151> 1997-01-27
; PRIOR APPLICATION NUMBER: PCT/US98/01445 <151> 1998-01-27
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-341-829A-9

Query Match 100.0%; Score 84; DB 17; Length 180;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNLTIRLT 18
Db 121 VLLKEFTVSGNLTIRLT 138

RESULT 6
US-09-392-714-25
; Sequence 25, Application US/09392714A
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Gure, Ali O.
; APPLICANT: Williamson, Barbara
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Cancer Associated Antigens and Uses
; FILE REFERENCE: L0461/7062
; CURRENT APPLICATION NUMBER: US/09/392,714A
; CURRENT FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: PCT/US98/14679
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-392-714-25

Query Match 100.0%; Score 84; DB 17; Length 180;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNLTIRLT 18
Db 121 VLLKEFTVSGNLTIRLT 138

RESULT 7
US-09-529-206-4
; Sequence 4, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269PC
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; CURRENT APPLICATION NUMBER: US/09/529,206
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-4

Query Match 100.0%; Score 84; DB 19; Length 180;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNLTIRLT 18
Db 121 VLLKEFTVSGNLTIRLT 138

RESULT 8
US-09-529-206A-3
; Sequence 3, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206A-3

Query Match 100.0%; Score 84; DB 19; Length 180;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNLTIRLT 18
Db 121 VLLKEFTVSGNLTIRLT 138

RESULT 9
US-09-529-206B-3
; Sequence 3, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
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; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-3

Query Match          100.0%; Score 84; DB 19; Length 180;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNLTIRLT 18
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Db 121 VLLKEFTVSGNLTIRLT 138

RESULT 10
US-09-561-571-3
; Sequence 3, Application US/09561571
; GENERAL INFORMATION:
; APPLICANT: CTL Immunotherapies Corp.
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; TITLE OF INVENTION: EPITOPE CLUSTERS
; FILE REFERENCE: CTIMM.010A
; CURRENT APPLICATION NUMBER: US/09/561,571
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-561-571-3

Query Match          100.0%; Score 84; DB 19; Length 180;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNLTIRLT 18
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Db 121 VLLKEFTVSGNLTIRLT 138

RESULT 11
US-09-751-798-8
; Sequence 8, Application US/09751798
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
; APPLICANT: Knuth, Alexander; Old, Lloyd J.
; TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
; TITLE OF INVENTION: Associated Proteins, Uses Thereof,
; TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
; TITLE OF INVENTION: Binding Peptides Derived Therefrom
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/751,798
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
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; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
US-09-751-798-8

Query Match          100.0%; Score 84; DB 21; Length 180;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNLTIRLT 18
   |||||
Db 121 VLLKEFTVSGNLTIRLT 138

RESULT 12
US-10-005-905-3
; Sequence 3, Application US/10005905
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; TITLE OF INVENTION: EPITOPE SYNCHRONIZATION IN ANTIGEN
; TITLE OF INVENTION: PRESENTING CELLS
; FILE REFERENCE: CTIMM.021CP1
; CURRENT APPLICATION NUMBER: US/10/005,905
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 09/561,074
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/560,465
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,572
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,571
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US01/13806
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-005-905-3

Query Match          100.0%; Score 84; DB 24; Length 180;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNLTIRLT 18
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Db 121 VLLKEFTVSGNLTIRLT 138

RESULT 13
US-10-023-182-8
; Sequence 8, Application US/10023182
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:22:11 ; Search time 64.42 Seconds
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28.270 Million cell updates/sec

Title: US-09-165-546A-9
Perfect score: 84
Sequence: 1 VLLKEFTVSGNILTIRLT 18

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	84	100.0	180	1	PCT-US02-13994-30		Sequence 30, Appl
2	84	100.0	180	5	US-09-807-512-8		Sequence 8, Appl
3	84	100.0	180	6	US-10-117-937-74		Sequence 74, Appl
4	65	77.4	180	5	US-09-807-512-4		Sequence 4, Appl
5	65	77.4	180	6	US-10-117-937-75		Sequence 75, Appl
6	65	77.4	180	6	US-10-146-473-69		Sequence 69, Appl
7	49	58.3	210	5	US-09-807-512-6		Sequence 6, Appl
8	49	58.3	210	6	US-10-117-937-76		Sequence 76, Appl
9	49	58.3	210	6	US-10-157-031-88		Sequence 88, Appl
10	48	57.1	10	6	US-10-117-937-186		Sequence 186, App
11	47	56.0	10	6	US-10-117-937-188		Sequence 188, App
12	44	52.4	9	5	US-09-344-040C-120		Sequence 120, App
13	43	51.2	9	6	US-10-117-937-189		Sequence 189, App
14	43	51.2	130	6	US-10-152-780-247		Sequence 247, App
15	42	50.0	9	5	US-09-344-040C-125		Sequence 125, App
16	42	50.0	9	6	US-10-117-937-185		Sequence 185, App
17	40	47.6	105	5	US-09-710-059-293		Sequence 293, App
18	40	47.6	105	5	US-09-722-069-293		Sequence 293, App
19	40	47.6	109	5	US-09-688-017-310		Sequence 310, App
20	39	46.4	144	5	US-09-704-302A-756		Sequence 756, App
21	39	46.4	265	7	US-60-360-039-15		Sequence 15, Appl
22	39	46.4	568	7	US-60-360-039-19183		Sequence 19183, A
23	39	46.4	653	7	US-60-360-039-5324		Sequence 5324, Ap
24	39	46.4	802	7	US-60-382-898-222		Sequence 222, App
25	39	46.4	881	7	US-60-360-039-3341		Sequence 3341, Ap
26	38.5	45.8	154	5	US-09-540-209B-8787		Sequence 8787, Ap

27	38.5	45.8	1772	5	US-09-573-655B-2363	Sequence 2363, Ap
28	38	45.2	165	5	US-09-540-209B-8201	Sequence 8201, Ap
29	38	45.2	257	5	US-09-935-625-8806	Sequence 8806, Ap
30	38	45.2	294	5	US-09-935-625-8398	Sequence 8398, Ap
31	38	45.2	299	5	US-09-935-625-9805	Sequence 9805, Ap
32	38	45.2	336	5	US-09-935-625-8397	Sequence 8397, Ap
33	38	45.2	549	7	US-60-360-039-19574	Sequence 19574, A
34	38	45.2	592	5	US-09-935-625-900	Sequence 900, App
35	38	45.2	592	5	US-09-935-625-5343	Sequence 5343, App
36	38	45.2	592	5	US-09-935-625-8099	Sequence 8099, Ap
37	38	45.2	592	5	US-09-935-625-25320	Sequence 25320, A
38	38	45.2	597	5	US-09-935-625-899	Sequence 899, App
39	38	45.2	597	5	US-09-935-625-5342	Sequence 5342, Ap
40	38	45.2	597	5	US-09-935-625-8098	Sequence 8098, Ap
41	38	45.2	597	5	US-09-935-625-25319	Sequence 25319, A
42	38	45.2	621	5	US-09-935-625-9810	Sequence 9810, Ap
43	38	45.2	663	5	US-09-935-625-9809	Sequence 9809, Ap
44	38	45.2	727	5	US-09-935-625-898	Sequence 898, App
45	38	45.2	727	5	US-09-935-625-5341	Sequence 5341, Ap

ALIGNMENTS

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RESULT 1
PCT-US02-13994-30
; Sequence 30, Application PC/TUS0213994
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research
; APPLICANT: Cornell Research Foundation, Inc.
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd
; APPLICANT: Scanlan, Matthew
; APPLICANT: Stockert, Elisabeth
; TITLE OF INVENTION: COLON CANCER ANTIGEN PANEL
; FILE REFERENCE: L00461/70105WO(JRV)
; CURRENT APPLICATION NUMBER: PCT/US02/13994
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US 09/849,602
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-13994-30

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Query Match      100.0%; Score 84; DB 1; Length 180;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 VLLKEFTVSGNILTIRLT 18
 |||||
 Db 121 VLLKEFTVSGNILTIRLT 138

RESULT 2
US-09-807-512-8
; Sequence 8, Application US/09807512-8
; GENERAL INFORMATION:
; APPLICANT: Schrier, Peter I.
; APPLICANT: Aarnoudse, Corlien
; APPLICANT: Heider, Karl-Heinz
; APPLICANT: Klade, Christoph
; TITLE OF INVENTION: Camel, An Alte
; TITLE OF INVENTION: Antigen-Lage
; FILE REFERENCE: 0652.2200000
; CURRENT APPLICATION NUMBER: US/09/
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: PCT/EP99
; PRIOR FILING DATE: 1999-10-15

; PRIOR APPLICATION NUMBER: EP 98119583.7
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-807-512-8

Query Match 100.0%; Score 84; DB 5; Length 180;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNLTIRLT 18
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Db 121 VLLKEFTVSGNLTIRLT 138

RESULT 3
US-10-117-937-74
; Sequence 74, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-74

Query Match 100.0%; Score 84; DB 6; Length 180;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNLTIRLT 18
|||
Db 121 VLLKEFTVSGNLTIRLT 138

RESULT 4
US-09-807-512-4
; Sequence 4, Application US/09807512
; GENERAL INFORMATION:
; APPLICANT: Schrier, Peter I.
; APPLICANT: Aarnoudse, Corlien
; APPLICANT: Heider, Karl-Heinz
; APPLICANT: Klade, Christoph
; TITLE OF INVENTION: Camel, An Alternative Translation Product of the Tumor
; FILE REFERENCE: Antigen-Lage 1
; FILE REFERENCE: 0652.2200000
; CURRENT APPLICATION NUMBER: US/09/807,512
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: PCT/EP99/07832
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: EP 98119583.7

; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-807-512-4

Query Match 77.4%; Score 65; DB 5; Length 180;
Best Local Similarity 76.5%; Pred. No. 0.0008;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LLKEFTVSGNLTIRLT 18
:|:|:|:|:|:|:|
Db 122 VLKDFTVSGNLTIRLT 138

RESULT 5
US-10-117-937-75
; Sequence 75, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-75

Query Match 77.4%; Score 65; DB 6; Length 180;
Best Local Similarity 76.5%; Pred. No. 0.0008;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LLKEFTVSGNLTIRLT 18
:|:|:|:|:|:|:|
Db 122 VLKDFTVSGNLTIRLT 138

RESULT 6
US-10-146-473-69
; Sequence 69, Application US/10146473
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Gout, Ivan
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Gure, Ali
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd
; TITLE OF INVENTION: Breast Cancer Antigens
; FILE REFERENCE: L00461/70130(JRV)
; CURRENT APPLICATION NUMBER: US/10/146,473
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/291,150
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 82

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 69
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-473-69

Query Match 77.4%; Score 65; DB 6; Length 180;
Best Local Similarity 76.5%; Pred. No. 0.0008;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LLKEFTVSGNLTIRLT 18
:|||||:|
Db 122 VLKDFTVSGNLLFIRLT 138

RESULT 7
US-09-807-512-6
; Sequence 6, Application US/09807512
; GENERAL INFORMATION:
; APPLICANT: Schrier, Peter I.
; APPLICANT: Aarnoudse, Corlien
; APPLICANT: Heider, Karl-Heinz
; APPLICANT: Klade, Christoph
; TITLE OF INVENTION: Camel, An Alternative Translation Product of the Tumor
; TITLE OF INVENTION: Antigen-Lage 1
; FILE REFERENCE: 0652.2200000
; CURRENT APPLICATION NUMBER: US/09/807,512
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: PCT/EP99/07832
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: EP 98119583.7
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-807-512-6

Query Match 58.3%; Score 49; DB 5; Length 210;
Best Local Similarity 75.0%; Pred. No. 0.59;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLKEFTVSGNIL 13
:|||||:|
Db 122 VLKDFTVSGNLL 133

RESULT 8
US-10-117-937-76
; Sequence 76, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 76
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-76

Query Match 58.3%; Score 49; DB 6; Length 210;
Best Local Similarity 75.0%; Pred. No. 0.59;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLKEFTVSGNIL 13
:|||||:|
Db 122 VLKDFTVSGNLL 133

RESULT 9
US-10-157-031-88
; Sequence 88, Application US/10157031
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobashev, A. V.
; APPLICANT: Krukovskaya, L. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequence
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157,031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-031-88

Query Match 58.3%; Score 49; DB 6; Length 210;
Best Local Similarity 75.0%; Pred. No. 0.59;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLKEFTVSGNIL 13
:|||||:|
Db 122 VLKDFTVSGNLL 133

RESULT 10
US-10-117-937-186
; Sequence 186, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 186
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-186

Query Match 57.1%; Score 48; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FTVSGNLT 15
| | | | | | | | | |
Db 1 FTVSGNLT 10

RESULT 11
US-10-117-937-188
; Sequence 188, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 188
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-188

Query Match 56.0%; Score 47; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSG 10
| | | | | | | | | |
Db 1 VLLKEFTVSG 10

RESULT 12
US-09-344-040C-120
; Sequence 120, Application US/09344040C
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Determining Expression of an SSX Gene, Peptides Derived From Said SSX Gene and Uses Thereof
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene and Uses Thereof
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 120
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-120

Query Match 52.4%; Score 44; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FTVSGNLT 14
| | | | | | | | | |
Db 1 FTVSGNLT 9

RESULT 13
US-10-117-937-189
; Sequence 189, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 189
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-189

Query Match 51.2%; Score 43; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLKEFTVSG 10
| | | | | | | | | |
Db 1 LLKEFTVSG 9

RESULT 14
US-10-152-780-247
; Sequence 247, Application US/10152780
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PM049C1n
; CURRENT APPLICATION NUMBER: US/10/152,780
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: 09/757,026
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 247
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (30)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-10-152-780-247

Query Match 51.2%; Score 43; DB 6; Length 130;
Best Local Similarity 56.2%; Pred. No. 3.9;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNLTIR 16
I: I: I I I I I I I I
Db 79 VVGKDLTVSGRILVVR 94

RESULT 15
US-09-344-040C-125
; Sequence 125, Application US/09344040C
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determin
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 125
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-125

Query Match 50.0%; Score 42; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TVSGNLTIR 15
I I I I I I I I I
Db 1 TVSGNLTIR 9

Search completed: July 3, 2002, 11:22:11
Job time: 943 sec

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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:09:45 ; Search time 49.27 Seconds
(without alignments)
8.923 Million cell updates/sec

Title: US-09-165-546A-9
Perfect score: 84
Sequence: 1 VLLKEFTVSGNILTIRLT 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	84	100.0	180	2 US-08-791-495-9	Sequence 9, Appli
3	84	100.0	180	4 US-08-937-263B-8	Sequence 8, Appli
4	65	77.4	180	2 US-08-791-495-7	Sequence 7, Appli
5	57	67.9	18	4 US-09-359-503-10	Sequence 10, Appl
6	56	66.7	18	4 US-09-359-503-13	Sequence 13, Appl
7	49	58.3	210	2 US-08-791-495-5	Sequence 5, Appli
8	38	45.2	334	1 US-08-118-270-22	Sequence 22, Appl
9	38	45.2	334	5 PCT-US93-08528-22	Sequence 22, Appl
10	37	44.0	142	4 US-09-404-390-6	Sequence 6, Appli
11	37	44.0	469	3 US-08-985-335-5	Sequence 5, Appli
12	37	44.0	469	3 US-08-985-335-9	Sequence 9, Appli
13	37	44.0	469	4 US-09-410-372-5	Sequence 5, Appli
14	37	44.0	469	4 US-09-410-372-9	Sequence 9, Appli
15	37	44.0	956	1 US-08-185-232A-2	Sequence 2, Appli
16	37	44.0	956	1 US-08-416-523-2	Sequence 2, Appli
17	37	44.0	956	3 US-08-789-478-2	Sequence 2, Appli
18	36	42.9	273	4 US-08-235-836C-11	Sequence 11, Appl
19	36	42.9	273	4 US-08-235-836C-89	Sequence 89, Appl
20	36	42.9	273	4 US-08-235-836C-140	Sequence 140, App
21	36	42.9	273	4 US-08-235-836C-142	Sequence 142, App
22	36	42.9	273	4 US-08-235-836C-144	Sequence 144, App
23	36	42.9	409	1 US-08-403-545-2	Sequence 2, Appli
24	36	42.9	409	4 US-08-404-381-2	Sequence 2, Appli
25	36	42.9	488	2 US-08-599-455B-5	Sequence 5, Appli
26	36	42.9	488	4 US-09-069-781B-5	Sequence 5, Appli
27	36	42.9	572	2 US-08-419-652-5	Sequence 5, Appli

28	36	42.9	572	4 US-09-401-476-4	Sequence 4, Appli
29	36	42.9	658	2 US-08-825-558-4	Sequence 4, Appli
30	36	42.9	708	1 US-07-797-556-2	Sequence 2, Appli
31	36	42.9	708	1 US-08-308-881-2	Sequence 2, Appli
32	36	42.9	708	2 US-09-058-263-2	Sequence 2, Appli
33	36	42.9	708	2 US-09-059-099-2	Sequence 2, Appli
34	36	42.9	708	3 US-09-058-264-2	Sequence 2, Appli
35	36	42.9	708	5 PCT-US95-06530-2	Sequence 2, Appli
36	36	42.9	803	4 US-09-063-035-2	Sequence 2, Appli
37	36	42.9	918	2 US-08-825-558-6	Sequence 6, Appli
38	35	41.7	273	1 US-08-137-175A-5	Sequence 5, Appli
39	35	41.7	273	4 US-08-479-017-5	Sequence 5, Appli
40	35	41.7	273	4 US-09-196-293-13	Sequence 13, Appl
41	35	41.7	273	4 US-08-209-603E-13	Sequence 13, Appl
42	35	41.7	330	1 US-08-118-270-19	Sequence 19, Appl
43	35	41.7	330	5 PCT-US93-08528-19	Sequence 19, Appl
44	35	41.7	338	2 US-08-441-857-10	Sequence 10, Appl
45	35	41.7	338	3 US-08-193-159-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-359-503-9
; Sequence 9, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid

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; TOPOLOGY: linear
US-09-359-503-9

Query Match 100.0%; Score 84; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNLTIRLT 18
   |||
Db 1 VLLKEFTVSGNLTIRLT 18

RESULT 2
US-08-791-495-9
; Sequence 9, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth , Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-9

Query Match 100.0%; Score 84; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. NO. 4.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNLTIRLT 18
   |||
Db 121 VLLKEFTVSGNLTIRLT 138

RESULT 3
US-08-937-263B-8
; Sequence 8, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
; APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
```

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; APPLICANT: Alexander, Knuth; Drijfhout, Jan W.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
; TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
; TITLE OF INVENTION: ITSELF, AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,263B
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sinn, Eric, Patent Agent
; REGISTRATION NUMBER: 40,177
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
US-08-937-263B-8

Query Match 100.0%; Score 84; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. NO. 4.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNLTIRLT 18
   |||
Db 121 VLLKEFTVSGNLTIRLT 138

RESULT 4
US-08-791-495-7
; Sequence 7, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth , Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-9

Query Match 100.0%; Score 84; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. NO. 4.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNLTIRLT 18
   |||
Db 121 VLLKEFTVSGNLTIRLT 138

RESULT 3
US-08-937-263B-8
; Sequence 8, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
; APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
```

```

; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-791-495-7

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Query Match          77.4%; Score 65; DB 2; Length 180;
Best Local Similarity 76.5%; Pred. NO. 0.00075;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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QY      2 LLKEFTVSGNILTIRLT 18
        :||:|||||:| ||||
Db     122 VLKDFTVSGNLLFIRLT 138
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RESULT 5
US-09-359-503-10
; Sequence 10, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958

```

; INFORMATION FOR SEQ ID NO: 10:
;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 18 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
US-09-359-503-10

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Query Match . 67.9%; Score.57; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	1	VLLKEFTVSGNI	12
Db	7	VLLKEFTVSGNI	18

RESULT 6
 US-09-359-503-13
 ; Sequence 13, Application US/09359503
 ; Patent No. 6251603
 ; GENERAL INFORMATION:
 ; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old,
 ; APPLICANT: Knuth, alexander
 ; TITLE OF INVENTION: Method for Determining Status
 ; TITLE OF INVENTION: Cancerous Condition By Determ
 ; TITLE OF INVENTION: a Patient Sample
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fulbright & Jaworski, L.L.P.
 ; STREET: 666 Fifth Avenue
 ; CITY: New York City
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10103
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
 ; COMPUTER: IBM
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: WordPerfect
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/359,503
 ; FILING DATE: July 23, 1999
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/165,546
 ; FILING DATE: October 2, 1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/062,422
 ; FILING DATE: April 17, 1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/937,263
 ; FILING DATE: September 15, 1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/752,182
 ; FILING DATE: 03-October-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hanson, No. 6251603man D.
 ; REGISTRATION NUMBER: 30,946
 ; REFERENCE/DOCKET NUMBER: LUD 5466.1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 318-3000
 ; TELEFAX: (212) 752-5958
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 18 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ;
 US-09-359-503-13

Query Match 66.7% Score 56; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0018;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TVSGNLTIRLT 18
|||||
Db 1 TVSGNLTIRLT 12

RESULT 7
US-08-791-495-5
; Sequence 5, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-5

Query Match 58.3%; Score 49; DB 2; Length 210;
Best Local Similarity 75.0%; Pred. No. 0.5;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLKEFTVSGNIL 13
:|||||
Db 122 VLKDFTVSGNLL 133

RESULT 8
US-08-118-270-22
; Sequence 22, Application US/08118270
; Patent No. 5508384
; GENERAL INFORMATION:
; APPLICANT: Murphy, Randall B.
; APPLICANT: Schuster, David I.
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300

; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/118,270
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 334 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-118-270-22

Query Match 45.2%; Score 38; DB 1; Length 334;
Best Local Similarity 57.1%; Pred. No. 66;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 LLKEFTVSGNLT 15
|: ||| ||:|
Db 10 LIMLFTVFGNVLVI 23

RESULT 9
PCT-US93-08528-22
; Sequence 22, Application PC/TUS9308528
; GENERAL INFORMATION:
; APPLICANT: New York University
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08528
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
; TELECOMMUNICATION INFORMATION:

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;
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 334 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US93-08528-22
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Query Match 45.2%; Score 38; DB 5; Length 334;
Best Local Similarity 57.1%; Pred. No. 66;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
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QY 2 LLKEFTVSGNLT 15
I: ||| ||:|
Db 10 LIMLFTVFGNVLVI 23
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RESULT 10
US-09-404-390-6
; Sequence 6, Application US/09404390A
; Patent No. 6359196
; GENERAL INFORMATION:
; APPLICANT: LOK, FINN
; APPLICANT: OLSEN, OLE
; APPLICANT: MEIJER, PER-JOHAN
; APPLICANT: CAMERON-MILLS, VERENA
; TITLE OF INVENTION: GERMINATION-SPECIFIC PLANT PROMOTERS
; FILE REFERENCE: 11225.8US02
; CURRENT APPLICATION NUMBER: US/09/404,390A
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Hordeum vulgare
US-09-404-390-6
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Query Match 44.0%; Score 37; DB 4; Length 142;
Best Local Similarity 50.0%; Pred. No. 36;
Matches 10; Conservative 5; Mismatches 3; Indels 2; Gaps 1;
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QY 1 VLLKEFTVSGNI--LTIRLT 18
I ||: ||:| :|||:|
Db 88 VKLKKQTVAGTMYVITIRVT 107
```

```
RESULT 11
US-08-985-335-5
; Sequence 5, Application US/08985335
; Patent No. 6080847
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,335
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0421 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 469 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: OVARUTUT01
; CLONE: 815087
; US-08-985-335-5
```

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Query Match 44.0%; Score 37; DB 3; Length 469;
Best Local Similarity 58.3%; Pred. No. 1.5e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 VLLKEFTVSGNI 12
:||||: ||:|
Db 333 MLLKEYLLSGDI 344
```

```
RESULT 12
US-08-985-335-9
; Sequence 9, Application US/08985335
; Patent No. 6080847
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,335
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
```

;; REFERENCE/DOCKET NUMBER: PF-0421 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650-855-0555
;; TELEFAX: 650-845-4166
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 469 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: GenBank
;; CLONE: 1384078
US-08-985-335-9

Query Match 44.0%; Score 37; DB 3; Length 469;
Best Local Similarity 58.3%; Pred. No. 1.5e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNI 12
:||||: |||:
Db 333 MLLKEYLLSGDI 344

RESULT 13
US-09-410-372-5
; Sequence 5, Application US/09410372
; Patent No. 6281334
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/410,372
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/985,335
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0421 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 469 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: OVERTUT01
; CLONE: 815087
US-09-410-372-5

Query Match 44.0%; Score 37; DB 4; Length 469;
Best Local Similarity 58.3%; Pred. No. 1.5e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNI 12
:||||: |||:
Db 333 MLLKEYLLSGDI 344

RESULT 14
US-09-410-372-9
; Sequence 9, Application US/09410372
; Patent No. 6281334
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/410,372
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/985,335
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0421 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 469 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1384078
US-09-410-372-9

Query Match 44.0%; Score 37; DB 4; Length 469;
Best Local Similarity 58.3%; Pred. No. 1.5e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNI 12
:||||: |||:
Db 333 MLLKEYLLSGDI 344

RESULT 15
US-08-185-232A-2
; Sequence 2, Application US/08185232A


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; Patent No. 5576205
; GENERAL INFORMATION:
; APPLICANT: KAMBOJ, Rajender
; APPLICANT: NUTT, Stephen
; APPLICANT: SHEKTER, Lee
; APPLICANT: WOSNICK, Michael
; TITLE OF INVENTION: KAINATE-BINDING HUMAN CNS RECEPTORS OF
; TITLE OF INVENTION: THE EAAL FAMILY
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K. Street, N.W. Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,232A
; FILING DATE: 24-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/750,090
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16777/150 ALLE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 956 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-185-232A-2

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Query Match 44.0%; Score 37; DB 1; Length 956;
Best Local Similarity 37.5%; Pred. NO. 3.3e+02;
Matches 6; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

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QY      2 LLKEFTVSGNILTIRL 17
        ||::| :| : |::|:
Db     178 LLRQFLISKDTLSVRM 193
```

Search completed: July 3, 2002, 11:09:46
Job time: 268 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:10:54 ; Search time 61.47 Seconds
(without alignments)
28.137 Million cell updates/sec

Title: US-09-165-546A-10
Perfect score: 92
Sequence: 1 PLPVPGVLLKEFTVSGNI 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	47	51.1	134	2	AH1877	hypothetical prote
2	46	50.0	345	1	QRSEUC	nucleotide-binding
3	46	50.0	349	2	AB0360	iron(III)-transpor
4	46	50.0	1048	2	H64459	hypothetical prote
5	46	50.0	2248	1	D42088	adenylate cyclase
6	45	48.9	172	2	S71273	blue copper-bindin
7	44	47.8	241	2	S74620	hypothetical prote
8	43.5	47.3	292	2	JC4741	mosquitocidal toxi
9	43	46.7	394	2	A75303	UDP-glucose 4-epim
10	42	45.7	102	2	G71025	hypothetical prote
11	42	45.7	128	2	H65171	hypothetical trans
12	42	45.7	349	2	T43920	yfuc protein [impo
13	42	45.7	1899	2	T32732	PAM C-terminal int
14	42	45.7	1919	2	T42098	PAM interacting pr
15	41.5	45.1	449	2	E75394	hypothetical prote
16	41	44.6	175	1	B69088	conserved hypothet
17	41	44.6	244	2	JC2379	cell-specific heli
18	41	44.6	248	2	G69111	conserved hypothet
19	41	44.6	259	2	AF2012	hypothetical prote
20	41	44.6	356	2	JC6558	outer membrane pro
21	41	44.6	483	1	VCBP13	minor coat protein
22	41	44.6	545	2	H83079	hypothetical prote
23	41	44.6	560	1	DOCGPO	NAD+--diphthamide
24	41	44.6	560	1	DOCGA	NAD+--diphthamide
25	41	44.6	679	2	T20713	hypothetical prote
26	41	44.6	1034	2	S50917	aminomethyltransfe
27	40.5	44.0	242	2	AD1952	lysine [imported]
28	40.5	44.0	836	2	T46070	hypothetical prote
29	40	43.5	166	2	C98266	phosphoribosylamin

30	40	43.5	166	2	AF3018	hypothetical prote
31	40	43.5	190	2	A69302	hypothetical prote
32	40	43.5	238	2	I40703	outer membrane pro
33	40	43.5	238	2	I62385	outer membrane pro
34	40	43.5	240	2	I62394	outer membrane pro
35	40	43.5	241	2	I62391	outer membrane pro
36	40	43.5	241	2	I62387	outer membrane pro
37	40	43.5	243	2	I84531	outer membrane pro
38	40	43.5	243	2	I62388	outer membrane pro
39	40	43.5	243	2	I62386	outer membrane pro
40	40	43.5	244	2	I62389	outer membrane pro
41	40	43.5	244	2	I62393	outer membrane pro
42	40	43.5	346	1	MMECA	outer membrane pro
43	40	43.5	346	2	A90759	outer membrane pro
44	40	43.5	346	2	G85622	outer membrane pro
45	40	43.5	350	1	MMEBAT	outer membrane pro

ALIGNMENTS

RESULT 1

AH1877 hypothetical protein all0569 [imported] - Anabaena sp. (strain PCC 7120)

C:Species: Anabaena sp.

A;Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002

C;Accession: AH1877

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu
Nakazaki, N.; Shimp, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AH1877

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-134 <KUR>

A;Cross-references: GB:BA000019; PIDN:BA072527.1; PID:g17129914; GSPDB:GN00179

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: all0569

C;Superfamily: conserved hypothetical protein slr2059; ferredoxin 2[4Fe-4S] homology

Query Match	51.1%;	Score 47;	DB 2;	Length 134;
Best Local Similarity	58.8%;	Pred. No. 1.4;		
Matches	10;	Conservative	2;	Mismatches 5; Indels 0; Gaps 0;
QY	2	LPVPGVLLKEFTVSGNI 18		
Db	16	MPVTYVLAKEFNVAANI 32		

RESULT 2

QRSEUC

nucleotide-binding protein sfuC - Serratia marcescens

C:Species: Serratia marcescens

C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999

C;Accession: C35108

R;Angerer, A.; Gaisser, S.; Braun, V.

J. Bacteriol. 172, 572-578, 1990

A;Title: Nucleotide sequences of the sfuA, sfuB, and sfuC genes of Serratia marcescen

A;Reference number: A35108; MUID:90130288

A;Accession: C35108

A;Molecule type: DNA

A;Residues: 1-345 <ANG>

A;Cross-references: GB:M33815; NID:g152859; PIDN:AAA26575.1; PID:g152862

C;Comment: This protein is the nucleotide-binding protein component of the binding pr
oss the outer membrane.

C;Genetics:

A;Gene: sfuC

C;Superfamily: inner membrane protein malk; ATP-binding cassette homology

C;Keywords: ATP; binding protein-dependent transport system; inner membrane; nucleoti

Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 PVPGVLLKEFTVSGN 17
|:|:| |:|:| |
Db 20 PMPGVTAKKYTVGEN 34

RESULT 7
S74620
hypothetical protein sl11032 - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C:Accession: S74620
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A:Reference number: S74322; MUID:97061201
A:Accession: S74620
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-241 <KAN>
A:Cross-references: EMBL:D90900; GB:AB001339; NID:gl651768; PIDN:BAA16772.1; PID:d101750
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 47.8%; Score 44; DB 2; Length 241;
Best Local Similarity 56.2%; Pred. No. 9.1;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 PVPGVLLKEFTVSGNI 18
|:|:| |:|:| |
Db 5 PVHSVSLSEYFVSGNV 20

RESULT 8
JC4741
mosquitocidal toxin Mtx2 precursor - Bacillus sphaericus
C:Species: Bacillus sphaericus
C:Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 15-Oct-1999
C:Accession: JC4741
R:Thanabalu, T.; Porter, A.G.
Gene 170, 85-89, 1996
A:Title: A Bacillus sphaericus gene encoding a novel type of mosquitocidal toxin of 31.8
A:Reference number: JC4741; MUID:96200861
A:Accession: JC4741
A:Molecule type: DNA
A:Residues: 1-292 <THA>
A:Cross-references: GB:U19898; NID:gl345085; PIDN:AAC44105.1; PID:gl345086
A:Experimental source: strain SSII-1
C:Comment: This protein is a mosquitocidal toxin. It is toxin to the larvae of Culex qui
C:Genetics:
A:Gene: mtx2
C:Keywords: toxin
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-292/Product: mosquitocidal toxin Mtx2 #status predicted <MAT>

Query Match 47.3%; Score 43.5; DB 2; Length 292;
Best Local Similarity 36.0%; Pred. No. 14;
Matches 9; Conservative 5; Mismatches 4; Indels 7; Gaps 1;

QY 1 PLPVP-----GVLLKEFTVSGNI 18
|:|:| |:|:| |
Db 183 PIPVPPHTKTRTDVYLNQVSIsgNV 207

RESULT 9
A75303
UDP-glucose 4-epimerase - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: A75303
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: A75303
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-394 <WHI>
A:Cross-references: GB:AE002053; GB:AE000513; NID:g6459999; PIDN:AAF11751.1; PID:g646
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR2202
A:Map position: 1
C:Superfamily: Escherichia coli UDPglucose 4-epimerase; UDPglucose 4-epimerase homolo

Query Match 46.7%; Score 43; DB 2; Length 394;
Best Local Similarity 61.5%; Pred. No. 23;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFT 13
|:|:| |:|:| |
Db 337 PLPLAGPLLRST 349

RESULT 10
G71025
hypothetical protein PH1499 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C:Accession: G71025
R:Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophili
A:Reference number: A71000; MUID:98344137
A:Accession: G71025
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-102 <KAW>
A:Cross-references: GB:AP000006; NID:g3236133; PIDN:BAA30607.1; PID:g3257924
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBa
C:Genetics:
A:Gene: PH1499
C:Superfamily: Pyrococcus horikoshii hypothetical protein PH1499

Query Match 45.7%; Score 42; DB 2; Length 102;
Best Local Similarity 41.2%; Pred. No. 7.6;
Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 LPVPGVLLKEFTVSGNI 18
|:|:| |:|:| |
Db 6 LPIPGSLISSNLSGTL 22

RESULT 11
H65171
hypothetical transcription regulator ibpA-gyrB intergenic region - Escherichia coli (
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999
C:Accession: H65171
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: H65171

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-128 <BLAT>
A:Cross-references: GB:AE000446; GB:U00096; NID:g2367261; PIDN:AAC76718.1; PID:g2367264;
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: yidW

Query Match 45.7%; Score 42; DB 2; Length 128;
Best Local Similarity 50.0%; Pred. No. 9.9;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
||| | :|| | ||
Db 27 PLPAEAEICEEFATSRNI 44

RESULT 12
T43920
Yfuc protein [imported] - Yersinia enterocolitica
C:Species: Yersinia enterocolitica
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 04-Mar-2000
C:Accession: T43920
R:Saken, E.M.; Rakin, A.V.; Heesemann, J.
submitted to the EMBL Data Library, November 1999
A:Description: Molecular characterization of a novel siderophore-independent iron transp
A:Reference number: Z22724
A:Accession: T43920
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-349 <SAK>
A:Cross-references: EMBL:Z47200; PIDN:CAA87396.1
A:Experimental source: strain WA-314
C:Genetics:
A:Gene: yfuc
C:Superfamily: inner membrane protein malk; ATP-binding cassette homology
C:Keywords: iron transport

Query Match 45.7%; Score 42; DB 2; Length 349;
Best Local Similarity 47.1%; Pred. No. 30;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 LPVPGVLLKEFTVSGNI 18
:| | | || :|||
Db 84 VPQDGALEFPHTAAGNI 100

RESULT 13
T32732
PAM C-terminal interactor protein, clone P-CIP10a - rat
N:Alternate names: Kalirin protein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 07-Dec-1999
C:Accession: T32732
R:Alam, M.R.; Johnson, R.C.; Darlington, D.N.; Hand, T.A.; Mains, R.E.; Eipper, B.A.
J. Biol. Chem. 272, 12667-12675, 1997
A>Title: Kalirin, a cytosolic protein with spectrin-like and GDP/GTP exchange factor-li
ssing enzyme.
A:Reference number: Z21214; MUID:97284746
A:Accession: T32732
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-1899 <ALA>
A:Cross-references: EMBL:U88157; NID:g2317897; PID:g2317898; PIDN:AAB66367.1
C:Genetics:
A:Gene: Kalirin
C:Function:
A:Description: may serve as part of a signal transduction system
A>Note: interacts with the cytosolic routing determinants of peptidylglycine -amidating

Query Match 45.7%; Score 42; DB 2; Length 1899;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 PGVLLKEFTVSGNI 18
||:| || : |||
Db 1293 PGILNKEHIIFGNI 1306

RESULT 14
T42098
PAM interacting protein P-CIP10, splice-form b - rat
N:Alternate names: kalirin
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 07-Dec-1999
C:Accession: T42098
R:Alam, M.R.; Johnson, R.C.; Darlington, D.N.; Hand, T.A.; Mains, R.E.; Eipper, B.A.
J. Biol. Chem. 272, 12667-12675, 1997
A>Title: Kalirin, a cytosolic protein with spectrin-like and GDP/GTP exchange factor-
ssing enzyme.
A:Reference number: Z21214; MUID:97284746
A:Accession: T42098
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-1919 <ALA>
A:Cross-references: EMBL:U88156; NID:g2317895; PID:g2317896; PIDN:AAB66366.1
C:Function:
A:Description: may be involved in a signal transduction system linking the catalytic
ransduction pathways
A>Note: interacts with the COOH-terminal domain of peptidylglycine alpha-amidating mo
C:Keywords: alternative splicing; signal transduction

Query Match 45.7%; Score 42; DB 2; Length 1919;
Best Local Similarity 57.1%; Pred. No. 2.1e+02;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 PGVLLKEFTVSGNI 18
||:| || : |||
Db 1313 PGILNKEHIIFGNI 1326

RESULT 15
E75394
hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C:Accession: E75394
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J
, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A>Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: E75394
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-449 <WHI>
A:Cross-references: GB:AE001989; GB:AE000513; NID:g6459202; PIDN:AAF11023.1; PID:g645
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1447
A:Map position: 1
C:Superfamily: Deinococcus radiodurans hypothetical protein DR1447

Query Match 45.1%; Score 41.5; DB 2; Length 449;
Best Local Similarity 50.0%; Pred. No. 49;
Matches 8; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

QY 3 PVPGVLLKEFTVSGNI 18
|:| | ||| |:
Db 106 PIPGA---NFTVQGNV 118

Search completed: July 3, 2002, 11:10:55
Job time: 317 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:24:43 ; Search time 29.65 Seconds
(without alignments)
23.506 Million cell updates/sec

Title: US-09-165-546A-10
Perfect score: 92
Sequence: 1 PLPVPGVLLKEFTVSGNI 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	92	100.0	180	1 CTAG_HUMAN	P78358 homo sapien
2	73	79.3	210	1 LAG1_HUMAN	O75638 homo sapien
3	46	50.0	345	1 SFUC_SERMA	P21410 serratia ma
4	46	50.0	2248	1 CYAL_DROME	P32870 drosophila
5	42	45.7	229	1 DGOR_ECOLI	P31460 escherichia
6	42	45.7	1663	1 HAPP_HUMAN	O60229 homo sapien
7	42	45.7	1919	1 HAPP_RAT	P97924 rattus norv
8	41	44.6	175	1 HES3_MOUSE	Q61657 mus musculu
9	41	44.6	344	1 OMPA_KLEPN	P24017 klebsiella
10	41	44.6	483	1 COA2_BPPF3	P03624 bacterioph
11	41	44.6	560	1 DTX_COROM	P00587 corynepha
12	41	44.6	567	1 DTX_CORBE	P00588 corynepha
13	41	44.6	1034	1 GCSP_YEAST	P49095 saccharomyc
14	41	44.6	1171	1 DPOL_HSVT1	Q9yus3 herpesvirus
15	41	44.6	1171	1 DPOL_HSVT2	Q9yus2 herpesvirus
16	40.5	44.0	130	1 BCCP_STRMU	P29337 streptococc
17	40	43.5	190	1 Y417_ARCFU	O29830 archaeoglob
18	40	43.5	238	1 OMPA_CITFR	P24016 citrobacter
19	40	43.5	241	1 OMPA_ESCBL	Q99124 escherichia
20	40	43.5	243	1 OMPA_ESCFE	P24747 escherichia
21	40	43.5	243	1 OMPA_ESCHE	P24754 escherichia
22	40	43.5	279	1 YADU_SALTY	O87663 salmonella
23	40	43.5	346	1 OMPA_ECOLI	P02934 escherichia
24	40	43.5	350	1 OMPA_ENTAE	P09146 enterobacte
25	40	43.5	350	1 OMPA_SALTY	P02936 salmonella
26	40	43.5	351	1 OMPA_SHIDY	P02935 shigella dy
27	40	43.5	543	1 PUR6_PICME	Q01930 pichia meth
28	40	43.5	547	1 GUN1_BUTFI	P20847 butyrivibri
29	40	43.5	552	1 PUR6_SCHPO	P15567 schizosacch
30	40	43.5	557	1 PUR6_DEBOC	P50504 debaryomyce
31	40	43.5	568	1 PUR6_CANAL	Q92210 candida alb
32	40	43.5	762	1 E13B_TRHA	P53626 trichoderma
33	39	42.4	265	1 IHA_SHEEP	P38440 ovis aries

ALIGNMENTS

RESULT 1

CTAG_HUMAN

ID CTAG_HUMAN STANDARD; PRT; 180 AA.

AC P78358;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Autoimmunogenic cancer/testis antigen NY-ESO-1.

GN CTAG.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97203161; PubMed=9050879;

RA Chen Y.-T., Scanlan M.J., Sahin U., Tuereci O., Gure A.O., Tsang S.,

RA Williamson B., Stockert E., Pfreundschuh M., Old L.J.;

RT "A testicular antigen aberrantly expressed in human cancers detected

RT by autologous antibody screening.";

RL Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Melanoma;

RX MEDLINE=98289662; PubMed=9626360;

RA Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,

RA de Plaen E., Boon T.;

RT "LAGE-1 a new gene with tumor specificity.";

RL Int. J. Cancer 76:903-908(1998).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=98430682; PubMed=9759882;

RA Wang R.-F., Johnston S.L., Zeng G., Topalian S.L.,

RA Schwartzentruber D.J., Rosenberg S.A.;

RT "A breast and melanoma-shared tumor antigen: T cell responses to

RT antigenic peptides translated from different open reading frames.";

RL J. Immunol. 161:3596-3606(1998).

CC -!- TISSUE SPECIFICITY: EXPRESSED IN TESTIS AND OVARY AND IN A WIDE

CC VARIETY OF CANCERS. DETECTED IN UTERINE MYOMETRIUM.

CC -!- SIMILARITY: STRONG, TO LAGE-1.

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CC -----

CC EMBL; U87459; AAB49693.1; -.

DR EMBL; AJ003149; CAA05908.1; -.

DR EMBL; AF038567; AAD05202.1; -.

DR MIM; 300156; -.

KW Transmembrane; Antigen.

FT DOMAIN 5 82

FT TRANSMEM 156 172

GLY-RICH.

POTENTIAL.

DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CA2+/calmodulin-responsive adenylate cyclase (EC 4.6.1.1) (ATP
DE pyrophosphate-lyase) (Rutabaga protein).
GN RUT.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CANTON-S; TISSUE=Head;
RX MEDLINE=92154664; PubMed=1739965;
RA Levin L.R., Han P.-L., Hwang P.M., Feinstein P.G., Davis R.L.,
RA Reed R.R.;
RT "The Drosophila learning and memory gene rutabaga encodes a
RT Ca2+/Calmodulin-responsive adenylyl cyclase.";
RL Cell 68:479-489(1992).
CC -!- FUNCTION: THIS A MEMBRANE-BOUND, CALMODULIN-SENSITIVE ADENYLYL
CC CYCLASE. INACTIVATION OF THIS CYCLASE LEADS TO A LEARNING AND
CC MEMORY DEFECT.
CC -!- CATALYTIC ACTIVITY: ATP = 3',5'-cyclic AMP + diphosphate.
CC -!- ENZYME REGULATION: ACTIVATED BY CA(2+)/CALMODULIN AND G PROTEIN.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: MUSHROOM BODIES OF THE FLY BRAIN.
CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
CC FAMILY.
CC -----
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CC -----
DR EMBL; M81887; AAA28844.1; -.
DR PIR; D42088; D42088.
DR HSSP; P19754; LAWK.
DR FlyBase; FBgn0003301; rut.
DR InterPro; IPR001054; Guanylt_cyclase.
DR Pfam; PF00211; guanylate_cyc; 2.
DR SMART; SM00044; CYCC; 2.
DR PROSITE; PS00452; GUANYLATE_CYCLASES_1; 2.
DR PROSITE; PS50125; GUANYLATE_CYCLASES_2; 2.
DR Lyase; CAMP synthesis; Transmembrane; Glycoprotein; Duplication.
KW DOMAIN 1 41 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 42 60 POTENTIAL.
FT TRANSMEM 65 84 POTENTIAL.
FT TRANSMEM 101 115 POTENTIAL.
FT TRANSMEM 122 142 POTENTIAL.
FT TRANSMEM 152 174 POTENTIAL.
FT TRANSMEM 186 206 POTENTIAL.
FT DOMAIN 207 705 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 706 726 POTENTIAL.
FT TRANSMEM 730 750 POTENTIAL.
FT TRANSMEM 770 791 POTENTIAL.
FT DOMAIN 792 813 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 814 834 POTENTIAL.
FT TRANSMEM 842 867 POTENTIAL.
FT TRANSMEM 868 888 POTENTIAL.
FT DOMAIN 889 2248 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 318 334 CATALYTIC (POTENTIAL).
FT DOMAIN 1013 1029 CATALYTIC (POTENTIAL).
FT DOMAIN 515 530 GLY-RICH.
FT DOMAIN 569 602 GLY-RICH.
FT DOMAIN 1278 1297 GLN-RICH.
FT DOMAIN 1767 1810 GLY/SER-RICH.
FT DOMAIN 2025 2040 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 2200 2241 GLN-RICH.
FT CARBOHYD 800 800 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 807 807 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT MUTAGEN 1026 1026 G->R: ABOLISHES CATALYTIC ACTIVITY.
SQ SEQUENCE 2248 AA; 248899 MW; E459C718BE018868 CRC64;

Query Match 50.0%; Score 46; DB 1; Length 2248;
Best Local Similarity 53.3%; Pred. No. 20;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 PVPGVLLKEFTVSGN 17
||| |::||: |
Db 1357 PVPSVMLREFNIEN 1371

RESULT 5
DGOR_ECOLI STANDARD; PRT; 229 AA.
AC P31460; P76735; O32529;
DT 01-JUL-1993 (Rel. 26, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Galactonate operon transcriptional repressor.
GN DGOR OR B3694/B3695.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MGL655;
RX MEDLINE=93315143; PubMed=7686882;
RA Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.;
RT "DNA sequence and analysis of 136 kilobases of the Escherichia coli
RT genome: organizational symmetry around the origin of replication.";
RL Genomics 16:551-561(1993).
RN [2]
RP REVISIONS.
RC STRAIN=K12 / MGL655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP CONCEPTUAL TRANSLATION.
RA Rudd K.E.;
RL Unpublished observations (JUL-1998).
CC -!- FUNCTION: REPRESSOR FOR THE DGORKAT OPERON. BINDS D-GALACTONATE AS
CC AN INDUCER.
CC -!- SIMILARITY: BELONGS TO THE GNTR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
CC -!- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; POTENTIAL FRAMESHIFTS
CC WERE CORRECTED TO PRODUCE THIS ORF.
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CC -----
DR EMBL; L10328; AAA62046.1; ALT_FRAME.
DR EMBL; AE000446; AAC76717.1; ALT_FRAME.
DR EMBL; AE000446; AAC76718.1; ALT_FRAME.
DR EcoGene; EG11718; dgor.
DR InterPro; IPR000524; HTH_Gntr.
DR Pfam; PF00392; gntr; 1.
DR SMART; SM00345; HTH_GNTR; 1.
DR PROSITE; PS00043; HTH_GNTR_FAMILY; 1.
KW Transcription regulation; DNA-binding; Repressor; Complete proteome.
FT DNA_BIND 31 50 H-T-H MOTIF (POTENTIAL).
FT


```
SQ SEQUENCE 229 AA; 25982 MW; BE4172369BB57B94 CRC64;

Query Match 45.7%; Score 42; DB 1; Length 229;
Best Local Similarity 50.0%; Pred. No. 7.6;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
   ||| | : || | ||
Db 27 PLPAEAEELCEEAFATSRNI 44

RESULT 6
HAPP_HUMAN STANDARD; PRT; 1663 AA.
AC O60229;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Huntingtin-associated protein-interacting protein (Duo protein).
GN HAPIP OR DUO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Frontal cortex;
RX MEDLINE=97449175; PubMed=9285789;
RA Colomer V., Engelender S., Sharp A.H., Duan K., Cooper J.K.,
RA Lanahan A., Lyford G., Worley P., Ross C.A.;
RT "Huntingtin-associated protein 1 (HAP1) binds to a Trio-like
RT polypeptide, with a rac1 guanine nucleotide exchange factor domain.";
RL Hum. Mol. Genet. 6:1519-1525(1997).
CC -!- FUNCTION: PROMOTES THE EXCHANGE OF GDP BY GTP (BY SIMILARITY).
CC -!- SUBUNIT: INTERACTS WITH HUNTINGTIN-ASSOCIATED PROTEIN 1 (HAP1).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- TISSUE SPECIFICITY: BRAIN-SPECIFIC. HIGHLY EXPRESSED IN CEREBRAL
CC CORTEX, PUTAMEN, AMYGDALA, HIPPOCAMPUS AND CAUDATE NUCLEUS. WEAKLY
CC EXPRESSED IN BRAIN STEM AND CEREBELLUM.
CC -!- DOMAIN: THE DBL/GEF DOMAIN CATALYZES NUCLEOTIDE EXCHANGE FOR RAC1
CC (BY SIMILARITY).
CC -!- MISCELLANEOUS: CALLED DUO BECAUSE THE ENCODED PROTEIN IS CLOSELY
CC RELATED TO BUT SHORTER THAN TRIO.
CC -!- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY DOMAIN (DH).
CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC -!- SIMILARITY: CONTAINS 4 SPECTRIN REPEATS.
CC -----
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CC -----
DR EMBL; U94190; AAC15791.1; -.
DR MIM; 604605; -.
DR InterPro; IPR001251; CRAL_TRIO.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000219; RhoGEF.
DR InterPro; IPR002017; Spectrin.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RhoGEF; 1.
DR Pfam; PF00435; spectrin; 8.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RhoGEF; 1.
DR SMART; SM00516; SEC14; 1.
DR SMART; SM00150; SPEC; 7.
DR PROSITE; PS00741; DH_1; FALSE_NEG.
DR PROSITE; PS50010; DH_2; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
KW Guanine-nucleotide releasing factor; Repeat.
```

```
FT REPEAT 281 388 SPECTRIN 1.
FT REPEAT 519 606 SPECTRIN 2.
FT REPEAT 861 962 SPECTRIN 3.
FT REPEAT 1101 1203 SPECTRIN 4.
FT DOMAIN 682 687 POLY-GLN.
FT DOMAIN 1281 1456 DH.
FT DOMAIN 1468 1580 PH.
SQ SEQUENCE 1663 AA; 192228 MW; FAE683734C83417C CRC64;

Query Match 45.7%; Score 42; DB 1; Length 1663;
Best Local Similarity 57.1%; Pred. No. 68;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 PGVLLKEFTVSGNI 18
   ||:| || : |||
Db 1320 PGILNKEHIIFGNI 1333

RESULT 7
HAPP_RAT STANDARD; PRT; 1919 AA.
AC P97924; O70135;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Huntingtin-associated protein-interacting protein (DUO protein)
DE (Kalirin) (PAM COOH-terminal interactor protein 10) (P-CIP10).
GN HAPIP OR DUO.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Hippocampus;
RX MEDLINE=97284746; PubMed=9139723;
RA Alam M.R., Johnson R.C., Darlington D.N., Hand T.A., Mains R.E.,
RA Eipper B.A.;
RT "Kalirin, a cytosolic protein with spectrin-like and GDP/GTP exchange
RT factor-like domains that interacts with peptidylglycine alpha-
RT amidating monooxygenase, an integral membrane peptide-processing
RT enzyme.";
RT J. Biol. Chem. 272:12667-12675(1997).
RL [2]
RN [2]
RP SEQUENCE OF 448-1124 FROM N.A.
RC TISSUE=Hippocampus;
RX MEDLINE=97067094; PubMed=8910496;
RA Alam M.R., Caldwell B.D., Johnson R.C., Darlington D.N., Mains R.E.,
RA Eipper B.A.;
RT "Novel proteins that interact with the COOH-terminal cytosolic
RT routing determinants of an integral membrane peptide-processing
RT enzyme.";
RT J. Biol. Chem. 271:28636-28640(1996).
RL [3]
RN [3]
RP SEQUENCE OF 658-1236 FROM N.A.
RC TISSUE=Hippocampus, and Brain cortex;
RX MEDLINE=97449175; PubMed=9285789;
RA Colomer V., Engelender S., Sharp A.H., Duan K., Cooper J.K.,
RA Lanahan A., Lyford G., Worley P., Ross C.A.;
RT "Huntingtin-associated protein 1 (HAP1) binds to a Trio-like
RT polypeptide, with a rac1 guanine nucleotide exchange factor domain.";
RL Hum. Mol. Genet. 6:1519-1525(1997).
CC -!- FUNCTION: PROMOTES THE EXCHANGE OF GDP BY GTP. MAY ACT AS PART OF
CC A SIGNAL TRANSDUCTION SYSTEM LINKING THE CATALYTIC DOMAINS OF PAM
CC IN THE LUMEN OF THE SECRETORY PATHWAY TO CYTOSOLIC FACTORS
CC REGULATING THE CYTOSKELETON AND SIGNAL TRANSDUCTION PATHWAYS.
CC -!- SUBUNIT: INTERACTS WITH THE C-TERMINAL OF PEPTIDYLGLYCINE ALPHA-
CC AMIDATING MONOOXYGENASE (PAM) AND WITH THE HUNTINGTIN-ASSOCIATED
CC PROTEIN 1 (HAP1).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; P-CIP10A AND P-CIP10B (SHOWN
CC HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
```

CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.
CC -!- DOMAIN: THE GEF DOMAIN CATALYZES NUCLEOTIDE EXCHANGE FOR RAC1 (BY
CC SIMILARITY).
CC -!- MISCELLANEOUS: CALLED DUO BECAUSE THE ENCODED PROTEIN IS CLOSELY
CC RELATED TO BUT SHORTER THAN TRIO.
CC -!- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY DOMAIN (DH).
CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC -!- SIMILARITY: CONTAINS 4 SPECTRIN-LIKE DOMAINS.
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CC -----
CC EMBL; U88157; AAB66367.1; -.
CC EMBL; U88156; AAB66366.1; -.
CC EMBL; U94189; AAC15790.1; -.
CC InterPro; IPR001251; CRAL_TRIO.
CC InterPro; IPR001849; PH.
CC InterPro; IPR000219; RhGEF.
CC InterPro; IPR001452; SH3.
CC InterPro; IPR002017; Spectrin.
CC Pfam; PF00169; PH; 1.
CC Pfam; PF00621; RhGEF; 1.
CC Pfam; PF00018; SH3; 1.
CC Pfam; PF00435; spectrin; 7.
CC SMART; SM00233; PH; 1.
CC SMART; SM00325; RhGEF; 1.
CC SMART; SM00516; SEC14; 1.
CC SMART; SM00326; SH3; 1.
CC SMART; SM00150; SPEC; 7.
CC PROSITE; PS00741; DH_1; FALSE_NEG.
CC PROSITE; PS50010; DH_2; 1.
CC PROSITE; PS50003; PH_DOMAIN; 1.
CC PROSITE; PS50002; SH3; 1.
KW Guanine-nucleotide releasing factor; Alternative splicing; Repeat;
KW SH3 domain.
KW DOMAIN 283 1196 4 X SPECTRIN-LIKE REPEATS.
FT REPEAT 283 390 1.
FT REPEAT 521 608 2.
FT REPEAT 863 955 3.
FT REPEAT 1094 1196 4.
FT DOMAIN 1274 1449 DH.
FT DOMAIN 1461 1573 PH.
FT DOMAIN 1639 1704 SH3.
FT VARSPLIC 1 25 MNPEGASEEGGAADSDVDAFFRTG -> MVLSG (IN
FT ISOFORM P-CIPIOA).
FT CONFLICT 943 943 E -> ESLFHATSLQ (IN REF. 3).
SQ SEQUENCE 1919 AA; 218840 MW; E4DBB818E890F453 CRC64;

Query Match 45.7%; Score 42; DB 1; Length 1919;
Best Local Similarity 57.1%; Pred. No. 80;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 PGVLLKEFTVSGNI 18
||:|:|:|:|
Db 1313 PGILNKEHIIFGNI 1326

RESULT 8
HES3_MOUSE
ID HES3_MOUSE STANDARD; PRT; 175 AA.
AC Q61657; O09150; O09083;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Transcription factor HES-3 (Hairy and enhancer of split 3).
GN HES3 OR HES-3.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=94354864; PubMed=8074710;
RA Sakagami T., Sakurada K., Sakai Y., Watanabe T., Nakanishi S.,
RA Kageyama R.;
RT "Structure and chromosomal locus of the mouse gene encoding a
RT cerebellar Purkinje cell-specific helix-loop-helix factor Hes-3.";
RL Biochem. Biophys. Res. Commun. 203:594-601(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RA Kageyama R.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: TRANSCRIPTIONAL REPRESSOR OF GENES THAT REQUIRE A BHLH
CC PROTEIN FOR THEIR TRANSCRIPTION.
CC -!- SUBUNIT: TRANSCRIPTION REPRESSION REQUIRES FORMATION OF A COMPLEX
CC WITH A CO-REPRESSOR PROTEIN (GROUCHO).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DOMAIN: HAS A PARTICULAR TYPE OF BASIC DOMAIN (PRESENCE OF A
CC HELIX-INTERRUPTING PROLINE) THAT BINDS TO THE N-BOX (CACNAG),
CC RATHER THAN THE CANONICAL E-BOX (CANNTG).
CC -!- DOMAIN: THE CARBOXYL-TERMINAL WRPW MOTIF IS A TRANSCRIPTIONAL
CC REPRESSION DOMAIN NECESSARY FOR THE INTERACTION WITH GROUCHO, A
CC TRANSCRIPTIONAL CO-REPRESSOR RECRUITED TO SPECIFIC TARGET DNA BY
CC HAIRY-RELATED PROTEINS.
CC -!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC TRANSCRIPTION FACTORS. "HAIRY" SUBFAMILY.
CC -----

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EMBL; D32200; BAA06899.1; -.
EMBL; D85169; BAA19799.1; -.
DR MGD; MGI:104877; Hes3.
DR InterPro; IPR003015; HLH_Myc.
DR InterPro; IPR001092; HLH_dim.
DR Pfam; PF00010; HLH; 1.
DR SMART; SM00353; HLH; 1.
DR PROSITE; PS00038; HELIX_LOOP_HELIX; 1.
KW Transcription regulation; DNA-binding; Nuclear protein; Repressor.
FT DNA_BIND 1 6 BASIC DOMAIN.
FT DOMAIN 7 50 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
FT DOMAIN 108 167 PRO-RICH.
FT DOMAIN 172 175 WRPW MOTIF (REQUIRED FOR ACTIVITY)
FT (BY SIMILARITY).
SQ SEQUENCE 175 AA; 19294 MW; 43B13B277BC17CB3 CRC64;

Query Match 44.6%; Score 41; DB 1; Length 175;
Best Local Similarity 61.5%; Pred. No. 8.3;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFT 13
||:|:|:|:|
Db 137 PLPLPGGLLESST 149

RESULT 9
OMPA_KLEPN
ID OMPA_KLEPN STANDARD; PRT; 344 AA.
AC P24017; O69435;
DT 01-MAR-1992 (Rel. 21, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Outer membrane protein A precursor (Outer membrane protein II).
GN OMPA.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RV 308;
RX MEDLINE=98192544; PubMed=9524233;
RA Nguyen T.N., Samuelson P., Sterky F., Merle-Poitte C., Robert A.,
RA Baussant T., Haeuw J.F., Uhlen M., Binz H., Stahl S.;
RT "Chromosomal sequencing using a PCR-based biotin-capture method
RT allowed isolation of the complete gene for the outer membrane protein
RT A of Klebsiella pneumoniae.";
RL Gene 210:93-101(1998).
RN [2]
RP SEQUENCE OF 93-335 FROM N.A.
RC STRAIN=LD119;
RX MEDLINE=92065252; PubMed=1955870;
RA Lawrence J.G., Ochman H., Hartl D.L.;
RT "Molecular and evolutionary relationships among enteric bacteria.";
RL J. Gen. Microbiol. 137:1911-1921(1991).
CC -!- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE
CC STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A
CC RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A PORIN
CC WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
CC SOLUTES (BY SIMILARITY).
CC -!- SUBUNIT: MONOMER (PROBABLE).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -!- SIMILARITY: BELONGS TO THE OMPA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AJ000998; CAA04450.1; -.
CC EMBL; M63355; AAA25119.1; -.
CC InterPro; IPR001145; Bac_OmpA.
CC InterPro; IPR000498; OmpA_tmem.
CC Pfam; PF00691; OmpA; 1.
CC Pfam; PF01389; OmpA_membrane; 1.
CC PRINTS; PR01021; OMPADOMAIN.
CC ProDom; PD000930; Bac_OmpA; 1.
CC PROSITE; PS01068; OMPA; 1.
KW Outer membrane; Transmembrane; Phage recognition; Signal; Repeat;
KW Porin.
FT SIGNAL 1 ? POTENTIAL.
FT CHAIN ? 344 OUTER MEMBRANE PROTEIN A.
FT TRANSMEM 15 28 POTENTIAL.
FT TRANSMEM 48 60 POTENTIAL.
FT TRANSMEM 63 78 POTENTIAL.
FT TRANSMEM 90 100 POTENTIAL.
FT TRANSMEM 104 119 POTENTIAL.
FT TRANSMEM 140 151 POTENTIAL.
FT TRANSMEM 157 173 POTENTIAL.
FT TRANSMEM 179 190 POTENTIAL.
FT DOMAIN 199 206 4 X 2 AA TANDEM REPEATS OF A-P.
FT REPEAT 199 200 1.
FT REPEAT 201 202 2.
FT REPEAT 203 204 3.
FT REPEAT 205 206 4.
FT DOMAIN 255 299 OMPA-LIKE.
FT DISULFID 309 321 BY SIMILARITY.
FT CONFLICT 335 335 Y -> I (IN REF. 2).
SQ SEQUENCE 344 AA; 37061 MW; AC88AAE3B7871B16 CRC64;

Query Match 44.6%; Score 41; DB 1; Length 344;
Best Local Similarity 38.9%; Pred. NO. 18;
Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
| | | | | | | | | |
Db 202 PAPAPEVATKHFTLKSDV 219

RESULT 10
COA2_BPPF3
ID COA2_BPPF3 STANDARD; PRT; 483 AA.
AC P03624;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last annotation update)
DE Minor coat protein (ORF 483).
OS Bacteriophage Pf3.
OC Viruses; ssDNA viruses; Inoviridae; Inovirus.
OX NCBI_TaxID=10872;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEW-YORK, AND NIJMEGEN;
RX MEDLINE=85293231; PubMed=3928901;
RA Luiten R.G.M., Putterman D.G., Schoenmakers J.G.G., Konings R.N.H.,
RA Day L.A.;
RT "Nucleotide sequence of the genome of Pf3, an IncP-1 plasmid-specific
RT filamentous bacteriophage of Pseudomonas aeruginosa.";
RL J. Virol. 56:268-276(1985).
CC -!- MISCELLANEOUS: THE STRAIN NIJMEGEN SEQUENCE IS SHOWN.
CC -----
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CC -----
CC EMBL; M11912; AAA88379.1; -.
CC EMBL; M19377; AAA88388.1; -.
CC PIR; A04232; VCBPI3.
KW Coat protein.
FT VARIANT 419 419 L -> F (IN STRAIN NEW-YORK).
SQ SEQUENCE 483 AA; 52197 MW; DCBBAA598BA700BB CRC64;

Query Match 44.6%; Score 41; DB 1; Length 483;
Best Local Similarity 36.0%; Pred. NO. 26;
Matches 9; Conservative 5; Mismatches 1; Indels 10; Gaps 1;

QY 3 PVPG-----VLLKEFTVSGN 17
| | | | | | | | | |
Db 139 PLPGGGSPVLMRPVILNEYTVTGS 163

RESULT 11
DTX_COROM
ID DTX_COROM STANDARD; PRT; 560 AA.
AC P00587;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Diphtheria toxin precursor (DT) (NAD(+)--diphthamide ADP-
DE ribosyltransferase) (EC 2.4.2.36).
DE Corynephage omega.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC Lambda phage group.
OX NCBI_TaxID=10714;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84041471; PubMed=6314249;
RA Ratti G., Rappuoli R., Giannini G.;


```
RT "The complete nucleotide sequence of the gene coding for diphtheria
RT toxin in the corynebacteriophage omega (tox+) genome.";
RL Nucleic Acids Res. 11:6589-6595(1983).
CC -!- CORYNEBACTERIUM DIPHTHERIAE, PRODUCED BY A PHAGE INFECTING
CC ACTIVITY, CATALYZES THE COVALENT ATTACHMENT OF THE ADP RIBOSE
CC MOIETY OF NAD TO ELONGATION FACTOR 2.
CC -!- CATALYTIC ACTIVITY: NAD(+) + peptide diphthamide = nicotinamide +
CC peptide N-(ADP-D-ribosyl)diphthamide.
CC -!- SUBUNIT: HOMODIMER.
CC -----
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CC -----
DR EMBL; V01536; CAA24778.1; -.
DR EMBL; M19546; AAA32181.1; -.
DR PIR; A00728; DOCGPO.
DR HSSP; P00588; LDDT.
DR InterPro; IPR000512; Diphtheria_tox.
DR Pfam; PF02763; Diphtheria_C; 1.
DR Pfam; PF01324; Diphtheria_R; 1.
DR Pfam; PF02764; Diphtheria_T; 1.
DR PRINTS; PR00769; DPTHRIATOXIN.
DR ProDom; PD025441; Diphtheria_tox; 1.
KW Toxin; Transferase; Glycosyltransferase; NAD; Signal.
FT SIGNAL 1 25
FT CHAIN 26 218
FT -----
FT CHAIN 219 560
FT -----
FT ACT_SITE 46 46
FT ACT_SITE 90 90
FT ACT_SITE 173 173
FT DISULFID 211 226
FT DISULFID 486 496
FT SEQUENCE 560 AA; 60814 MW; 51F5718361B94EAB CRC64;

Query Match 44.6%; Score 41; DB 1; Length 560;
Best Local Similarity 50.0%; Pred. No. 30;
Matches 9; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

QY 1 PLPVPGVLLKEFTVSGNI 18
   |||: |||| | : | :
Db 451 PLPIAGVLLP--TIPGKL 466

RESULT 12
DTX_CORBE
ID DTX_CORBE STANDARD; PRT; 567 AA.
AC P00588;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Diphtheria toxin precursor (DT) (NAD(+)-diphthamide ADP-
DE ribosyltransferase) (EC 2.4.2.36).
OS Corynebacteriophage beta.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC Lambda phage group.
OX NCBI_TaxID=10703;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84070728; PubMed=6316330;
RA Greenfield L., Bjorn M.J., Horn G., Fong D., Buck G.A., Collier R.J.,
RA Kaplan D.A.;
RT "Nucleotide sequence of the structural gene for diphtheria toxin
RT carried by corynebacteriophage beta.";
```

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RL Proc. Natl. Acad. Sci. U.S.A. 80:6853-6857(1983).
RN [2]
RP SEQUENCE OF 33-225.
RX MEDLINE=79194138; PubMed=221484;
RA Delange R.J., Williams L.C., Drazin R.E., Collier R.J.;
RT "The amino acid sequence of fragment A, an enzymically active
RT fragment of diphtheria toxin. III. The chymotryptic peptides, the
RT peptides derived by cleavage at tryptophan residues, and the complete
RT sequence of the protein.";
RL J. Biol. Chem. 254:5838-5842(1979).
RN [3]
RP ACTIVE SITE TRP-185.
RX MEDLINE=77134904; PubMed=849463;
RA Michel A., Dirx J.;
RT "Occurrence of tryptophan in the enzymically active site of
RT diphtheria toxin fragment A.";
RL Biochim. Biophys. Acta 491:286-295(1977).
RN [4]
RP ACTIVE SITE TYR-97.
RX MEDLINE=91115874; PubMed=1990001;
RA Papini E., Santucci A., Schiavo G., Domenighini M., Neri P.,
RA Rappuoli R., Montecucco C.;
RT "Tyrosine 65 is photolabeled by 8-azidoadenine and 8-azidoadenosine
RT at the NAD binding site of diphtheria toxin.";
RL J. Biol. Chem. 266:2494-2498(1991).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=92269934; PubMed=1589020;
RA Choe S., Bennett M.J., Fujii G., Curmi P.M.G., Kantardjiev K.A.,
RA Collier R.J., Eisenberg D.;
RT "The crystal structure of diphtheria toxin.";
RL Nature 357:216-222(1992).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=96155972; PubMed=8573568;
RA Bell C.E., Eisenberg D.;
RT "Crystal structure of diphtheria toxin bound to nicotinamide adenine
RT dinucleotide.";
RL Biochemistry 35:1137-1149(1996).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=97164901; PubMed=9012663;
RA Bell C.E., Eisenberg D.;
RT "Crystal structure of nucleotide-free diphtheria toxin.";
RL Biochemistry 36:481-488(1997).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.65 ANGSTROMS) OF COMPLEX WITH RECEPTOR.
RX MEDLINE=98324089; PubMed=9659904;
RA Louie G.V., Yang W., Bowman M.E., Choe S.;
RT "Crystal structure of the complex of diphtheria toxin with an
RT extracellular fragment of its receptor.";
RL Mol. Cell 1:67-78(1997).
CC -!- FUNCTION: DIPHTHERIA TOXIN, PRODUCED BY A PHAGE INFECTING
CC CORYNEBACTERIUM DIPHTHERIAE, IS A PROENZYME THAT, AFTER
CC ACTIVATION, CATALYZES THE COVALENT ATTACHMENT OF THE ADP RIBOSE
CC MOIETY OF NAD TO ELONGATION FACTOR 2.
CC -!- CATALYTIC ACTIVITY: NAD(+) + peptide diphthamide = nicotinamide +
CC peptide N-(ADP-D-ribosyl)diphthamide.
CC -!- SUBUNIT: HOMODIMER.
CC -----
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CC -----
DR EMBL; X00703; CAA25302.1; -.
DR EMBL; K01722; AAA32182.1; ALT_INIT.
DR PIR; A00729; DOCGA.
DR PIR; A05128; A05128.
DR PDB; 1DDT; 31-JUL-94.
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DR PDB; 1MDT; 31-JUL-94.
DR PDB; 1DTP; 01-NOV-94.
DR PDB; 1TOX; 10-JUN-96.
DR PDB; 1SGK; 23-DEC-96.
DR PDB; 1XDT; 25-FEB-98.
DR InterPro; IPR000512; Diphtheria_tox.
DR Pfam; PF02763; Diphtheria_C; 1.
DR Pfam; PF01324; Diphtheria_R; 1.
DR Pfam; PF02764; Diphtheria_T; 1.
DR PRINTS; PR00769; DPTHRIATOXIN.
DR ProDom; PD025441; Diphtheria_tox; 1.
KW Toxin; Transferase; Glycosyltransferase; NAD; Signal; 3D-structure.
FT SIGNAL 1 32
FT CHAIN 33 225
FRAGMENT A (RESPONSIBLE FOR ENZYMATIC
ADP-RIBOSYLATION OF ELONGATION FACTOR 2).
FT CHAIN 226 567
FRAGMENT B (RESPONSIBLE FOR BINDING OF
TOXIN TO CELL RECEPTORS AND ENTRY OF
FRAGMENT A).
FT ACT_SITE 53 53
FT ACT_SITE 97 97
FT ACT_SITE 180 180
FT ACT_SITE 185 185
MODIFICATION INACTIVATES ENZYME; MAY BE
CONCERNED WITH CATALYSIS OR WITH BINDING
OF ELONGATION FACTOR 2.
FT DISULFID 218 233
FT DISULFID 493 503
FT CONFLICT 178 180
FT SEQUENCE 567 AA; 61601 MW; CAF82A75EA693FF8 CRC64;

Query Match 44.6%; Score 41; DB 1; Length 567;
Best Local Similarity 50.0%; Pred. No. 31;
Matches 9; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

QY 1 PLPVPGVLLKKEFTVSGNI 18
|||: |||| | : | :
Db 458 PLPIAGVLLP--TIPGKL 473

RESULT 13
GCSP_YEAST
ID GCSP_YEAST STANDARD; PRT; 1034 AA.
AC P49095;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glycine dehydrogenase [decarboxylating], mitochondrial precursor
DE (EC 1.4.4.2) (Glycine decarboxylase) (Glycine cleavage system P-
protein).
GN GCV2 OR GSD2 OR YMR189W OR YM9646.01.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96120340; PubMed=7498764;
RA Sinclair D.A., Dawes I.W.;
RT "Genetics of the synthesis of serine from glycine and the utilization
of glycine as sole nitrogen source by Saccharomyces cerevisiae.";
RL Genetics 140:1213-1222(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Pearson D., Bowman S., Barrell B.G., Rajandream M.A.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THE GLYCINE CLEAVAGE SYSTEM CATALYSES THE DEGRADATION OF
GLYCINE. THE P PROTEIN BINDS THE ALPHA-AMINO GROUP OF GLYCINE
THROUGH ITS PYRIDOXAL PHOSPHATE COFACTOR; CO(2) IS RELEASED AND
THE REMAINING METHYLAMINE MOIETY IS THEN TRANSFERRED TO THE
LIPOAMIDE COFACTOR OF THE H PROTEIN.
CC -!- CATALYTIC ACTIVITY: Glycine + lipoylprotein = S-
aminomethyldihydrolipoylprotein + CO(2).
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```
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
CC -!- SIMILARITY: TO OTHER GLYCINE CLEAVAGE SYSTEM P-PROTEIN.
CC -----
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CC -----
CC EMBL; U20641; AAB18933.1; -.
CC EMBL; Z47815; CAA87810.1; -.
CC SGD; S0004801; GCV2.
CC InterPro; IPR003437; GDC-P.
CC Pfam; PF02347; GDC-P; 1.
KW Oxidoreductase; Mitochondrion; Pyridoxal phosphate; Transit peptide.
FT TRANSIT 1 ?
FT CHAIN ? 1034 GLYCINE DEHYDROGENASE [DECARBOXYLATING].
FT BINDING 773 773 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 1034 AA; 114451 MW; F4D52642B0BDA041 CRC64;

Query Match 44.6%; Score 41; DB 1; Length 1034;
Best Local Similarity 56.2%; Pred. No. 59;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 PVPGVLLKKEFTVSGNI 18
|||| | : | | | :
Db 920 PVPGTLMIEPTESNL 935

RESULT 14
DPOL_HSVT1
ID DPOL_HSVT1 STANDARD; PRT; 1171 AA.
AC Q9YU53;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA polymerase (EC 2.7.7.7).
GN DPOL.
OS Herpesvirus tupaia (Strain 1) (THV-1).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae.
OX NCBI_TaxID=132677;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99094630; PubMed=9880021;
RA Springfield C., Tidona C.A., Kehm R., Bahr U., Darai G.;
RT "Identification and characterization of the Tupaia herpesvirus DNA
polymerase gene.";
RL J. Gen. Virol. 79:3049-3053(1998).
CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
+ [DNA](N).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
CC -----
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CC -----
CC EMBL; AF074327; AAD08666.1; -.
CC InterPro; IPR002064; DNA_pol_B.
CC Pfam; PF00136; DNA_pol_B; 1.
CC Pfam; PF03104; DNA_pol_B_exo; 1.
CC PRINTS; PR00106; DNAPOLB.
CC SMART; SM00486; POLBc; 1.
CC PROSITE; PS00116; DNA_POLYMERASE_B; 1.
```

KW Transferase; DNA-directed DNA polymerase; DNA replication;
KW DNA-binding; Nuclear protein.
SQ SEQUENCE 1171 AA; 128622 MW; CDC0480FEACFC7EC CRC64;

Query Match 44.6%; Score 41; DB 1; Length 1171;
Best Local Similarity 70.0%; Pred. No. 68;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PVPGVLLKEF 12
|:||||: ||
Db 366 PIPGVLVYEF 375

RESULT 15
DPOL_HSVT2 STANDARD; PRT; 1171 AA.
AC Q9YUS2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA polymerase (EC 2.7.7.7).
GN DPOL.
OS Herpesvirus tupaia (Strain 2) (THV-2).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae.
OX NCBI_TaxID=132678;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99094630; PubMed=9880021;
RA Springfield C., Tidona C.A., Kehm R., Bahr U., Darai G.;
RT "Identification and characterization of the Tupaia herpesvirus DNA
polymerase gene.";
RL J. Gen. Virol. 79:3049-3053(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99319892; PubMed=10392721;
RA Bahr U., Springfield C., Tidona C.A., Darai G.;
RT "Structural organization of a conserved gene cluster of Tupaia
herpesvirus encoding the DNA polymerase, glycoprotein B, a probable
processing and transport protein, and the major DNA binding protein.";
RL Virus Res. 60:123-136(1999).
CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + {DNA}(N).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; AF074328; AAD08667.1; -.
DR EMBL; AF084543; AAD42936.1; -.
DR InterPro; IPR002064; DNA_pol_B.
DR Pfam; PF00136; DNA_pol_B; 1.
DR Pfam; PF03104; DNA_pol_B_exo; 1.
DR PRINTS; PR00106; DNAPOLB.
DR SMART; SM00486; POLBc; 1.
DR PROSITE; PS00116; DNA_POLYMERASE_B; 1.
KW Transferase; DNA-directed DNA polymerase; DNA replication;
KW DNA-binding; Nuclear protein.
SQ SEQUENCE 1171 AA; 128590 MW; D2D64897FD5E7DE8 CRC64;

Query Match 44.6%; Score 41; DB 1; Length 1171;
Best Local Similarity 70.0%; Pred. No. 68;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PVPGVLLKEF 12

Db 366 PIPGVLVYEF 375
|:||||: ||

Search completed: July 3, 2002, 11:24:44
Job time: 891 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:24:07 ; Search time 107.89 Seconds
(without alignments)
28.862 Million cell updates/sec

Title: US-09-165-546A-10
Perfect score: 92
Sequence: 1 PLPVPGVLLKEFTVSGNI 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues 562222
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertibrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archheap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	92	100.0	142	4	Q9NY13	Q9ny13 homo sapien
2	73	79.3	180	4	Q9Y479	Q9y479 homo sapien
3	73	79.3	210	4	Q9BU80	Q9bu80 homo sapien
4	73	79.3	210	4	Q9UJ89	Q9uj89 homo sapien
5	48	52.2	248	2	O68978	O68978 sphingomona
6	48	52.2	323	2	Q47914	Q47914 flavobacter
7	47	51.1	290	4	O95848	O95848 homo sapien
8	46	50.0	373	13	Q90723	Q90723 gallus gall
9	46	50.0	373	13	Q98950	Q98950 gallus gall
10	46	50.0	1048	17	Q58677	Q58677 methanococc
11	46	50.0	2248	5	Q9VY17	Q9vy17 drosophila
12	45	48.9	172	10	Q39131	Q39131 arabidopsis
13	44	47.8	179	16	Q92T95	Q92t95 rhizobium m
14	44	47.8	241	16	P72757	P72757 synecocyst
15	44	47.8	343	5	Q9VSZ4	Q9vsz4 drosophila
16	43.5	47.3	292	2	Q45422	Q45422 bacillus sp

17	43.5	47.3	292	2	Q45470	Q45470 bacillus sp
18	43.5	47.3	292	2	Q45473	Q45473 bacillus sp
19	43.5	47.3	292	2	Q45474	Q45474 bacillus sp
20	43.5	47.3	292	2	Q45475	Q45475 bacillus sp
21	43.5	47.3	292	2	Q45476	Q45476 bacillus sp
22	43	46.7	367	1	Q48924	Q48924 methanosarc
23	43	46.7	394	16	Q9RSC3	Q9rsc3 deinococcus
24	43	46.7	526	2	Q52405	Q52405 pseudomonas
25	42	45.7	102	17	O59168	O59168 pyrococcus
26	42	45.7	349	2	Q56927	Q56927 yersinia en
27	42	45.7	630	10	Q9LSU7	Q9lsu7 arabidopsis
28	42	45.7	994	5	Q9BLN0	Q9bln0 theileria a
29	42	45.7	1013	11	Q9JIH3	Q9jih3 rattus norv
30	42	45.7	1167	5	Q9Y067	Q9y067 theileria a
31	42	45.7	1654	11	Q9JIG0	Q9jig0 rattus norv
32	42	45.7	2376	11	Q9JIF2	Q9jif2 rattus norv
33	42	45.7	2959	11	Q9JIF1	Q9jif1 rattus norv
34	41.5	45.1	250	2	Q9RK82	Q9rk82 streptomyce
35	41.5	45.1	449	16	Q9RUE0	Q9rue0 deinococcus
36	41	44.6	175	17	O27691	O27691 methanother
37	41	44.6	199	11	Q9D7Y6	Q9d7y6 mus musculu
38	41	44.6	200	11	Q9JHC5	Q9jhc5 mus musculu
39	41	44.6	248	17	O27858	O27858 methanother
40	41	44.6	332	10	Q9SH07	Q9sh07 arabidopsis
41	41	44.6	381	16	Q986Y7	Q986y7 rhizobium l
42	41	44.6	457	10	Q94LK1	Q94lk1 oryza sativ
43	41	44.6	472	10	Q9SM43	Q9sm43 spinacia ol
44	41	44.6	535	9	Q9MBL8	Q9mb18 corynephage
45	41	44.6	545	16	Q9HVN7	Q9hvn7 pseudomonas

ALIGNMENTS

RESULT 1
Q9NY13
ID Q9NY13 PRELIMINARY; PRT; 142 AA.
AC Q9NY13;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE HYPOTHETICAL 13.9 KDA PROTEIN (FRAGMENT).
GN LAGE-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lethe B.G.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AJ275978; CAB76945.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 142 AA; 13895 MW; 27EBE922AC4ACC7B CRC64;

Query Match 100.0%; Score 92; DB 4; Length 142;
Best Local Similarity 100.0%; Pred. NO. 8.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
| | | | | | | | | | | | | | | | | |
Db 89 PLPVPGVLLKEFTVSGNI 106

RESULT 2
Q9Y479
ID Q9Y479 PRELIMINARY; PRT; 180 AA.
AC Q9Y479;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

```
DE LAGE-1S PROTEIN (CANCER/TESTIS ANTIGEN 2).
GN LAGE1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MELANOMA;
RX MEDLINE=99325550; PubMed=10399963;
RA Aarnoudse C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.;
RT "Interleukin-2-induced, melanoma-specific T cells recognize CAMEL, an
RT unexpected translation product of LAGE-1."
RL Int. J. Cancer 82:442-448(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Aradhya S., Bardaro T., Galgoczy P., Yamagata T., Esposito T.,
RA Patlan H., Ciccodicola A., Kenwick S., Platzer M., D'Urso M.,
RA Nelson D.L.;
RT "Multiple pathogenic and benign genomic rearrangements occur at a 35-
RT kb duplication involving the NEMO and the LAGE2 genes.";
RL Hum. Mol. Genet. 0:0-0(2001).
DR EMBL; AJ012834; CAA10194.1; -.
DR EMBL; AF277315; AAL27015.1; -.
SQ SEQUENCE 180 AA; 18236 MW; 9077FAF953543A25 CRC64;

Query Match 79.3%; Score 73; DB 4; Length 180;
Best Local Similarity 72.2%; Pred. No. 0.00018;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
   ||| || :||:|||||:
Db 115 PLPRPGAVLKDFTVSGNL 132

RESULT 3
Q9BU80
ID Q9BU80 PRELIMINARY; PRT; 210 AA.
AC Q9BU80;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CANCER/TESTIS ANTIGEN 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA, CHORIOCARCINOMA;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002833; AAH02833.1; -.
SQ SEQUENCE 210 AA; 21089 MW; 8FB5BF04FB04E8BE CRC64;

Query Match 79.3%; Score 73; DB 4; Length 210;
Best Local Similarity 72.2%; Pred. No. 0.00021;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
   ||| || :||:|||||:
Db 115 PLPRPGAVLKDFTVSGNL 132

RESULT 4
Q9UJ89
ID Q9UJ89 PRELIMINARY; PRT; 210 AA.
AC Q9UJ89;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
```

```
DE LAGE-1L PROTEIN.
GN LAGE-1L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MELANOMA;
RX MEDLINE=99325550; PubMed=10399963;
RA Aarnoudse C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.;
RT "Interleukin-2-induced, melanoma-specific T cells recognize CAMEL, an
RT unexpected translation product of LAGE-1."
RL Int. J. Cancer 82:442-448(1999).
DR EMBL; AJ012835; CAA10196.1; -.
SQ SEQUENCE 210 AA; 21060 MW; 1DD0B1829735B60A CRC64;

Query Match 79.3%; Score 73; DB 4; Length 210;
Best Local Similarity 72.2%; Pred. No. 0.00021;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
   ||| || :||:|||||:
Db 115 PLPRPGAVLKDFTVSGNL 132

RESULT 5
O68978
ID O68978 PRELIMINARY; PRT; 248 AA.
AC O68978;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PENTACHLOROPHENOL 4-MONOXYGENASE REDUCTASE (FRAGMENT).
GN PCPD.
OS Sphingomonas sp. UG30.
OC Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
OC Sphingomonas.
OX NCBI_TaxID=76070;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG30;
RX MEDLINE=99237251; PubMed=10220902;
RA Leung K.T., Campbell S., Gan Y., White D.C., Lee H., Trevors J.T.;
RT "The role of the Sphingomonas species UG30 pentachlorophenol-4-
RT monooxygenase in p-nitrophenol degradation.";
RL FEMS Microbiol. Lett. 173:247-253(1999).
DR EMBL; AF059680; AAC15880.1; -.
DR HSSP; P33164; 2PIA.
DR InterPro; IPR001834; Cyt_B5_reductase.
DR InterPro; IPR001433; Oxidored_FAD.
DR InterPro; IPR000951; Phdiox_reductase.
DR InterPro; IPR001221; Phe_hydroxylase.
DR Pfam; PF00970; FAD_binding_6; 1.
DR Pfam; PF00175; NAD_binding; 1.
DR PRINTS; PR00409; PHDIOXRDTASE.
DR PRINTS; PR00410; PHEHYDRXLASE.
KW Monooxygenase.
FT NON_TER 248 248
SQ SEQUENCE 248 AA; 27111 MW; 200F44B5C125AEDE CRC64;

Query Match 52.2%; Score 48; DB 2; Length 248;
Best Local Similarity 56.2%; Pred. No. 4.6;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 PVPGVLLKEFTVSGNI 18
   | |||:| ||| :|
Db 29 PEPGVILPEFTAGAH 44

RESULT 6
```

Q47914 ID Q47914 PRELIMINARY; PRT; 323 AA.
AC Q47914;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PENTACHLOROPHENOL 4-MONOOXYGENASE REDUCTASE.
GN PCPD.
OS Flavobacterium sp. (strain ATCC 39723).
OC Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
OC Sphingobium.
OX NCBI_TaxID=46429;
RN [1]
RP SEQUENCE FROM N.A.
RA Lange C.C., Orser C.S.;
RT "Molecular analysis of pentachlorophenol degradation by Flavobacterium
RT sp. strain ATCC 39723.";
RL Thesis (1994), Microbiology, Molecular Biology and Biochemistry.,
CC -!- COFACTOR: BINDS A 2FE-2S CLUSTER (BY SIMILARITY).
DR EMBL; U12290; AAA68938.1; -.
DR HSSP; P33164; 2PIA.
DR InterPro; IPR000564; 2Fe2S_ferredoxin.
DR InterPro; IPR001834; Cyt_B5_reductase.
DR InterPro; IPR001041; Ferredoxin.
DR InterPro; IPR001433; Oxidored_FAD.
DR InterPro; IPR000951; Phdiox_reductase.
DR Pfam; PF00970; FAD_binding_6; 1.
DR Pfam; PF00111; fer2; 1.
DR Pfam; PF00175; NAD_binding; 1.
DR PRINTS; PR00409; PHDIOXRDTASE.
DR PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
KW Iron-sulfur; Monooxygenase.
SQ SEQUENCE 323 AA; 35187 MW; DCA5758E26BBAF2 CRC64;

Query Match 52.2%; Score 48; DB 2; Length 323;
Best Local Similarity 56.2%; Pred. No. 6.1;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 PVPGVLLKEFTVSGNI 18
I :|||:| ||| :|
Db 29 PEPGVLPETAGAH 44

RESULT 7
O95848 ID O95848 PRELIMINARY; PRT; 290 AA.
AC O95848;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 31.5 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20130121; PubMed=10662552;
RA Deng Y., Madan A., Banta A., Friedman C., Trask B., Hood L., Li L.;
RT "Characterization, Chromosomal Localization, and the Complete 30-kb
RT DNA Sequence of the Human Jagged2 (JAG2) Gene.";
RL Genomics 63:133-138(2000).
DR EMBL; AF111170; AAD15563.1; -.
DR InterPro; IPR000086; NUDIX_hydrolase.
DR Pfam; PF00293; NUDIX; 1.
KW Hypothetical protein.
SQ SEQUENCE 290 AA; 31520 MW; 835D48C3460771EC CRC64;

Query Match 51.1%; Score 47; DB 4; Length 290;
Best Local Similarity 81.8%; Pred. No. 8;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKE 11
| :|||:| ||| :|
Db 6 PLPVPGLLLLE 16

RESULT 8
Q90723 ID Q90723 PRELIMINARY; PRT; 373 AA.
AC Q90723;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GROWTH FACTOR CVG1.
GN CVG1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WHITE LEGHORN;
RA Shah S.B., Hume C.R., Dodd J.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; U55871; AAB01194.1; -.
DR HSSP; P12643; 3BMP.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR001839; TGF-beta.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR ProDom; PD000357; TGF-beta; 1.
DR SMART; SM00204; TGFB; 1.
DR PROSITE; PS00250; TGF_BETA; 1.
KW Glycoprotein.
SQ SEQUENCE 373 AA; 41405 MW; E2ACFCCCD3A4C8B5 CRC64;

Query Match 50.0%; Score 46; DB 13; Length 373;
Best Local Similarity 30.0%; Pred. No. 16;
Matches 12; Conservative 3; Mismatches 3; Indels 22; Gaps 1;

Qy 1 PLPVPGVL-----LKEFTVSGNI 18
| :|||:| ||| :|
Db 50 PIPVPSVLWRIFQKRSPATNRDPVDGCRVEEFNVPNGI 89

RESULT 9
Q98950 ID Q98950 PRELIMINARY; PRT; 373 AA.
AC Q98950;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CVG1 PROTEIN.
GN CVG1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97147815; PubMed=8939612;
RA Seleiro E.A., Connolly D.J., Cooke J.;
RT "Early developmental expression and experimental axis determination by
RT the chicken Vgl gene.";
RL Curr. Biol. 6:1476-1486(1996).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; U73003; AAC60038.1; -.

Query Match 50.0%; Score 46; DB 13; Length 373;
Best Local Similarity 30.0%; Pred. No. 16;
Matches 12; Conservative 3; Mismatches 3; Indels 22; Gaps 1;

DR HSSP; P12643; 3BMP.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR001839; TGF-beta.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR ProDom; PD000357; TGF-beta; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA; 1.
KW Glycoprotein.
SQ SEQUENCE 373 AA; 41503 MW; 9FADC8212145602E CRC64;

Query Match 50.0%; Score 46; DB 13; Length 373;
Best Local Similarity 30.0%; Pred. No. 16;
Matches 12; Conservative 3; Mismatches 3; Indels 22; Gaps 1;

QY 1 PLPVPGL-----LKEFTVSGNI 18
|:|||||
Db 50 PIPVPSVLWIRIFQKRSPATNRDPVDCRVEFNVPGNI 89
:|||||

RESULT 10
Q58677
ID Q58677 PRELIMINARY; PRT; 1048 AA.
AC Q58677;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE HYPOTHETICAL PROTEIN MJ1281.
GN MJ1281.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP REVISIONS.
RC STRAIN=DSM 2661;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii.";
RL Science 273:1058-1073(1996).
DR EMBL; U67568; AAB99287.1; -.
DR TIGR; MJ1281; -.
KW Hypothetical protein; Complete proteome.
FT DOMAIN 598 601 POLY-GLU.
SQ SEQUENCE 1048 AA; 121014 MW; 14138CFDCE6A8A76 CRC64;

Query Match 50.0%; Score 46; DB 17; Length 1048;
Best Local Similarity 56.2%; Pred. No. 47;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 PVPGVLLKEFTVSGNI 18
| | | :||| :|||
Db 827 PFPVQIKEFFENGNI 842

RESULT 11
Q9VY17
ID Q9VY17 PRELIMINARY; PRT; 2248 AA.
AC Q9VY17; Q9TWA7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE RUT PROTEIN (ADENYLYL CYCLASE HOMOLOG CLONE AC-12F).
GN RUT OR CG9533.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foslter A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE OF 1075-1110 FROM N.A.
RX MEDLINE=92154664; PubMed=1739965;
RA Levin L.R., Han P.L., Hwang P.M., Feinstein P.G., Davis R.L.,
RA Reed R.R.;
RT "The Drosophila learning and memory gene rutabaga encodes a
Ca2+/Calmodulin-responsive adenylyl cyclase.";
RL Cell 68:479-489(1992).

DR EMBL; AE003497; AAF48388.1; -.
DR HSSP; P19754; 1AWK.
DR FlyBase; FBgn0003301; rut.
DR InterPro; IPR001054; Guanylt_cyclase.
DR Pfam; PF00211; guanylate_cyc; 2.
DR SMART; SM00044; CYCC; 2.
DR PROSITE; PS00452; GUANYLATE_CYCLASES_1; 2.
DR PROSITE; PS0125; GUANYLATE_CYCLASES_2; 2.
KW Lyase.
SQ SEQUENCE 2248 AA; 248823 MW; F7E6B4656A2D073C CRC64;

Query Match 50.0%; Score 46; DB 5; Length 2248;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 PVPGVLLKEFTVSGN 17
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Db 1356 VPFSVMLREFNIEN 1370

RESULT 12
Q39131 PRELIMINARY; PRT; 172 AA.
AC Q39131;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE LAMIN (AT5G15350/F8M21_240).
GN F8M21_240.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Willis G.;
RL Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Nersissian A.M., Valentine J.S.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
RA Rudd S., Lemcke K., Mayer K.F.X.;
RL Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,
RA Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis cDNA clones."
RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; X97023; CAA65750.1; -.
DR EMBL; U77721; AAC32930.1; -.
DR EMBL; AL353993; CAB89345.1; -.
DR EMBL; AF424627; AAL11620.1; -.
DR HSSP; P00303; 2CBP.
DR InterPro; IPR003245; Cu_bind_like.
DR Pfam; PF02298; Cu_bind_like; 1.
DR ProDom; PD003122; Cu_bind_like; 1.
KW Hypothetical protein.

SQ SEQUENCE 172 AA; 19435 MW; 4BD9B88FF0A4AE06 CRC64;

Query Match 48.9%; Score 45; DB 10; Length 172;
Best Local Similarity 53.3%; Pred. No. 10;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 PVPGVLLKEFTVSGN 17
||||| |::||| |
Db 20 PMPGVTAKKTVGEN 34

RESULT 13
Q92T95 PRELIMINARY; PRT; 179 AA.
AC Q92T95;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL TRANSMEMBRANE PROTEIN SMC02591.
GN SMC02591.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21368234; PubMed=11474104;
RA Galibert F., Finan T.M., Long S.R., Puehler A., Abola P., Ampe F.,
RA Barloy-Hubler F., Barnett M.J., Becker A., Boistard P., Bothe G.,
RA Boutry M., Bowser L., Buhrmester J., Cadieu E., Capela D., Chain P.,
RA Cowie A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F.,
RA Gloux S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M.,
RA Hernandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D.,
RA Kahn M.L., Kalman S., Keating D.H., Kiss E., Komp C., Lelaure V.,
RA Masuy D., Palm C., Peck M.C., Pohl T.M., Portetelle D., Purnelle B.,
RA Ramsperger U., Surzycki R., Thebault P., Vandenbol M.,
RA Vorhoelter F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J.;
RT "The composite genome of the legume symbiont Sinorhizobium meliloti."
RL Science 293:668-672(2001).
DR EMBL; AL591782; CAC41459.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 179 AA; 19154 MW; 5BCAF074259DF31B CRC64;

Query Match 47.8%; Score 44; DB 16; Length 179;
Best Local Similarity 72.7%; Pred. No. 16;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKE 11
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Db 115 PLPLPGRLLRE 125

RESULT 14
P72757 PRELIMINARY; PRT; 241 AA.
AC P72757;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE HYPOTHETICAL 25.1 KDA PROTEIN.
GN CCMN OR SLL1032.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirose M., Sugiyama M., Sugiyama S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,

RA Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
DR EMBL; D90900; BAA16772.1; -;
DR InterPro; IPR001451; Hexapep_transf.
DR Pfam; PF00132; hexapep; 3.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 241 AA; 25057 MW; 2555A88B4EB8B9D4 CRC64;

Query Match 47.8%; Score 44; DB 16; Length 241;
Best Local Similarity 56.2%; Pred. No. 21;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 PVPGVLLKEFTVSGNI 18
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Db 5 PVHSVSLSEYFVSGNV 20

RESULT 15
Q9VSZ4
ID Q9VSZ4 PRELIMINARY; PRT; 343 AA.
AC Q9VSZ4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE CG3437 PROTEIN.
GN CG3437.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abiril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu P., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Styrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003552; AAF50264.1; -;
DR FlyBase; FBgn0035998; CG3437.
SQ SEQUENCE 343 AA; 40044 MW; 261F026B93975169 CRC64;

Query Match 47.8%; Score 44; DB 5; Length 343;
Best Local Similarity 81.8%; Pred. NO. 31;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PGVLLKEFTVS 15
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Db 39 PGVLVKEFTRS 49

Search completed: July 3, 2002, 11:24:08
Job time: 915 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:08:49 ; Search time 136.43 Seconds
(without alignments)
14.655 Million cell updates/sec

Title: US-09-165-546A-10
Perfect score: 92
Sequence: 1 PLPVPGVLLKEFTVSGNI 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	100.0	18	AAU01541	HLA-DR53 recognisi
2	92	100.0	18	AAB69941	Human NY-ESO-1 HLA
3	92	100.0	25	AAE07718	Human NY ESO-1 MHC
4	92	100.0	27	AAE07717	Human NY ESO-1 MHC
5	92	100.0	180	AAW69665	Human NY-ESO-1 pro
6	92	100.0	180	AAW62584	Cancer associated
7	92	100.0	180	AAW05965	Human cancer antig
8	92	100.0	180	AAB03154	Human oesophageal
9	92	100.0	180	AAW70862	Human tumour antig
10	92	100.0	180	AAW52430	Human tumour antig
11	92	100.0	180	AAG67164	Amino acid sequenc

12	92	100.0	180	22	AAE07714	Human NY ESO-1 pro
13	92	100.0	180	22	AAU01535	Human NY-ESO-1 tum
14	92	100.0	180	22	AAB69946	Human NY-ESO-1 pro
15	92	100.0	397	22	AAE13122	NY-ESO-1C-HER-2 me
16	85	92.4	20	22	AAE07729	Human NY ESO-1 MHC
17	82	89.1	16	22	AAE07779	Human NY ESO-1 pep
18	82	89.1	17	22	AAE07753	Human NY ESO-1 pep
19	82	89.1	20	22	AAE07746	Human ESO p111-130
20	81.5	88.6	19	21	AAW52437	Human tumour antig
21	80	87.0	16	22	AAE07754	Human NY ESO-1 rel
22	76	82.6	17	22	AAE07719	Human NY ESO-1 MHC
23	75	81.5	15	22	AAE07721	Human NY ESO-1 MHC
24	75	81.5	15	22	AAE07780	Human NY ESO-1 pep
25	73	79.3	180	19	AAW69664	Human LAGE-1 clone
26	73	79.3	180	21	AAW70860	Human LAGE-1 splic
27	73	79.3	210	19	AAW69663	Human LAGE-1 clone
28	73	79.3	210	21	AAW70861	Human LAGE-1 unspl
29	72	78.3	16	22	AAE07720	Human NY ESO-1 MHC
30	71	77.2	14	22	AAE07722	Human NY ESO-1 MHC
31	71	77.2	14	22	AAE07781	Human NY ESO-1 pep
32	68	73.9	15	22	AAE07748	Human NY ESO-1 pep
33	64	69.6	13	22	AAE07723	Human NY ESO-1 MHC
34	64	69.6	13	22	AAE07782	Human NY ESO-1 pep
35	63	68.5	14	22	AAE07749	Human NY ESO-1 pep
36	60	65.2	12	22	AAE07724	Human NY ESO-1 MHC
37	60	65.2	12	22	AAE07783	Human NY ESO-1 pep
38	57	62.0	13	22	AAE07750	Human NY ESO-1 pep
39	57	62.0	18	22	AAE07769	Human NY ESO-1 HLA
40	57	62.0	18	22	AAU01540	HLA-DR53 recognisi
41	57	62.0	18	22	AAB69940	Human NY-ESO-1 HLA
42	53	57.6	11	22	AAE07725	Human NY ESO-1 MHC
43	53	57.6	11	22	AAE07784	Human NY ESO-1 pep
44	53	57.6	15	22	AAE07726	Human NY ESO-1 MHC
45	53	57.6	15	22	AAE07786	Human NY ESO-1 pep

ALIGNMENTS

RESULT 1
AAU01541
ID AAU01541 standard; Peptide; 18 AA.
XX
AC AAU01541;
XX
DT 18-JUL-2001 (first entry)
XX
DE HLA-DR53 recognising NY-ESO-1 peptide #3.
XX
KW NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
KW human leukocyte antigen-determining region; disease progression;
KW disease regression; disease onset; body tissue; body fluid; enzyme label;
KW radioactive label; monoclonal antibody.
OS Homo sapiens.
XX
PN WO200123560-A2.
XX
PD 05-APR-2001.
XX
PF 26-SEP-2000; 2000WO-US26411.
XX
PR 29-SEP-1999; 99US-0408036.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Tureci O, Sahin U, Pfreundschuh M;
XX
DR WPI; 2001-266156/27.
XX
PT Polypeptides binding to major histocompatibility complex class II human
PT leukocyte antigen-determining region molecule having amino acid

PT sequence found in tumour rejection antigen precursor used for
PT stimulating proliferation of helper T cells -
PS Example 13; Page 19; 62pp; English.
XX
CC The sequence represents a human NY-ESO-1 tumour rejection antigen
CC precursor fragment which recognises and binds to HLA-DR53. NY-ESO-1 and
CC SSX-2 polypeptides, or fragments of, bind to major histocompatibility
CC complex (MHC) Class II molecules such as human leukocyte
CC antigen-determining region (HLA-DR) molecules and stimulate proliferation
CC of helper T cells. The peptides can be administered to an HLA-DR positive
CC subject in order to stimulate the helper T cells. An MHC Class II
CC HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell or
CC present in free form is useful for this stimulation. The nucleic acid is
CC useful for screening for a cancerous condition, which involves contacting
CC a subject sample to a cell line transfected with the immunoreactive cell
CC (helper T cell), where interaction is indicative of cancer. In addition,
CC a sample from a patient (for example, a body fluid or tissue) can be
CC monitored for the amount of the complex present in the bloodstream. This
CC is useful for determining regression, progression or onset of a cancerous
CC condition. The method involves contacting the sample with a radioactive
CC labelled or enzyme labelled monoclonal antibody which specifically binds
CC with the complex.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 92; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
| | | | | | | | | | | | | | | |
Db 1 plpvpgvllkeftvsgni 18

RESULT 2
AAB69941
ID AAB69941 standard; Peptide; 18 AA.
XX
AC AAB69941;
XX
DT 27-APR-2001 (first entry)
XX
DE Human NY-ESO-1 HLA-DR53 binding motif #3.
XX
KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW non-small cell lung carcinoma; tumour status determination.
XX
OS Homo sapiens.
XX
PN WO200107917-A1.
XX
PD 01-FEB-2001.
XX
PF 14-JUL-2000; 2000WO-US19220.
XX
PR 23-JUL-1999; 99US-0359503.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.
XX
PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
XX
DR WPI; 2001-182822/18.
XX
PT Method useful for determining the status (e.g. progression, regression
PT or stability of the disease) of a cancerous condition, involves
PT determining the levels of NY-ESO-1 specific antibodies in a sample
PT taken from a patient -
XX

PS Example 16; Page 27; 50pp; English.
XX
CC The present sequence is given in a specification relating to a method
CC for determining the status of a cancerous condition in a patient
CC with a tumour that expresses NY-ESO-1. The method comprises assaying a
CC sample taken from the patient for antibodies that specifically bind to
CC the NY-ESO-1 and comparing the value obtained to a prior value obtained
CC from assay of a prior sample taken from the patient. Any difference
CC between the values is indicative of a change in status of the cancerous
CC condition. The method is useful for determining whether a cancerous
CC condition is progressing, regressing or remaining stable, in particular
CC in patients receiving treatment for a melanoma, adenocarcinoma,
CC non-small cell lung carcinoma or bladder carcinoma.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 92; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
| | | | | | | | | | | | | | | |
Db 1 plpvpgvllkeftvsgni 18

RESULT 3
AAE07718
ID AAE07718 standard; peptide; 25 AA.
XX
AC AAE07718;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human NY ESO-1 MHC class II restricted T cell epitope #4.
XX
KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.
XX
OS Homo sapiens.
XX
PN WO200155393-A2.
XX
PD 02-AUG-2001.
XX
PF 26-JAN-2001; 2001WO-US02765.
XX
PR 28-JAN-2000; 2000US-0179004.
PR 29-SEP-2000; 2000US-0237107.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang R, Rosenberg SA, Zeng G;
XX
DR WPI; 2001-496851/54.
XX
PT New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -
XX
PS Claim 4; Page 16; 134pp; English.
XX
CC The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and

CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or hapten and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is MHC
CC class II restricted T cell epitope of human NY ESO-1 protein.
XX
SQ Sequence 25 AA;

Query Match 100.0%; Score 92; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
Db 3 plpvpgvllkeftvsgni 20
|||||

RESULT 4
AAE07717
ID AAE07717 standard; peptide; 27 AA.
XX
AC AAE07717;
XX

DT 06-NOV-2001 (first entry)
XX

DE Human NY ESO-1 MHC class II restricted T cell epitope #3.
XX

KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.
XX

OS Homo sapiens.
XX

PN WO200155393-A2.
XX

PD 02-AUG-2001.
XX

PF 26-JAN-2001; 2001WO-US02765.
XX

PR 28-JAN-2000; 2000US-0179004.
XX

PR 29-SEP-2000; 2000US-0237107.
XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX

PI Wang R, Rosenberg SA, Zeng G;
XX

PI WPI; 2001-496851/54.
XX

DR New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
XX useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -
PT
XX

PS Claim 4; Page 15; 134pp; English.
XX

CC The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also

CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or hapten and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is MHC
CC class II restricted T cell epitope of human NY ESO-1 protein.
XX
SQ Sequence 27 AA;

Query Match 100.0%; Score 92; DB 22; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.5e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
Db 5 plpvpgvllkeftvsgni 22
|||||

RESULT 5
AAW69665
ID AAW69665 standard; Protein; 180 AA.
XX
AC AAW69665;
XX

DT 27-OCT-1998 (first entry)
XX

DE Human NY-ESO-1 protein sequence, formerly known as LL-1.2 clone.
XX

KW Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour.
XX

OS Homo sapiens.
XX

PN WO9832855-A1.
XX

PD 30-JUL-1998.
XX

PF 27-JAN-1998; 98WO-US01445.
XX

PR 27-JAN-1997; 97US-0791495.
XX

PA (LUDW-) LUDWIG INST CANCER RES.
XX

PI Boon-Falleur T, De Smet C, Godelaine D, Lethe B;
PI Lucas S;
XX

DR WPI; 1998-427951/36.
XX

DR N-PSDB; AAV50348.
XX

PT New isolated LAGE-1 tumour associated nucleic acids - used to
PT develop products for the diagnosis and treatment of LAGE-1
PT associated disorders, particularly tumours
XX

PS Example 2; Page 57-58; 73pp; English.
XX

CC The present sequence represents human NY-ESO-1, formerly known as LL-1.2
CC clone, which is used in an example from the present invention which
CC describes LAGE-1 tumour associated protein (TAP). The present invention
CC also describes: (1) a method for treating a subject with a disorder
CC characterised by expression of a LAGE-1 nucleic acid molecule or an
CC expression product, comprising administering to the subject autologous
CC cytolytic T cells to ameliorate the disorder, where the cytolytic T
CC cells are specific for complexes of an HLA molecule and a LAGE-1 TAP or
CC an immunogenic fragment; (2) a method for treating a subject with a
CC disorder characterised by expression of a LAGE-1 nucleic acid molecule
CC or an expression product, comprising administering a LAGE-1 TAP or an
CC immunogenic fragment to ameliorate the disorder; and (3) a method for
CC selectively enriching a population of T cells with cytolytic T cells
CC specific for a LAGE-1 TAP comprising contacting an isolated population
CC of T cells with an agent presenting a complex of a LAGE TAP or an
CC immunogenic fragment and a HLA presenting molecule to selectively
CC enrich the isolated population of T cells with the cytolytic T cells.
CC The methods and products from the present invention can be used for the
CC diagnosis and treatment of LAGE-1 associated disorders, particularly

CC ovarian, pancreatic and thyroid cancers. Melanoma is treated by
CC inducing cancer-specific T cells in vitro for subsequent return to
CC a patient.
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 92; DB 20; Length 180;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
Db 115 plpvpgvllkeftvsgni 132

RESULT 8
AAB03154
ID AAB03154 standard; Protein; 180 AA.
XX
AC AAB03154;
DT 23-OCT-2000 (first entry)
XX
DE Human oesophageal cancer-associated antigen NY-ESO-1.
XX
KW Oesophageal cancer associated antigen; NY-ESO-1; human;
KW immunogen; oesophageal carcinoma; melanoma; ovary; testis;
KW transmembrane domain; antibody; diagnostic marker; drug delivery target.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 7
FT Modified-site 9 /note= "Potential N-myristoylation site"
FT Modified-site 11 /note= "Potential N-myristoylation site"
FT Modified-site 98 /note= "Potential O-phosphorylation site"
FT Modified-site 134 /note= "Potential O-phosphorylation site"
FT Modified-site 138 /note= "Potential O-phosphorylation site"
FT Domain /note= "Potential O-phosphorylation site"
FT /note= "Potential transmembrane domain"
XX
PN US6069233-A.
XX
PD 30-MAY-2000.
XX
PF 26-JAN-1998; 98US-0013150.
XX
PR 03-OCT-1996; 96US-0725381.
XX
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Scanlan M, Gure AO, Chen Y, Tureci O, Sahin U, Pfreundschuh M;
PI Old LJ;
XX
DR WPI; 2000-410880/35.
DR N-PSDB; AAA61483.
XX
PT New isolated esophageal cancer-associated antigen useful as markers for
PT producing antibodies and as targets for identifying abnormal
PT conditions, e.g. infections and cancer -
XX
PS Example 5; Fig 3; 9pp; English.
XX
CC This sequence represents a human oesophageal cancer-associated antigen,

CC NY-ESO-1. The cDNA encoding this sequence was isolated from a
CC cDNA library prepared from a specimen of well-to-moderately
CC differentiated squamous cell cancer of the oesophagus. Expression
CC analysis demonstrated that NY-ESO-1 was expressed in oesophageal
CC carcinoma, certain melanoma cell lines and in normal ovary and testis
CC tissue, but not in normal colon, kidney, liver or brain tissue. Analysis
CC of the amino acid sequence of the protein indicates that the protein has
CC a transmembrane domain, several N-myristoylation sites and
CC O-phosphorylation sites and that it contains antigenic sequences in the
CC N-terminal half of the protein. The antigen is useful as an immunogen
CC when combined with an adjuvant, in both precursor and post-
CC translationally modified forms, and may be used to generate anti-NY-ESO-1
CC antibodies. It can also be used as a diagnostic marker for oesophageal
CC cancer, and can be utilised as a marker for the targetted delivery of
CC therapeutic agents to oesophageal cancer cells. It can also be used to
CC generate diagnostic or therapeutic agents.
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 92; DB 21; Length 180;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
Db 115 plpvpgvllkeftvsgni 132

RESULT 9
AAY70862
ID AAY70862 standard; Protein; 180 AA.
XX
AC AAY70862;
DT 31-JUL-2000 (first entry)
XX
DE Human tumour antigen, NY-ESO-1 protein.
XX
KW NY-ESO-1; CAMEL; CTL-recognised Antigen on MELanoma; human; cancer; CTL;
KW cytotoxic T lymphocyte; tumour-associated antigen; LAGE-1; anticancer;
KW melanoma; immunotherapy; immune response.
XX
OS Homo sapiens.
XX
PN WO200023584-A1.
XX
PD 27-APR-2000.
XX
PF 15-OCT-1999; 99WO-EP07832.
XX
PR 16-OCT-1998; 98EP-0119583.
XX
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
PA (UYHO-) UNIV HOSPITAL LEIDEN.
XX
PI Schrier PI, Aarnoudse CA, Heider K, Klade C;
XX
DR WPI; 2000-339685/29.
DR N-PSDB; AAD00152.
XX
PT Tumor-associated antigen useful for cancer immunotherapy is encoded by
PT the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA -
XX
PS Example 3; Page 62-63; 73pp; English.
XX
CC The present sequence is the human NY-ESO-1 protein, a tumour antigen,
CC identified by screening an esophagus carcinoma cDNA library. This protein
CC is derived from open reading frame (ORF)-1 that contain epitopes of
CC tumour specific T-cells. NY-ESO-1 is expressed in different tumour types,
CC but not in healthy tissues except in testis. It also shows homology with
CC the CAMEL (Cytotoxic T lymphocytes (CTL)-recognised Antigen on MELanoma)
CC protein, a tumour-associated antigen. The tumour-associated antigen

CC displayed on melanoma cells is recognised by cytotoxic T lymphocytes.
CC This sequence has anticancer activity. CAMEL tumour antigen and
CC immunogenic peptides derived from it are useful for cancer immunotherapy.
CC They have the potential to induce an immune response, by eliciting a
CC CTL response. The DNA molecule is used for the construction of
CC recombinant or fusion proteins.
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 92; DB 21; Length 180;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
| | | | | | | | | | | | | | | | | |
Db 115 plpvpgvllkeftvsgni 132

RESULT 10
AAY52430
ID AAY52430 standard; Protein; 180 AA.
XX
AC AAY52430;
XX
DT 15-FEB-2000 (first entry)
XX
DE Human tumour antigen NY-ESO-1.
XX
KW Cancer; tumour; antigen; MHC; major histocompatibility complex;
KW T-cell; cytotoxic; helper; stimulation; proliferation; treatment;
KW diagnosis; prevention; melanoma; breast cancer; ovarian cancer;
KW prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer;
KW lymphoma.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 44..53
FT /note= "Peptide presented by MHC Class I HLA-B7"
FT Peptide 60..68
FT /note= "Peptide presented by MHC Class I HLA-B7"
FT Peptide 60..69
FT /note= "Peptide presented by MHC Class I HLA-B7"
FT Peptide 63..72
FT /note= "Peptide presented by MHC Class I HLA-B7"
FT Peptide 79..87
FT /note= "Peptide presented by MHC Class I HLA-B7, HLA-B8
FT and HLA-B35"
FT Peptide 79..88
FT /note= "Peptide presented by MHC Class I HLA-B7"
FT Peptide 82..90
FT /note= "Peptide presented by MHC Class I HLA-A1"
FT Peptide 82..91
FT /note= "Peptide presented by MHC Class I HLA-A1"
FT Peptide 83..91
FT /note= "Peptide presented by MHC Class I HLA-B44"
FT Peptide 84..92
FT /note= "Peptide presented by MHC Class I HLA-B7, HLA-B8
FT and HLA-B35"
FT Peptide 87..96
FT /note= "Peptide presented by MHC Class I HLA-A1"
FT Peptide 88..96
FT /note= "Peptide presented by MHC Class I HLA-B44"
FT Peptide 96..104
FT /note= "Peptide presented by MHC Class I HLA-B7"
FT Peptide 100..108
FT /note= "Peptide presented by MHC Class I HLA-B44"
FT Peptide 102..110
FT /note= "Peptide presented by MHC Class I HLA-B44"
FT Peptide 107..116
FT /note= "Peptide presented by MHC Class I HLA-A24"
FT Peptide 110..118

FT Peptide /note= "Peptide presented by MHC Class I HLA-B52"
FT 113..121
FT /note= "Peptide presented by MHC Class I HLA-B7"
FT 113..122
FT /note= "Peptide presented by MHC Class I HLA-B7 and
FT HLA-B52"
FT 115..124
FT /note= "Peptide presented by MHC Class I HLA-A3"
FT 118..126
FT /note= "Peptide presented by MHC Class I HLA-B35"
FT 124..133
FT /note= "Peptide presented by MHC Class I HLA-B52"
FT 125..133
FT /note= "Peptide presented by MHC Class I HLA-A24"
FT 138..147
FT /note= "Peptide presented by MHC Class I HLA-B8"
FT 139..147
FT /note= "Peptide presented by MHC Class I HLA-B7"
FT 145..153
FT /note= "Peptide presented by MHC Class I HLA-A24 and
FT HLA-B52"
FT 153..162
FT /note= "Peptide presented by MHC Class I HLA-B52"
FT 154..162
FT /note= "Peptide presented by MHC Class I HLA-B52"
FT 154..163
FT /note= "Peptide presented by MHC Class I HLA-B52"
FT 156..167
FT /note= "Peptide (AAY52434) presented by MHC Class I
FT HLA-A2" Peptide 158..166
FT /note= "Peptide presented by MHC Class I HLA-A3"
FT 159..167
FT /note= "Peptide presented by MHC Class I HLA-A3"
FT 162..170
FT /note= "Peptide presented by MHC Class I HLA-B52"
XX
PN WO9953938-A1.
XX
PD 28-OCT-1999.
XX
PF 24-MAR-1999; 99WO-US06875.
XX
PR 17-APR-1998; 98US-0062422.
PR 02-OCT-1998; 98US-0165546.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
PI Gure A, Ritter G;
XX
DR WPI; 2000-038483/03.
DR N-PSDB; AAZ38380.
XX
PT Novel peptides which bind to MHC class I and MHC class II molecules,
PT useful for therapeutic and diagnostic purposes -
XX
PS Claim 30; Fig 3; 49pp; English.
XX
CC This sequence represents a human tumour antigen, NY-ESO-1, the cDNA
CC encoding which was isolated from an oesophagus squamous cell cancer cDNA
CC library. Tissue localisation studies revealed it to be expressed at
CC high levels in normal ovary and testis but not in normal colon, kidney,
CC liver, brain, oesophagus and skin. It was expressed in certain tumours
CC and tumour cell lines with some degree of frequency - these included
CC melanoma specimens and cell lines, and breast and bladder cancer
CC specimens, with expression in other tumour types being sporadic.
CC Peptides derived from NY-ESO-1 are bound by both MHC (major
CC histocompatibility complex) Class I and Class II molecules for
CC presentation to T-cells. Peptides AAY52431-Y52434 bind to Class I HLA-A2
CC molecules, thereby stimulating proliferation of cytotoxic T-cells, while
CC peptides AAY52435-Y52440 bind to Class II HLA-DR53 molecules, stimulating
CC helper T-cell proliferation. The peptides derived from NY-ESO-1 may be
CC used in methods and compositions used for the treatment, diagnosis and

RESULT 13
AAU01535
ID AAU01535 standard; Protein; 180 AA.
XX
AC AAU01535;
XX
DT 18-JUL-2001 (first entry)
XX
DE Human NY-ESO-1 tumour rejection antigen precursor protein.
XX
KW NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
KW human leukocyte antigen-determining region; disease progression;
KW disease regression; disease onset; body tissue; body fluid; enzyme label;
KW radioactive label; monoclonal antibody.
XX
OS Homo sapiens.
XX
FH XX
FT Key Location/Qualifiers
FT Modified-site 7 /note= "Myristoylated"
FT Modified-site 9 /note= "Myristoylated"
FT Modified-site 11 /note= "Phosphorylated"
FT Modified-site 98 /note= "Phosphorylated"
FT Modified-site 134 /note= "Phosphorylated"
FT Modified-site 138 /note= "Phosphorylated"
FT /note= "Phosphorylated"
XX WO200123560-A2.
PN
XX
PD 05-APR-2001.
XX
PF 26-SEP-2000; 2000WO-US26411.
XX
PR 29-SEP-1999; 99US-0408036.
XX (LUDW-) LUDWIG INST CANCER RES.
PA
PI Tureci O, Sahin U, Pfreundschuh M;
XX
DR WPI; 2001-266156/27.
DR N-PSDB; AAS02254.
XX
PT Polypeptides binding to major histocompatibility complex class II human
PT leukocyte antigen-determining region molecule having amino acid
PT sequence found in tumour rejection antigen precursor used for
PT stimulating proliferation of helper T cells -
XX
PS Claim 4; Fig 3; 62pp; English.
XX
CC The sequence represents a human NY-ESO-1 tumour rejection antigen
CC precursor. NY-ESO-1 and SSX-2 polypeptides, or fragments of, bind to
CC major histocompatibility complex (MHC) Class II molecules such as human
CC leukocyte antigen-determining region (HLA-DR) molecules and stimulate
CC proliferation of helper T cells. The peptides can be administered to an
CC HLA-DR positive subject in order to stimulate the helper T cells. An MHC
CC Class II HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell
CC or present in free form is useful for this stimulation. The nucleic acid
CC is useful for screening for a cancerous condition, which involves
CC contacting a subject sample to a cell line transfected with the
CC immunoreactive cell (helper T cell), where interaction is indicative of
CC cancer. In addition, a sample from a patient (for example, a body fluid
CC or tissue) can be monitored for the amount of the complex present in the
CC bloodstream. This is useful for determining regression, progression or
CC onset of a cancerous condition. The method involves contacting the sample
CC with a radioactive labelled or enzyme labelled monoclonal antibody which
CC specifically binds with the complex.
XX

SQ Sequence 180 AA;

Query Match 100.0%; Score 92; DB 22; Length 180;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
Db 115 plpvpgvllkeftvsgni 132
|||||
RESULT 14
AAB69946
ID AAB69946 standard; Protein; 180 AA.
XX
AC AAB69946;
XX
DT 27-APR-2001 (first entry)
XX
DE Human NY-ESO-1 protein.
XX
KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW non-small cell lung carcinoma; tumour status determination.
XX
OS Homo sapiens.
XX
PN WO200107917-A1.
XX
PD 01-FEB-2001.
XX
PF 14-JUL-2000; 2000WO-US19220.
XX
PR 23-JUL-1999; 99US-0359503.
XX (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.
XX
PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
XX
DR WPI; 2001-182822/18.
DR N-PSDB; AAF58634.
XX
PT Method useful for determining the status (e.g. progression, regression
PT or stability of the disease) of a cancerous condition, involves
PT determining the levels of NY-ESO-1 specific antibodies in a sample
PT taken from a patient -
XX
PS Example 5; Fig 3; 50pp; English.
XX
CC The present sequence is human NY-ESO-1 protein. It is provided in a
CC specification relating to a method for determining the status of a
CC cancerous condition in a patient with a tumour that expresses NY-ESO-1.
CC The method comprises assaying a sample taken from the patient for
CC antibodies that specifically bind to the NY-ESO-1 and comparing the
CC value obtained to a prior value obtained from assay of a prior sample
CC taken from the patient. Any difference between the values is indicative
CC of a change in status of the cancerous condition. The method is useful
CC for determining whether a cancerous condition is progressing, regressing
CC or remaining stable, in particular in patients receiving treatment for a
CC melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder
CC carcinoma.
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 92; DB 22; Length 180;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18

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Db      115 plpvpgvllkeftvsgni 132
|||||
RESULT 15
AAE13122
ID      AAE13122 standard; Protein; 397 AA.
XX
AC      AAE13122;
XX
DT      28-JAN-2002 (first entry)
XX
DE      NY-ESO-IC-HER-2 membrane distal intracellular domain fusion protein.
XX
KW      Immunostimulatory fusion protein; IFP; antigen component; therapy;
KW      immunostimulatory component; T-cell mediated immune response; DC;
KW      dendritic cell; colon cancer; breast carcinoma; ovarian cancer;
KW      human; HER-2 membrane distal intracellular domain; NY-ESO-IC;
KW      autoimmunogenic cancer/testis antigen.
XX
OS      Homo sapiens.
XX
PN      WO200174855-A2.
XX
PD      11-OCT-2001.
XX
PF      30-MAR-2001; 2001WO-US10515.
XX
PR      30-MAR-2000; 2000US-193504P.
XX
PA      (DEND-) DENDREON CORP.
XX
PI      Laus R, Vidovic D, Graddis T;
XX
DR      WPI; 2001-662965/76.
DR      N-PSDB; AAD21573.
XX
PT      An immunostimulatory fusion protein comprising the intracellular domain
PT      of HER-2 and an antigen elicits an immune response to the antigen and
PT      is useful for the treatment of associated cancer associated -
XX
PS      Disclosure; Page 54-55; 59pp; English.
XX
CC      The invention relates to immunostimulatory fusion proteins (IFP) and
CC      nucleic acid molecules encoding such proteins. The IFPs comprise a
CC      polypeptide antigen component and an immunostimulatory component derived
CC      from the intracellular domain of HER-2 protein which is effective to
CC      elicit a protective dendritic cell (DC)-induced T-cell mediated cellular
CC      immune response to the antigen. IFP or superactivated dendritic cells
CC      are used to treat cancer e.g. breast carcinoma, ovarian and colon cancer
CC      associated with a particularly antigen. The present sequence is a
CC      fusion protein which comprises human autoimmunogenic
CC      cancer/testis antigen, NY-ESO-IC and mature human HER-2 membrane distal
CC      intracellular domain.
XX
SQ      Sequence 397 AA;
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Query Match 100.0%; Score 92; DB 22; Length 397;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 PLPVPGVLLKEFTVSGNI 18
|||||
Db      115 plpvpgvllkeftvsgni 132
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:21:00 ; Search time 599.92 Seconds
(without alignments)
10.561 Million cell updates/sec

Title: US-09-165-546A-10
Perfect score: 92
Sequence: 1 PLPVPGVLLKEFTVSGNI 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980361 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/2/paa/US07_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US080_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US081_COMB.pep:*

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23: /cgn2_6/ptodata/2/paa/US099_COMB.pep:*

24: /cgn2_6/ptodata/2/paa/US100_COMB.pep:*

25: /cgn2_6/ptodata/2/paa/US101_COMB.pep:*

26: /cgn2_6/ptodata/2/paa/US60_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match	Length DB	ID	Description
1	92	100.0	18	15 US-09-165-546A-10	Sequence 10, Appl
2	92	100.0	18	18 US-09-408-036B-9	Sequence 9, Appli
3	92	100.0	61	19 US-09-529-206-55	Sequence 55, Appl
4	92	100.0	61	19 US-09-529-206A-55	Sequence 55, Appl
5	92	100.0	61	19 US-09-529-206B-55	Sequence 55, Appl
6	92	100.0	122	26 US-60-336-968-17	Sequence 17, Appl
7	92	100.0	180	11 US-08-791-495-9	Sequence 9, Appli

8	92	100.0	180	17	US-09-341-829A-9	Sequence 9, Appli
9	92	100.0	180	17	US-09-392-714-25	Sequence 25, Appl
10	92	100.0	180	19	US-09-529-206-4	Sequence 4, Appli
11	92	100.0	180	19	US-09-529-206A-3	Sequence 3, Appli
12	92	100.0	180	19	US-09-529-206B-3	Sequence 3, Appli
13	92	100.0	180	19	US-09-561-571-3	Sequence 3, Appli
14	92	100.0	180	21	US-09-751-798-8	Sequence 8, Appli
15	92	100.0	180	24	US-10-005-905-3	Sequence 3, Appli
16	92	100.0	180	24	US-10-023-182-8	Sequence 8, Appli
17	92	100.0	180	24	US-10-026-066-3	Sequence 3, Appli
18	92	100.0	180	26	US-60-336-968-11	Sequence 11, Appl
19	92	100.0	397	22	US-09-821-883-27	Sequence 27, Appl
20	73	79.3	180	11	US-08-791-495-7	Sequence 7, Appli
21	73	79.3	180	17	US-09-341-829A-7	Sequence 7, Appli
22	73	79.3	210	11	US-08-791-495-5	Sequence 5, Appli
23	73	79.3	210	17	US-09-341-829A-5	Sequence 5, Appli
24	57	62.0	18	15	US-09-165-546A-9	Sequence 9, Appli
25	57	62.0	18	18	US-09-408-036B-8	Sequence 8, Appli
26	52	56.5	10	19	US-09-529-206-88	Sequence 88, Appl
27	52	56.5	10	19	US-09-529-206A-88	Sequence 88, Appl
28	52	56.5	10	19	US-09-529-206B-88	Sequence 88, Appl
29	47	51.1	392	20	US-09-605-703B-1772	Sequence 1772, Ap
30	47	51.1	392	21	US-09-738-626-4181	Sequence 4181, Ap
31	47	51.1	417	1	PCT-US01-03800A-2300	Sequence 2300, Ap
32	47	51.1	417	1	PCT-US01-04098A-3105	Sequence 3105, Ap
33	47	51.1	1204	1	PCT-US01-04098A-1137	Sequence 1137, Ap
34	47	51.1	1616	26	US-60-230-445-1415	Sequence 1415, Ap
35	46	50.0	192	19	US-09-540-236-3746	Sequence 3746, Ap
36	46	50.0	192	26	US-60-128-476-3087	Sequence 3087, Ap
37	46	50.0	204	26	US-60-324-109-22319	Sequence 22319, A
38	46	50.0	493	26	US-60-146-394-1639	Sequence 1639, Ap
39	46	50.0	523	26	US-60-341-955-4	Sequence 4, Appli
40	46	50.0	547	16	US-09-252-691-9925	Sequence 9925, Ap
41	46	50.0	547	16	US-09-252-691C-9925	Sequence 9925, Ap
42	46	50.0	634	26	US-60-341-955-2	Sequence 2, Appli
43	46	50.0	636	26	US-60-341-955-6	Sequence 6, Appli
44	46	50.0	1575	26	US-60-167-217-20426	Sequence 20426, A
45	46	50.0	1575	26	US-60-173-464-16643	Sequence 16643, A

ALIGNMENTS

RESULT 1

US-09-165-546A-10

; Sequence 10, Application US/09165546A

; GENERAL INFORMATION:

; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao, Canlan, Matt; Gure, Ali, Old, Lloyd, Ritter, Gerd

; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CLASS II MOLECULES, AND USES THEREOF

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FULBRIGHT & JAWORSKI LLP

; STREET: 666 Fifth Avenue

; CITY: New York City

; STATE: New York

; COUNTRY: USA

; ZIP: 10158

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage

; COMPUTER: IBM

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: WordPerfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/165,546A

; FILING DATE: 02-Oct-1998

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/062,422

; FILING DATE: April 17, 1998

; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-165-546A-10

Query Match 100.0%; Score 92; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
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Db 1 PLPVPGVLLKEFTVSGNI 18

RESULT 2
US-09-408-036B-9
; Sequence 9, Application US/09408036B
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Isolated Peptides Which Bind to MHC Class II Molecules and Uses T
; FILE REFERENCE: LUD 5624
; CURRENT APPLICATION NUMBER: US/09/408,036B
; CURRENT FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/165,546
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 9
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-408-036B-9

Query Match 100.0%; Score 92; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
| | | | | | | | | | | | | | | |
Db 1 PLPVPGVLLKEFTVSGNI 18

RESULT 3
US-09-529-206-55
; Sequence 55, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08

; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-55

Query Match 100.0%; Score 92; DB 19; Length 61;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
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Db 39 PLPVPGVLLKEFTVSGNI 56

RESULT 4
US-09-529-206A-55
; Sequence 55, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206A-55

Query Match 100.0%; Score 92; DB 19; Length 61;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
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Db 39 PLPVPGVLLKEFTVSGNI 56

RESULT 5
US-09-529-206B-55
; Sequence 55, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-55

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Query Match      100.0%; Score 92; DB 19; Length 61;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
Db 39 PLPVPGVLLKEFTVSGNI 56

RESULT 6
US-60-336-968-17
; Sequence 17, Application US/60336968
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: CTLIMM.022PR
; CURRENT APPLICATION NUMBER: US/60/336,968
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-336-968-17

Query Match      100.0%; Score 92; DB 26; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
Db 58 PLPVPGVLLKEFTVSGNI 75

RESULT 7
US-08-791-495-9
; Sequence 9, Application US/08791495
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-9

Query Match      100.0%; Score 92; DB 11; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
Db 115 PLPVPGVLLKEFTVSGNI 132

RESULT 8
US-09-341-829A-9
; Sequence 9, Application US/09341829A
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-341-829A-9

Query Match      100.0%; Score 92; DB 17; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
Db 115 PLPVPGVLLKEFTVSGNI 132

RESULT 9
US-09-392-714-25
; Sequence 25, Application US/09392714A
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Gure, Ali O.
; APPLICANT: Williamson, Barbara
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Cancer Associated Antigens and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: L0461/7062
; CURRENT APPLICATION NUMBER: US/09/392,714A
; CURRENT FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: PCT/US98/14679
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 25
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[illegible]

;; APPLICANT: Knuth, Alexander; Old, Lloyd J.
;; TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
;; TITLE OF INVENTION: Associated Proteins, Uses Thereof,
;; TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
;; TITLE OF INVENTION: Binding Peptides Derived Therefrom
;; NUMBER OF SEQUENCES: 8
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fulbright & Jaworski, L.L.P.
;; STREET: 666 Fifth Avenue
;; CITY: New York City
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
;; COMPUTER: IBM
;; OPERATING SYSTEM: PC-DOS
;; SOFTWARE: WordPerfect
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/751,798
;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/062,422
;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/725,182
;; FILING DATE: October 3, 1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hanson, Norman D.
;; REGISTRATION NUMBER: 30,946
;; REFERENCE/DOCKET NUMBER: LUD 5466.3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 318-3168
;; TELEFAX: (212) 752-5958
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 180
;; TYPE: amino acid
;; TOPOLOGY: linear
;; US-09-751-798-8

Query Match 100.0%; Score 92; DB 21; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
| | | | | | | | | | | | | | | | | | | | | |
Db 115 PLPVPGVLLKEFTVSGNI 132

RESULT 15
US-10-005-905-3
; Sequence 3, Application US/10005905
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; TITLE OF INVENTION: EPITOPE SYNCHRONIZATION IN ANTIGEN
; TITLE OF INVENTION: PRESENTING CELLS
; FILE REFERENCE: CTLIMM.021CPI
; CURRENT APPLICATION NUMBER: US/10/005,905
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 09/561,074
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/560,465
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,572
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,571
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US01/13806
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 89

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-005-905-3

Query Match 100.0%; Score 92; DB 24; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
| | | | | | | | | | | | | | | | | | | | | |
Db 115 PLPVPGVLLKEFTVSGNI 132

Search completed: July 3, 2002, 11:21:01
Job time: 888 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:22:11 ; Search time 64.42 Seconds
(without alignments)
28.270 Million cell updates/sec

Title: US-09-165-546A-10
Perfect score: 92
Sequence: 1 PLPVPGVLLKEFTVSGNI 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 308740 seqs, 101176262 residues

Total number of hits satisfying chosen parameters: 308740

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92	100.0	180	1	PCT-US02-13994-30
2	92	100.0	180	5	US-09-807-512-8
3	92	100.0	180	6	US-10-117-937-74
4	73	79.3	180	5	US-09-807-512-4
5	73	79.3	180	6	US-10-117-937-75
6	73	79.3	180	6	US-10-146-473-69
7	73	79.3	210	5	US-09-807-512-6
8	73	79.3	210	6	US-10-117-937-76
9	73	79.3	210	6	US-10-157-031-88
10	52	56.5	10	6	US-10-117-937-183
11	52	56.5	10	6	US-10-117-937-191
12	47	51.1	9	6	US-10-117-937-178
13	47	51.1	10	6	US-10-117-937-179
14	47	51.1	10	6	US-10-117-937-188
15	47	51.1	808	6	US-10-104-047-2654
16	45	48.9	9	6	US-10-117-937-182
17	45	48.9	9	6	US-10-117-937-190
18	45	48.9	629	5	US-09-704-302A-927
19	43.5	47.3	8360	6	US-10-132-134-34
20	43	46.7	9	6	US-10-117-937-187
21	43	46.7	9	6	US-10-117-937-189
22	43	46.7	66	5	US-09-540-209B-5890
23	42	45.7	144	5	US-09-540-209B-9634
24	42	45.7	287	5	US-09-540-209B-9099
25	42	45.7	337	7	US-60-360-039-8700
26	42	45.7	562	7	US-60-360-039-13736

27	42	45.7	627	7	US-60-382-898-135	Sequence 135, App
28	41	44.6	88	5	US-09-540-209B-6861	Sequence 6861, Ap
29	41	44.6	185	6	US-10-104-047-2222	Sequence 2222, Ap
30	41	44.6	344	5	US-09-831-061-2	Sequence 2, Appli
31	41	44.6	344	6	US-10-088-720-2	Sequence 2, Appli
32	41	44.6	452	6	US-10-088-720-4	Sequence 4, Appli
33	41	44.6	679	7	US-60-360-039-5703	Sequence 5703, Ap
34	40.5	44.0	783	7	US-60-360-039-9817	Sequence 9817, Ap
35	40.5	44.0	836	7	US-60-382-898-305	Sequence 305, App
36	40	43.5	8	6	US-10-117-937-180	Sequence 180, App
37	40	43.5	8	6	US-10-117-937-184	Sequence 184, App
38	40	43.5	252	5	US-09-573-655B-721	Sequence 721, App
39	40	43.5	386	7	US-60-360-039-13877	Sequence 13877, A
40	40	43.5	398	7	US-60-360-039-12011	Sequence 12011, A
41	40	43.5	1523	1	PCT-US02-08253-244	Sequence 244, App
42	40	43.5	1523	5	US-09-970-944-29	Sequence 29, Appl
43	40	43.5	1523	6	US-10-006-063A-198	Sequence 198, App
44	40	43.5	1523	6	US-10-006-117A-198	Sequence 198, App
45	40	43.5	1523	6	US-10-006-130A-198	Sequence 198, App

ALIGNMENTS

RESULT 1
PCT-US02-13994-30
; Sequence 30, Application PC/TUS0213994
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research
; APPLICANT: Cornell Research Foundation, Inc.
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd
; APPLICANT: Scanlan, Matthew
; APPLICANT: Stockert, Elisabeth
; TITLE OF INVENTION: COLON CANCER ANTIGEN PANEL
; FILE REFERENCE: L00461/70105WO(JRV)
; CURRENT APPLICATION NUMBER: PCT/US02/13994
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US 09/849,602
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-13994-30

Query Match 100.0%; Score 92; DB 1; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
Db 115 PLPVPGVLLKEFTVSGNI 132

RESULT 2

US-09-807-512-8
; Sequence 8, Application US/09807512
; GENERAL INFORMATION:
; APPLICANT: Schrier, Peter I.
; APPLICANT: Aarnoudse, Corlien
; APPLICANT: Heider, Karl-Heinz
; APPLICANT: Klade, Christoph
; TITLE OF INVENTION: Camel, An Alternative Translation Product of the Tumor
; TITLE OF INVENTION: Antigen-Lage 1
; FILE REFERENCE: 0652.2200000
; CURRENT APPLICATION NUMBER: US/09/807,512
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: PCT/EP99/07832
; PRIOR FILING DATE: 1999-10-15

; PRIOR APPLICATION NUMBER: EP 98119583.7
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-807-512-8

Query Match 100.0%; Score 92; DB 5; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
|||||
Db 115 PLPVPGVLLKEFTVSGNI 132

RESULT 3
US-10-117-937-74
; Sequence 74, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLLMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-74

Query Match 100.0%; Score 92; DB 6; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
|||||
Db 115 PLPVPGVLLKEFTVSGNI 132

RESULT 4
US-09-807-512-4
; Sequence 4, Application US/09807512
; GENERAL INFORMATION:
; APPLICANT: Schrier, Peter I.
; APPLICANT: Aarnoudse, Corlien
; APPLICANT: Heider, Karl-Heinz
; APPLICANT: Klade, Christoph
; TITLE OF INVENTION: Camel, An Alternative Translation Product of the Tumor Antigen-Lage 1
; FILE REFERENCE: 0652.2200000
; CURRENT APPLICATION NUMBER: US/09/807,512
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: PCT/EP99/07832
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: EP 98119583.7

; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-807-512-4

Query Match 79.3%; Score 73; DB 5; Length 180;
Best Local Similarity 72.2%; Pred. No. 0.00031;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
|||||
Db 115 PLPRPGAVLKDFTVSGNL 132

RESULT 5
US-10-117-937-75
; Sequence 75, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLLMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-75

Query Match 79.3%; Score 73; DB 6; Length 180;
Best Local Similarity 72.2%; Pred. No. 0.00031;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
|||||
Db 115 PLPRPGAVLKDFTVSGNL 132

RESULT 6
US-10-146-473-69
; Sequence 69, Application US/10146473
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Gout, Ivan
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Gure, Ali
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd
; TITLE OF INVENTION: Breast Cancer Antigens
; FILE REFERENCE: L00461/70130(JRV)
; CURRENT APPLICATION NUMBER: US/10/146,473
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/291,150
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 82

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 69
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-473-69

Query Match 79.3%; Score 73; DB 6; Length 180;
Best Local Similarity 72.2%; Pred. No. 0.00031;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
||| || :||:|||||:
Db 115 PLPRPGAVLKDFTVSGNL 132

RESULT 7

US-09-807-512-6
; Sequence 6, Application US/09807512
; GENERAL INFORMATION:
; APPLICANT: Schrier, Peter I.
; APPLICANT: Aarnoudse, Corlien
; APPLICANT: Heider, Karl-Heinz
; - APPLICANT: Klage, Christoph
; TITLE OF INVENTION: Camel, An Alternative Translation Product of the Tumor
; TITLE OF INVENTION: Antigen-Lage 1
; FILE REFERENCE: 0652.2200000
; CURRENT APPLICATION NUMBER: US/09/807,512
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: PCT/EP99/07832
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: EP 98119583.7
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-807-512-6

Query Match 79.3%; Score 73; DB 5; Length 210;
Best Local Similarity 72.2%; Pred. No. 0.00036;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
||| || :||:|||||:
Db 115 PLPRPGAVLKDFTVSGNL 132

RESULT 8

US-10-117-937-76
; Sequence 76, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 76
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-76

Query Match 79.3%; Score 73; DB 6; Length 210;
Best Local Similarity 72.2%; Pred. No. 0.00036;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
||| || :||:|||||:
Db 115 PLPRPGAVLKDFTVSGNL 132

RESULT 9

US-10-157-031-88
; Sequence 88, Application US/10157031
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobashev, A. V.
; APPLICANT: Krukovskaya, L. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated sequenc
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157,031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-031-88

Query Match 79.3%; Score 73; DB 6; Length 210;
Best Local Similarity 72.2%; Pred. No. 0.00036;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
||| || :||:|||||:
Db 115 PLPRPGAVLKDFTVSGNL 132

RESULT 10

US-10-117-937-183
; Sequence 183, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 183
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-183

Query Match 56.5%; Score 52; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PVPGVLLKEF 12
| | | | | | | | | |
Db 1 PVPGVLLKEF 10

RESULT 11
US-10-117-937-191
; Sequence 191, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 191
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-191

Query Match 56.5%; Score 52; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PVPGVLLKEF 12
| | | | | | | | | |
Db 1 PVPGVLLKEF 10

RESULT 12
US-10-117-937-178
; Sequence 178, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-117-937-178

Query Match 51.1%; Score 47; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLL 9
| | | | | | | | |
Db 1 PLPVPGVLL 9

RESULT 13
US-10-117-937-179
; Sequence 179, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 179
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-179

Query Match 51.1%; Score 47; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLL 9
| | | | | | | | |
Db 2 PLPVPGVLL 10

RESULT 14
US-10-117-937-188
; Sequence 188, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 188
; LENGTH: 10
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-117-937-188

Query Match 51.1%; Score 47; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VLLKEFTVSG 16
| | | | | | | | | |
Db 1 VLLKEFTVSG 10

RESULT 15
US-10-104-047-2654
; Sequence 2654, Application US/10104047
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2654
; LENGTH: 808
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2654

Query Match 51.1%; Score 47; DB 6; Length 808;
Best Local Similarity 57.1%; Pred. No. 24;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 PVPGVLLKEFTVSG 16
| | | | | | | | | |
Db 50 PVPGLLLREYLYGG 63

Search completed: July 3, 2002, 11:22:12
Job time: 944 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:09:46 ; Search time 49.27 Seconds
(without alignments)
8.923 Million cell updates/sec

Title: US-09-165-546A-10
Perfect score: 92
Sequence: 1 PLPVPGVLLKEFTVSGNI 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				% Query		Description	
Result No.	Score	Match	Length	DB	ID		
1	92	100.0	18	4	US-09-359-503-10	Sequence 10, Appli	
2	92	100.0	180	2	US-08-791-495-9	Sequence 9, Appli	
3	92	100.0	180	4	US-08-937-263B-8	Sequence 8, Appli	
4	73	79.3	180	2	US-08-791-495-7	Sequence 7, Appli	
5	73	79.3	210	2	US-08-791-495-5	Sequence 5, Appli	
6	57	62.0	18	4	US-09-359-503-9	Sequence 9, Appli	
7	41	44.6	150	2	US-08-564-972-63	Sequence 63, Appli	
8	41	44.6	180	2	US-08-564-972-57	Sequence 57, Appli	
9	41	44.6	331	2	US-08-564-972-9	Sequence 9, Appli	
10	41	44.6	335	4	US-08-836-500A-2	Sequence 2, Appli	
11	41	44.6	535	2	US-08-564-972-1	Sequence 1, Appli	
12	41	44.6	535	4	US-09-171-969-9	Sequence 9, Appli	
13	40	43.5	695	1	US-08-164-839-8	Sequence 8, Appli	
14	40	43.5	695	1	US-08-583-799-8	Sequence 8, Appli	
15	40	43.5	696	1	US-08-164-839-10	Sequence 10, Appli	
16	40	43.5	696	1	US-08-583-799-10	Sequence 10, Appli	
17	40	43.5	1523	4	US-09-182-024A-2	Sequence 2, Appli	
18	39	42.4	20	2	US-08-564-972-47	Sequence 47, Appli	
19	39	42.4	688	4	US-08-973-273-26	Sequence 26, Appli	
20	39	42.4	747	4	US-08-973-273-3	Sequence 3, Appli	
21	38	41.3	331	2	US-08-997-080-182	Sequence 182, App	
22	38	41.3	331	2	US-08-997-362-182	Sequence 182, App	
23	38	41.3	331	4	US-09-095-855-182	Sequence 182, App	
24	38	41.3	331	4	US-09-324-542-182	Sequence 182, App	
25	38	41.3	349	2	US-08-483-926A-12	Sequence 12, Appli	
26	38	41.3	367	2	US-08-737-045-14	Sequence 14, Appli	
27	38	41.3	367	3	US-08-932-871B-2	Sequence 2, Appli	

28	38	41.3	367	3	US-09-476-919-2	Sequence 2, Appli
29	38	41.3	367	4	US-08-780-311A-2	Sequence 2, Appli
30	37	40.2	15	4	US-08-981-392-59	Sequence 59, Appli
31	37	40.2	469	3	US-08-985-335-5	Sequence 5, Appli
32	37	40.2	469	3	US-08-985-335-9	Sequence 9, Appli
33	37	40.2	469	4	US-09-410-372-5	Sequence 5, Appli
34	37	40.2	469	4	US-09-410-372-9	Sequence 9, Appli
35	37	40.2	544	4	US-08-687-590-30	Sequence 30, Appli
36	37	40.2	552	1	US-07-999-280A-22	Sequence 22, Appli
37	37	40.2	552	1	US-07-999-280A-24	Sequence 24, Appli
38	37	40.2	552	1	US-08-426-279-22	Sequence 22, Appli
39	37	40.2	552	1	US-08-426-279-24	Sequence 24, Appli
40	37	40.2	552	1	US-08-401-013-22	Sequence 22, Appli
41	37	40.2	552	1	US-08-401-013-24	Sequence 24, Appli
42	37	40.2	552	3	US-08-426-570-22	Sequence 22, Appli
43	37	40.2	552	3	US-08-426-570-24	Sequence 24, Appli
44	37	40.2	552	3	US-08-425-876-22	Sequence 22, Appli
45	37	40.2	552	3	US-08-425-876-24	Sequence 24, Appli

ALIGNMENTS

RESULT 1
US-09-359-503-10
; Sequence 10, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid

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; TOPOLOGY: linear
US-09-359-503-10

Query Match 100.0%; Score 92; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
   |||||
Db 1 PLPVPGVLLKEFTVSGNI 18

RESULT 2
US-08-791-495-9
; Sequence 9, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth , Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-9

Query Match 100.0%; Score 92; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
   |||||
Db 115 PLPVPGVLLKEFTVSGNI 132

RESULT 3
US-08-937-263B-8
; Sequence 8, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
; APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
```

```
; APPLICANT: Alexander, Knuth; Drijfhout, Jan W.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
; TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
; TITLE OF INVENTION: ITSELF, AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,263B
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sinn, Eric, Patent Agent
; REGISTRATION NUMBER: 40,177
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-937-263B-8

Query Match 100.0%; Score 92; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
   |||||
Db 115 PLPVPGVLLKEFTVSGNI 132

RESULT 4
US-08-791-495-7
; Sequence 7, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth , Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
```


;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Van Amsterdam, John R.
;; REGISTRATION NUMBER: 40,212
;; REFERENCE/DOCKET NUMBER: L0461/7005
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-720-3500
;; TELEFAX: 617-720-2441
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 180 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-791-495-7

Query Match 79.3%; Score 73; DB 2; Length 180;
Best Local Similarity 72.2%; Pred. No. 3.9e-05;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKFTVSGNI 18
||| || :||:|||||
Db 115 PLPRPGAVLKDFTVSGNL 132

RESULT 5
US-08-791-495-5
; Sequence 5, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-5

Query Match 79.3%; Score 73; DB 2; Length 210;
Best Local Similarity 72.2%; Pred. No. 4.6e-05;

Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 PLPVPGVLLKFTVSGNI 18
||| || :||:|||||
Db 115 PLPRPGAVLKDFTVSGNL 132

RESULT 6
US-09-359-503-9
; Sequence 9, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-359-503-9

Query Match 62.0%; Score 57; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VLLKFTVSGNI 18
|||||
Db 1 VLLKFTVSGNI 12

RESULT 7
US-08-564-972-63
; Sequence 63, Application US/08564972

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; Patent No. 5843462
; GENERAL INFORMATION:
; APPLICANT: Conti-Fine, B. M.
; TITLE OF INVENTION: DIPHTHERIA TOXIM EPITOPES
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
; STREET: P.O. Box 2938
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/564,972
; FILING DATE: 30-NOV-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 600.344US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; TELEX:
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: C-terminal
; ORIGINAL SOURCE:
; US-08-564-972-63

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Query Match	44.6%;	Score 41;	DB 2;	Length 150;
Best Local Similarity	50.0%;	Pred. No. 10;		
Matches	9;	Conservative	3;	Mismatches
			4;	Indels
			2;	Gaps
				1;

QY 1 PLPVPGVLLKEFTVSGNI 18
|||: |||| | : | :
Db 41 PLPIAGVLLP--TIPGKL 56

RESULT 8
 US-08-564-972-57
 ; Sequence 57, Application US/08564972
 ; Patent No. 5843462
 ; GENERAL INFORMATION:
 ; APPLICANT: Conti-Fine, B. M.
 ; TITLE OF INVENTION: DIPHTHERIA TOXIM EPITOPES
 ; NUMBER OF SEQUENCES: 79
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
 ; STREET: P.O. Box 2938
 ; CITY: Minneapolis
 ; STATE: MN
 ; COUNTRY: USA
 ; ZIP: 55402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible

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; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/564,972
; FILING DATE: 30-NOV-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 600.344US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; TELEX:
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-564-972-57

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Query Match	44.6%;	Score 41;	DB 2;	Length 180;
Best Local Similarity	50.0%;	Pred. No. 13;		
Matches	9;	Conservative	3;	Mismatches 4;
				Indels 2;
				Gaps 1;

QY 1 PLPVPGVLLKEFTVSGNI 18
 |||: |||| | : | :
 Db 156 PLPIAGVLLP--TIPGKL 171

RESULT 9
US-08-564-972-9
; Sequence 9, Application US/08564972
; Patent No. 5843462
; GENERAL INFORMATION:
; APPLICANT: Conti-Fine, B. M.
; TITLE OF INVENTION: DIPHTHERIA TOXIM EPITOPES
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
; STREET: P.O. Box 2938
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/564,972
; FILING DATE: 30-NOV-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 600.344US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331

```

;
; TELEFAX: 612-339-3061
;
; TELEX:
;
; INFORMATION FOR SEQ ID NO: 9:
;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 331 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   FRAGMENT TYPE: C-terminal
;   ORIGINAL SOURCE:
;
; US-08-564-972-9

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Query Match	44.6%	Score 41;	DB 2;	Length 331;
Best Local Similarity	50.0%	Pred. No. 26;		
Matches 9;	Conservative	3;	Mismatches	4;
			Indels	2;
			Gaps	1;

Qy 1 PLPVPGVLLKEFTVSGNI 18
|||: |||| | : | :
Db 222 PLPIAGVLLP--TIPGKL 237

```

RESULT 10
US-08-836-500A-2
; Sequence 2, Application US/08836500A
; Patent No. 6197929
; GENERAL INFORMATION:
; APPLICANT: Binz, Hans
; APPLICANT: Baussant, Thierry
; APPLICANT: Haeuw, Jean-Francois
; APPLICANT: Nguyen Ngoc, Thien
; TITLE OF INVENTION: Carrier Protein Having an Adjuvant
; TITLE OF INVENTION: Effect, Immunogenic Complex Containing It, Process for
; TITLE OF INVENTION: Their Preparation, Nucleotide Sequence and Vaccines
; Patent No. 6197929
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rockey, Milhamow & Katz, Ltd.
; STREET: 180 N. Stetson, 2 Prudential Plaza, Suite
; STREET: 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,500A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Katz, Martin L.
; REGISTRATION NUMBER: 25,011
; REFERENCE/DOCKET NUMBER: PIE1514P0180US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 335 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-836-500A-2

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Query Match 44.68; Score 41; DB 4; Length 335;

Best Local Similarity	38.9%;	Pred. No. 26;
Matches	7; Conservative	3; Mismatches
		8; Indels
		Gaps 0;

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QY      1 PLPVPGVLLKEFTVSGNI 18
        | | | | | | | |
Db     193 PAPAPEVATKHFTLKSDV 210
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RESULT 11
US-08-564-972-1
; Sequence 1, Application US/08564972
; Patent No. 5843462
; GENERAL INFORMATION:
; APPLICANT: Conti-Fine, B. M.
; TITLE OF INVENTION: DIPHERIA TOXIM EPITOPES
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
; STREET: P.O. Box 2938
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/564,972
; FILING DATE: 30-NOV-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 600.344US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; TELEX:

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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 535 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   FRAGMENT TYPE: internal
;   ORIGINAL SOURCE:
US-08-564-972-1

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Query Match 44.6%; Score 41; DB 2; Length 535;
Best Local Similarity 50.0%; Pred. No. 45;
Matches 9; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

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QY      1 PLPVPGVLLKEFTVSGNI 18
      |||: |||| | : | :
Db     426 PLPIAGVLLP--TIPGKL 441
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RESULT 12
US-09-171-969-9
; Sequence 9, Application US/09171969
; Patent No. 6284533
; GENERAL INFORMATION:
; APPLICANT: Thomas, Lawrence J.
; TITLE OF INVENTION: PLASMID-BAS

; TELEPHONE: (703)412-3000
; TELEFAX: (703)413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 695 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-583-799-8

Query Match 43.5%; Score 40; DB 1; Length 695;
Best Local Similarity 40.0%; Pred. No. 91;
Matches 12; Conservative 3; Mismatches 3; Indels 12; Gaps 2;

QY 1 PLPVP-----GVL-LKEFTVSGNI 18
||||| |:| || :||:|
Db 610 PLPVPLNRGVFTVEGAGLLSTKEIRISGS 639

RESULT 15
US-08-164-839-10
; Sequence 10, Application US/08164839
; Patent No. 5514573
; GENERAL INFORMATION:
; APPLICANT: YASUEDA, HISASHI
; APPLICANT: NAKANISHI, KAZUO
; APPLICANT: MOTOKI, MASAO
; APPLICANT: NAGASE, KAZUO
; APPLICANT: MATSUI, HIROSHI
; TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
; TITLE OF INVENTION: FROM FISH
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/164,839
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/004,729
; FILING DATE: 14-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5514573man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-599-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)412-3000
; TELEFAX: (703)413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 696 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-164-839-10

Query Match 43.5%; Score 40; DB 1; Length 696;
Best Local Similarity 40.0%; Pred. No. 91;

Matches 12; Conservative 3; Mismatches 3; Indels 12; Gaps 2;
QY 1 PLPVP-----GVL-LKEFTVSGNI 18
||||| |:| || :||:|
Db 611 PLPVPLNRGVFTVEGAGLLSTKEIRISGS 640

Search completed: July 3, 2002, 11:09:47
Job time: 269 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:10:55 ; Search time 61.47 Seconds
(without alignments)
28.137 Million cell updates/sec

Title: US-09-165-546A-11
Perfect score: 105
Sequence: 1 GAASGLNGCCRCGARGPE 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	48.6	312	2 T25048	hypothetical prote
2	50	47.6	1561	2 T00248	zinc finger protei
3	49	46.7	300	2 T19929	hypothetical prote
4	49	46.7	301	2 B31219	collagen 2 - Caen
5	48.5	46.2	308	2 T37286	collagen 40 - Caen
6	48.5	46.2	1589	2 C44766	defective chorion-
7	48	45.7	299	2 T19564	hypothetical prote
8	48	45.7	316	2 T20497	hypothetical prote
9	48	45.7	333	2 T20436	hypothetical prote
10	47.5	45.2	416	2 T32458	hypothetical prote
11	47	44.8	236	2 F84586	hypothetical prote
12	47	44.8	281	2 T04522	hypothetical prote
13	47	44.8	476	2 A54743	transcription fact
14	47	44.8	542	2 T05988	hypothetical prote
15	46.5	44.3	824	2 B38423	protein-glutamine
16	46	43.8	299	2 T22705	hypothetical prote
17	46	43.8	299	2 T24833	hypothetical prote
18	46	43.8	299	2 T25407	hypothetical prote
19	45.5	43.3	304	2 T22482	hypothetical prote
20	45	42.9	176	2 D71336	probable peptidyl-
21	45	42.9	266	2 T22706	hypothetical prote
22	45	42.9	307	2 T16842	hypothetical prote
23	45	42.9	309	2 T28708	hypothetical prote
24	45	42.9	769	2 A41029	integrin beta-8 ch
25	44	41.9	76	2 S17560	metallothionein-li
26	44	41.9	189	2 T48828	hypothetical prote
27	44	41.9	214	1 KNNT2S	glycine-rich prote
28	44	41.9	267	2 T08204	carbonate dehydrat
29	44	41.9	268	2 A86988	conserved hypothet

30	44	41.9	269	2 S72590	hypothetical prote
31	44	41.9	381	2 T27806	hypothetical prote
32	44	41.9	441	2 T35788	probable transcrip
33	44	41.9	1039	2 B71342	hypothetical prote
34	43.5	41.4	74	2 T33085	hypothetical prote
35	43.5	41.4	128	2 AF2671	conserved hypothet
36	43.5	41.4	142	2 D97453	hypothetical prote
37	43.5	41.4	316	2 S08169	collagen col-12 pr
38	43.5	41.4	316	2 S08170	collagen col-13 pr
39	43	41.0	54	2 S72975	glutamate decarbox
40	43	41.0	95	2 D69121	hypothetical prote
41	43	41.0	152	2 T18975	hypothetical prote
42	43	41.0	162	2 S07658	hypothetical prote
43	43	41.0	162	2 S07655	hypothetical prote
44	43	41.0	174	2 B48454	cathepsin B-like c
45	43	41.0	174	2 E84378	hypothetical prote

ALIGNMENTS

RESULT 1

T25048
hypothetical protein T21B4.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T25048
R:Smyle, R.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19974
A:Accession: T25048
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-312 <WIL>
A:Cross-references: EMBL:Z81124; PIDN:CAB03369.1; GSPDB:GN00020; CESP:T21B4.2
A:Experimental source: clone T21B4
C:Genetics:
A:Gene: CESP:T21B4.2
A:Map position: 2
A:Introns: 21/1; 53/3
C:Superfamily: unassigned collagens

Query Match 48.6%; Score 51; DB 2; Length 312;
Best Local Similarity 52.6%; Pred. No. 10;
Matches 10; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

Qy 1 GAASGLNGCCRC--GARGP 17
+ + + + + + + + + +
Db 111 GGGGGGGGGCCCGIGAAGP 129

RESULT 2

T00248
zinc finger protein wizL - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 05-Nov-1999
C:Accession: T00248
R:Matsumoto, K.; Ishii, N.; Yoshida, S.; Shiosaka, S.; Wanaka, A.; Tohyama, M.
submitted to the EMBL Data Library, March 1998
A:Description: Molecular cloning and distinct developmental expression pattern of spl
A:Reference number: Z14130
A:Accession: T00248
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-1561 <MAT>
A:Cross-references: EMBL:AB012265; NID:d1227740; PIDN:BAA32790.1; PID:d1033756
A:Experimental source: brain
C:Genetics:
A:Gene: wiz

Query Match 47.6%; Score 50; DB 2; Length 1561;

Best Local Similarity 52.9%; Score 49; DB 2; Length 300;
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGP 17
|:||||| | || |
Db 326 GDSSGLNTCVHCGFTAP 342

RESULT 3
T19929
hypothetical protein C44C10.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T19929
R;Cottage, A.
submitted to the EMBL Data Library, February 1996
A;Reference number: Z19197
A;Accession: T19929
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-300 <WIL>
A;Cross-references: EMBL:Z69787; PIDN:CAA93642.1; GSPDB:GN00028; CESP:C44C10.1
A;Experimental source: clone C44C10
C;Genetics:
A;Gene: CESP:C44C10.1
A;Map position: X
C;Superfamily: unassigned collagens

Query Match 46.7%; Score 49; DB 2; Length 300;
Best Local Similarity 52.6%; Pred. No. 18;
Matches 10; Conservative 1; Mismatches 6; Indels 2; Gaps 1;

QY 1 GAASGLNGCCRCG--ARGP 17
|: | ||| || | ||
Db 97 GSFSSQGGCCGCVSAAGP 115

RESULT 4
B31219
collagen 2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 21-Jul-2000
C;Accession: B31219; T37289; T26033; T37288
R;Kramer, J.M.; Cox, G.N.; Hirsh, D.
Cell 30, 599-606, 1982
A;Title: Comparisons of the complete sequences of two collagen genes from Caenorhabditis
A;Reference number: A90826; MUID:83050944
A;Accession: B31219
A;Molecule type: DNA
A;Residues: 1-301 <KRA>
A;Cross-references: GB:V00148; NID:g6683; PIDN:CAA23464.1; PID:g6684
A;Accession: T37289
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-301 <KR3>
A;Cross-references: EMBL:V00148; NID:g6683; PIDN:CAA23464.1; PID:g6684
R;Coles, L.
submitted to the EMBL Data Library, December 1995
A;Reference number: Z20141
A;Accession: T26033
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-301 <WIL>
A;Cross-references: EMBL:Z68301; PIDN:CAA92620.1; GSPDB:GN00022; CESP:W01B6.7
A;Experimental source: clone W01B6
R;Kramer, J.M.; Cox, G.N.; Hirsh, D.
J. Biol. Chem. 260, 1945-1951, 1985
A;Title: Expression of the Caenorhabditis elegans collagen genes col-1 and col-2 is deve
A;Reference number: Z21668; MUID:85105075
A;Accession: T37288
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA

A;Residues: 1-301 <KR2>
A;Cross-references: EMBL:J01048; NID:g156261; PIDN:AAA27990.1; PID:g156262
C;Genetics:
A;Gene: col-2
A;Map position: 4
A;Introns: 94/1
C;Superfamily: unassigned collagens

Query Match 46.7%; Score 49; DB 2; Length 301;
Best Local Similarity 47.1%; Pred. No. 18;
Matches 8; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGP 17
|: | ||| | ||
Db 93 GGGGCGDCCNPGPPGP 109

RESULT 5
T37286
collagen 40 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C;Accession: T37286
R;Levy, A.D.; Kramer, J.M.
Gene 137, 281-285, 1993
A;Title: Identification, sequence and expression patterns of the Caenorhabditis eleg
A;Reference number: Z21667; MUID:94131298
A;Accession: T37286
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-308 <LEV>
A;Cross-references: EMBL:L15419; NID:g289663; PIDN:AAA17726.1; PID:g289664
C;Genetics:
A;Gene: col-40
A;Map position: II
A;Introns: 72/3
C;Function:
A;Description: involved in cuticle assembly
C;Superfamily: unassigned collagens

Query Match 46.2%; Score 48.5; DB 2; Length 308;
Best Local Similarity 50.0%; Pred. No. 22;
Matches 12; Conservative 1; Mismatches 4; Indels 7; Gaps 2;

QY 1 GAASGLNG-----CCRC--GARGP 17
|||:| | || | || ||
Db 98 GAAAGEGGGGGCCSCCGIGAAGP 121

RESULT 6
C44766
defective chorion-1 fcl77 protein precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 24-Sep-1998
C;Accession: C44766
R;Waring, G.L.; Hawley, R.J.; Schoenfeld, T.
Dev. Biol. 142, 1-12, 1990
A;Title: Multiple proteins are produced from the dec-1 eggshell gene in Drosophila by
A;Reference number: A44766; MUID:91032553
A;Accession: C44766
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1589 <WAR>
A;Cross-references: GB:M35889; NID:g157185; PID:g157186
C;Genetics:
A;Gene: FlyBase:dec-1
A;Cross-references: FlyBase:FBgn0000427

Query Match 46.2%; Score 48.5; DB 2; Length 1589;
Best Local Similarity 37.1%; Pred. No. 69;

Matches 13; Conservative 1; Mismatches 4; Indels 17; Gaps 2;

QY 1 GAASGLN-----GC-----CRCGARGPE 18
| :||| |
Db 994 GQEAGLNATTSKGGCGRLDCLGSRRCGRRGLE 1028

RESULT 7
Tl9564
hypothetical protein C29F4.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T19564
R:Kershaw, J.
submitted to the EMBL Data Library, January 1996
A:Reference number: Z19143
A:Accession: T19564
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-299 <WIL>
A:Cross-references: EMBL:Z68335; PIDN:CAA92729.1; GSPDB:GN00022; CESP:C29F4.1
A:Experimental source: clone C29F4
C:Genetics:
A:Gene: CESP:C29F4.1
A:Map position: 4
A:Introns: 27/3
C:Superfamily: unassigned collagens

Query Match 45.7%; Score 48; DB 2; Length 299;
Best Local Similarity 57.9%; Pred. No. 25;
Matches 11; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

QY 1 GAAS--GLNGCCRCGARGP 17
|||| | : || |||
Db 89 GAASAGGCDACCLPGAAGP 107

RESULT 8
T20497
hypothetical protein F02D10.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T20497
R:Swinburne, J.
submitted to the EMBL Data Library, November 1995
A:Reference number: Z19283
A:Accession: T20497
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-316 <WIL>
A:Cross-references: EMBL:Z67990; PIDN:CAA91932.1; GSPDB:GN00028; CESP:F02D10.1
A:Experimental source: clone F02D10
C:Genetics:
A:Gene: CESP:F02D10.1
A:Map position: X
A:Introns: 56/3
C:Superfamily: unassigned collagens

Query Match 45.7%; Score 48; DB 2; Length 316;
Best Local Similarity 47.1%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGP 17
| | ||| | ||
Db 108 GGGGGCTGCCNPGPPG 124

RESULT 9
T20436
hypothetical protein E03G2.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T20436
R:McMurray, A.
submitted to the EMBL Data Library, November 1995
A:Reference number: Z19275
A:Accession: T20436
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-333 <WIL>
A:Cross-references: EMBL:Z68113; PIDN:CAA92150.1; GSPDB:GN00028; CESP:E03G2.4
A:Experimental source: clone E03G2
C:Genetics:
A:Gene: CESP:E03G2.4
A:Map position: X
A:Introns: 30/3; 49/3; 183/3; 274/1; 319/1
C:Superfamily: unassigned collagens

Query Match 45.7%; Score 48; DB 2; Length 333;
Best Local Similarity 47.1%; Pred. No. 27;
Matches 8; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGP 17
| : ||| || |
Db 130 GSQGGGGCGCGGQSPP 146

RESULT 10
T32458
hypothetical protein T13B5.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T32458
R:Maggi, L.
submitted to the EMBL Data Library, September 1997
A:Description: The sequence of C. elegans cosmid T13B5.
A:Reference number: Z21172
A:Accession: T32458
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-416 <MAG>
A:Cross-references: EMBL:AF026211; PIDN:AAB71295.1; GSPDB:GN00020; CESP:T13B5.4
A:Experimental source: strain Bristol N2; clone T13B5
C:Genetics:
A:Gene: CESP:T13B5.4
A:Map position: 2
A:Introns: 20/1; 85/3; 314/3

Query Match 45.2%; Score 47.5; DB 2; Length 416;
Best Local Similarity 50.0%; Pred. No. 36;
Matches 12; Conservative 1; Mismatches 4; Indels 7; Gaps 2;

QY 1 GAASGLNG-----CCRC--GARGP 17
|||:| | || | |||
Db 111 GAAAGGGGGGGSCCGCGIGAAGP 134

RESULT 11
F84586
hypothetical protein At2g20230 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: F84586
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: AB4420; MUID:20083487
A:Accession: F84586
A:Status: preliminary
A:Molecule type: DNA

A;Residues: 1-236 <STO>
A;Cross-references: GB:AE002093; NID:94512712; PIDN:AAD21765.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g20230
A;Map position: 2

Query Match 44.8%; Score 47; DB 2; Length 236;
Best Local Similarity 63.6%; Pred. No. 28;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 AASGLNGCCRC 12
||:|||||
Db 87 AAEAINGCCCLC 97

RESULT 12
T04522
hypothetical protein F16A16.120 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
C;Accession: T04522
R;Bevan, M.; Brandt, P.; Dose, S.; Jarke, D.; Scharfe, M.; Schon, O.; Hoheisel, J.; Mewes, H.W.; Mayer, K.
submitted to the Protein Sequence Database, February 1999
A;Reference number: Z15376
A;Accession: T04522
A;Molecule type: DNA
A;Residues: 1-281 <BEV>
A;Cross-references: EMBL:AL035353
A;Experimental source: cultivar Columbia; BAC clone F16A16
C;Genetics:
A;Map position: 4
A;Introns: 110/2; 143/3; 170/3; 205/3; 268/3
A;Note: F16A16.120

Query Match 44.8%; Score 47; DB 2; Length 281;
Best Local Similarity 63.6%; Pred. No. 32;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 AASGLNGCCRC 12
||:|||||
Db 132 AAEAINGCCCLC 142

RESULT 13
A54743
transcription factor HFK1 - human
C;Species: Homo sapiens (man)
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 12-Sep-1997
C;Accession: A54743
R;Murphy, D.B.; Wiese, S.; Burfeind, P.; Schmundt, D.; Mattei, M.G.; Schulz-Schaeffer, W.
Genomics 21, 551-557, 1994
A;Title: Human brain factor 1, a new member of the fork head gene family.
A;Reference number: A54743; MUID:95048332
A;Accession: A54743
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-476 <MUR>
A;Cross-references: GB:X74142
C;Genetics:
A;Gene: GDB:FKHL4; HBF-1; HFK1
A;Cross-references: GDB:433550
A;Map position: 14q12-14q12
C;Superfamily: unassigned fork head proteins; fork head DNA-binding domain homology
F;169-260/Domain: fork head DNA-binding domain homology <FHD>

Query Match 44.8%; Score 47; DB 2; Length 476;
Best Local Similarity 58.8%; Pred. No. 47;
Matches 10; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

QY 1 GAASGLNGCCRCGARG 17

Db 113 GAKAG--GCCRPGELGP 127
||:| ||||| ||

RESULT 14
T05988
hypothetical protein F17M5.130 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 17-Nov-2000
C;Accession: T05988
R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hoheisel, J.; Mewes, H.W.; Mayer, K.
submitted to the Protein Sequence Database, March 1999
A;Reference number: Z15263
A;Accession: T05988
A;Molecule type: DNA
A;Residues: 1-542 <BEV>
A;Cross-references: EMBL:AL035678; GSPDB:GN00062; ATSP:F17M5.130
A;Experimental source: cultivar Columbia; BAC clone F17M5
C;Genetics:
A;Gene: ATSP:F17M5.130
A;Map position: 4
A;Introns: 30/3
C;Superfamily: ATP-dependent RNA helicase DBP1

Query Match 44.8%; Score 47; DB 2; Length 542;
Best Local Similarity 57.1%; Pred. No. 51;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 ASGLNGCCRCGARG 16
|||: || || |
Db 495 ASGVKGCAYCGGLG 508

RESULT 15
B38423
protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 04-Feb-2000
C;Accession: B38423
R;Phillips, M.A.; Stewart, B.E.; Qin, Q.; Chakravarty, R.; Floyd, E.E.; Jetten, A.M.;
Proc. Natl. Acad. Sci. U.S.A. 87, 9333-9337, 1990
A;Title: Primary structure of keratinocyte transglutaminase.
A;Reference number: A38423; MUID:91067700
A;Accession: B38423
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-824 <PHI>
A;Cross-references: GB:M57263; NID:g205098; PIDN:AAA63495.1; PID:g205099
C;Superfamily: protein-glutamine gamma-glutamyltransferase
C;Keywords: aminoacyltransferase
F;323-325/Region: cell attachment (R-G-D) motif
F;385/Active site: Cys #status predicted

Query Match 44.3%; Score 46.5; DB 2; Length 824;
Best Local Similarity 56.2%; Pred. No. 80;
Matches 9; Conservative 0; Mismatches 2; Indels 5; Gaps 1;

QY 8 GCCRCGAR----GPE 18
||| || | |||
Db 51 GCCSCGNRADDWDWGPE 66

Search completed: July 3, 2002, 11:10:56
Job time: 318 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:24:44 ; Search time 29.65 Seconds
(without alignments)
23.506 Million cell updates/sec

Title: US-09-165-546A-11
Perfect score: 105
Sequence: 1 GAASGLNGCCRCGARGPE 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	105	100.0	180	1	CTAG_HUMAN	P78358 homo sapien
2	58	55.2	210	1	LAG1_HUMAN	O75638 homo sapien
3	49	46.7	301	1	CC02_CAEEL	P17656 caenorhabdi
4	48.5	46.2	308	1	CC40_CAEEL	P34804 caenorhabdi
5	48.5	46.2	1589	1	DC13_DROME	P18171 drosophila
6	47	44.8	477	1	FXGB_HUMAN	P55315 homo sapien
7	46.5	44.3	824	1	TGLK_RAT	P23606 rattus norv
8	45	42.9	176	1	SLYD_TREPA	O83369 treponema p
9	45	42.9	266	1	YXWK_CAEEL	Q21184 caenorhabdi
10	45	42.9	769	1	ITB8_HUMAN	P26012 homo sapien
11	44	41.9	76	1	MT1_MAIZE	P30571 zea mays (m
12	44	41.9	214	1	GRP2_NICSY	P27484 nicotiana s
13	44	41.9	1039	1	Y304_TREPA	O83326 treponema p
14	43.5	41.4	316	1	CC12_CAEEL	P20630 caenorhabdi
15	43.5	41.4	316	1	CC13_CAEEL	P20631 caenorhabdi
16	43	41.0	174	1	CYS3_OSTOS	Q06544 ostertagia
17	43	41.0	302	1	CCDC_CAEEL	P17657 caenorhabdi
18	43	41.0	492	1	SES1_HUMAN	Q9y6p5 homo sapien
19	43	41.0	508	1	CILA_KLEPN	P45413 klebsiella
20	43	41.0	684	1	Y492_MYCTU	Q11157 mycobacteri
21	43	41.0	1958	1	UBR1_SCHPO	O60152 schizosacch
22	42	40.0	1016	1	PCR2_SCHPO	P36583 schizosacch
23	42	40.0	1174	1	KPC1_COCHE	O42632 cochliobolu
24	41.5	39.5	212	1	SLYD_AERHY	O07046 aeromonas h
25	41.5	39.5	315	1	YV67_CAUCR	Q9a3n5 caulobacter
26	41	39.0	53	1	RS14_METVA	P14041 methanococc
27	41	39.0	55	1	FER_CLOSP	P00197 clostridium
28	41	39.0	56	1	RS14_PYRHO	O74093 pyrococcus
29	41	39.0	105	1	YM74_MYCTU	Q50689 mycobacteri
30	41	39.0	201	1	GR2B_ARATH	Q38896 arabidopsis
31	41	39.0	295	1	CAC3_HAECO	P16253 haemonchus
32	41	39.0	560	1	EPS_MOUSE	Q64355 mus musculu
33	41	39.0	561	1	EPS_HUMAN	O43281 homo sapien

RESULT 1

CTAG_HUMAN

ID	CTAG_HUMAN	STANDARD;	PRT;	180 AA.
AC	P78358;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Autoimmunogenic cancer/testis antigen NY-ESO-1.			
GN	CTAG.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97203161; PubMed=9050879;			
RA	Chen Y.-T., Scanlan M.J., Sahin U., Tuereci O., Gure A.O., Tsang S.,			
RA	Williamson B., Stockert E., Pfreundschuh M., Old L.J.;			
RT	"A testicular antigen aberrantly expressed in human cancers detected			
RT	by autologous antibody screening."			
RL	Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Melanoma;			
RX	MEDLINE=98289662; PubMed=9626360;			
RA	Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,			
RA	de Plaen E., Boon T.;			
RT	"LAGE-1 a new gene with tumor specificity."			
RL	Int. J. Cancer 76:903-908(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98430682; PubMed=9759882;			
RA	Wang R.-F., Johnston S.L., Zeng G., Topalian S.L.,			
RA	Schwartzentruber D.J., Rosenberg S.A.;			
RT	"A breast and melanoma-shared tumor antigen: T cell responses to			
RT	antigenic peptides translated from different open reading frames."			
RL	J. Immunol. 161:3596-3606(1998).			
CC	-!- TISSUE SPECIFICITY: EXPRESSED IN TESTIS AND OVARY AND IN A WIDE			
CC	VARIETY OF CANCERS. DETECTED IN UTERINE MYOMETRIUM.			
CC	-!- SIMILARITY: STRONG, TO LAGE-1.			

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CC	EMBL; U87459; AAB49693.1; -.
DR	EMBL; AJ003149; CAA05908.1; -.
DR	EMBL; AF038567; AAD05202.1; -.
DR	MIM; 300156; -.
KW	Transmembrane; Antigen.
FT	DOMAIN 5 82
FT	TRANSMEM 156 172
FT	GLY-RICH. POTENTIAL.

O88508 mus musculu
Q9y6k1 homo sapien
P14099 bos taurus
O14727 homo sapien
O88879 mus musculu
P15800 rattus norv
P80251 mytilus edu
P80252 mytilus edu
P20730 bombyx mori
P56747 homo sapien
P41975 oryctolagus
Q9nry6 homo sapien

ALIGNMENTS

Query Match 46.7%; Score 49; DB 1; Length 301;
Best Local Similarity 47.1%; Pred. No. 4.3;
Matches 8; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGP 17
I :||| I ||
Db 93 GGGGGCDGCCNPGPPGP 109

RESULT 4

CC40_CAEEL STANDARD; PRT; 308 AA.
AC P34804;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Cuticle collagen 40.
GN COL-40.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=94131298; PubMed=82999960;
RA Levy A.D., Kramer J.M.;
RT "Identification, sequence and expression patterns of the
Caenorhabditis elegans col-36 and col-40 collagen-encoding genes.";
RL Gene 137:281-285(1993).
CC -!- FUNCTION: NEMATODE CUTICLES ARE COMPOSED LARGELY OF COLLAGEN-LIKE
PROTEINS. THE CUTICLE FUNCTIONS BOTH AS AN EXOSKELETON AND AS A
BARRIER TO PROTECT THE WORM FROM ITS ENVIRONMENT.
CC -!- SUBUNIT: COLLAGEN POLYPEPTIDE CHAINS ARE COMPLEXED WITHIN THE
CUTICLE BY DISULFIDE BONDS AND OTHER TYPES OF COVALENT CROSS-
LINKS.
CC -!- SIMILARITY: TO OTHER COLLAGENS. STRONG, TO OTHER CUTICLE
COLLAGENS.

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EMBL; L15419; AAA17726.1; -.
InterPro; IPR002486; Col_cuticle_N.
InterPro; IPR000087; Collagen.
Pfam; PF01391; Collagen; 2.
Pfam; PF01484; Col_cuticle_N; 1.
KW Cuticle; Connective tissue; Repeat; Multigene family; Collagen.
FT DOMAIN 102 109
FT DOMAIN 117 146
FT DOMAIN 165 191
FT DOMAIN 195 227
FT DOMAIN 232 258
FT DOMAIN 261 296
SQ SEQUENCE 308 AA; 29278 MW; FD29BB718D2116D2 CRC64;

Query Match 46.2%; Score 48.5; DB 1; Length 308;
Best Local Similarity 50.0%; Pred. No. 5.1;
Matches 12; Conservative 1; Mismatches 4; Indels 7; Gaps 2;

QY 1 GAASGLNG----CCRC--GARGP 17
|||:| I || I || I ||
Db 98 GAAAGEGGGGGCCSCGIGAGAP 121

RESULT 5

DC13_DROME

ID DC13_DROME STANDARD; PRT; 1589 AA.
AC P18171;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Defective chorion-1 protein, FC177 isoform precursor.
GN DEC-1.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=91032553; PubMed=1699826;
RA Waring G.L., Hawley R.J., Schoenfeld T.;
RT "Multiple proteins are produced from the dec-1 eggshell gene in
Drosophila by alternative RNA splicing and proteolytic cleavage
events.";
RL Dev. Biol. 142:1-12(1990).
RN [2]
RP DEVELOPMENTAL STAGE.
RX MEDLINE=88243015; PubMed=3378704;
RA Hawley R.J., Waring G.L.;
RT "Cloning and analysis of the dec-1 female-sterile locus, a gene
required for proper assembly of the Drosophila eggshell.";
RL Genes Dev. 2:341-349(1988).
CC -!- FUNCTION: THE DEC-1 FEMALE-STERILE LOCUS PROTEIN IS REQUIRED
FOR PROPER ASSEMBLY OF THE DROSOPHILA EGGSHELL.
CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; FC106 (AC P18170), FC125 (AC
P18169) AND FC177 (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
SPLICING.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED DURING EMBRYONIC STAGE 11.

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EMBL; M35889; AAA28448.1; -.
FlyBase; FBgn0000427; dec-1.
KW Chorion; Eggshell; Repeat; Alternative splicing; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 1589 DEFECTIVE CHORION-1 PROTEIN, FC177
ISOFORM.
FT DOMAIN 493 788 12 X 26 AA APPROXIMATE TANDEM REPEATS,
GLU, MET-RICH.
FT REPEAT 493 518 1.
FT REPEAT 519 544 2.
FT REPEAT 545 570 3.
FT REPEAT 571 596 4.
FT REPEAT 597 622 5.
FT REPEAT 623 652 6 (APPROXIMATE).
FT REPEAT 653 680 7 (APPROXIMATE).
FT REPEAT 681 696 8 (APPROXIMATE).
FT REPEAT 697 720 9 (APPROXIMATE).
FT REPEAT 721 733 10 (APPROXIMATE).
FT REPEAT 734 758 11 (APPROXIMATE).
FT REPEAT 759 788 12 (APPROXIMATE).
SQ SEQUENCE 1589 AA; 179506 MW; 70EC9F991E8D802A CRC64;

Query Match 46.2%; Score 48.5; DB 1; Length 1589;
Best Local Similarity 37.1%; Pred. No. 18;
Matches 13; Conservative 1; Mismatches 4; Indels 17; Gaps 2;

QY 1 GAASGLN-----GC-----CRCGARGPE 18
I :||| I || I || I ||
Db 994 GQEAGLNATTSGCGGGRDLCLGRCRCRRGLE 1028


```
RESULT 6
FXGB_HUMAN
ID FXGB_HUMAN STANDARD; PRT; 477 AA.
AC P55315;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Forkhead box protein GLB (Forkhead-related protein FKHL1)
DE (Transcription factor BF-1) (Brain factor 1) (BF1) (HPK1).
GN FOXGLB OR FKHL1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95048332; PubMed=7959731;
RA Murphy D.B., Wiese S., Burfeind P., Schmundt D., Mattei M.-G.,
RA Schulz-Schaeffer W., Thies U.;
RT "Human brain factor 1, a new member of the fork head gene family.";
RL Genomics 21:551-557(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95322450; PubMed=7599184;
RA Wiese S., Murphy D.B., Schlung A., Burfeind P., Schmundt D.,
RA Schnulle V., Mattei M.-G., Thies U.;
RT "The genes for human brain factor 1 and 2, members of the fork head
RT gene family, are clustered on chromosome 14q.";
RL Biochim. Biophys. Acta 1262:105-112(1995).
CC -!- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE ESTABLISHMENT OF THE
CC REGIONAL SUBDIVISION OF THE DEVELOPING BRAIN AND IN THE
CC DEVELOPMENT OF THE TELENCEPHALON. SEQUENCE-SPECIFIC DNA-BINDING
CC PROTEIN WITH A DISTINCT BINDING SPECIFICITY (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
CC -----
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CC -----
DR EMBL; X74142; CAA52239.1; -.
DR HSSP; Q63245; 2HFH.
DR TRANSFAC; T02350; -.
DR MIM; 164874; -.
DR InterPro; IPR001766; Fork_head.
DR Pfam; PF00250; Fork_head; 1.
DR PRINTS; PR00053; FORKHEAD.
DR SMART; SM00339; FH; 1.
DR PROSITE; PS00657; FORK_HEAD_1; 1.
DR PROSITE; PS00658; FORK_HEAD_2; 1.
DR PROSITE; PS50039; FORK_HEAD_3; 1.
KW Transcription regulation; DNA-binding; Nuclear protein;
KW Developmental protein.
FT DOMAIN 33 57 HIS-RICH.
FT DOMAIN 58 80 PRO-RICH.
FT DOMAIN 72 75 POLY-GLN.
FT DOMAIN 99 102 POLY-LEU.
FT DNA_BIND 168 259 FORK-HEAD.
SQ SEQUENCE 477 AA; 51340 MW; 71CFD0BD069CFAD5 CRC64;
```

```
Query Match 44.8%; Score 47; DB 1; Length 477;
Best Local Similarity 58.8%; Pred. No. 12;
Matches 10; Conservative 1; Mismatches 4; Indels 2; Gaps 1;
```

```
QY 1 GAASGLNGCCRCGARGP 17
|| :| |||| | ||
Db 113 GAKAG--GCCRPGLGP 127

RESULT 7
TGLK_RAT
ID TGLK_RAT STANDARD; PRT; 824 AA.
AC P23606;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Protein-glutamine gamma-glutamyltransferase K (EC 2.3.2.13)
DE (Transglutaminase K) (TGase K) (TGK) (Epidermal TGase).
GN TGM1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91067700; PubMed=1979171;
RA Phillips M.A., Stewart B.E., Qin Q., Chakravarty R., Floyd E.E.,
RA Jetten A.M., Rice R.H.;
RT "Primary structure of keratinocyte transglutaminase.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:9333-9337(1990).
CC -!- FUNCTION: CATALYZES THE CROSS-LINKING OF PROTEINS AND THE
CC CONJUGATION OF POLYAMINES TO PROTEINS. RESPONSIBLE FOR CROSS-
CC LINKING EPIDERMAL PROTEINS DURING FORMATION OF THE STRATUM
CC CORNEUM.
CC -!- CATALYTIC ACTIVITY: Protein glutamine + alkylamine = protein N5-
CC alkylglutamine + NH(3).
CC -!- COFACTOR: CALCIUM.
CC -!- SUBCELLULAR LOCATION: Membrane-bound.
CC -!- SIMILARITY: BELONGS TO THE TRANSGLUTAMINASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M57263; AAA63495.1; -.
DR PIR; B38423; B38423.
DR HSSP; P00488; LQRK.
DR InterPro; IPR002931; Transglut_core.
DR InterPro; IPR001102; Transglutmnse.
DR Pfam; PF00927; Transglutamin_C; 1.
DR Pfam; PF00868; Transglutamin_N; 1.
DR Pfam; PF01841; Transglut_core; 1.
DR SMART; SM00460; TGC; 1.
DR PROSITE; PS00547; TRANSGLUTAMINASES; 1.
KW Transferase; Acyltransferase; Calcium-binding; Membrane.
FT ACT_SITE 385 385 BY SIMILARITY.
SQ SEQUENCE 824 AA; 90769 MW; A7D81C148CEFD938 CRC64;

Query Match 44.3%; Score 46.5; DB 1; Length 824;
Best Local Similarity 56.2%; Pred. No. 21;
Matches 9; Conservative 0; Mismatches 2; Indels 5; Gaps 1;
```

```
QY 8 GCCRCGAR-----GPE 18
||| || | |||
Db 51 GCCSCGNRADDWDWGPE 66
```

```
RESULT 8
SLYD_TREPA
ID SLYD_TREPA STANDARD; PRT; 176 AA.
AC O83369;
DT 15-JUL-1999 (Rel. 38, Created)
```

DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FKBP-type peptidyl-prolyl cis-trans isomerase slyD (EC 5.2.1.8)
DE (PPIase) (Rotamase).
GN SLYD OR TP0349.
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=NICHOLS;
RX MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
RA McDonald L., Artlich P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;

RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete";

RL Science 281:375-388(1998).

CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS (BY

CC SIMILARITY).

CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC

CC PEPTIDE BONDS IN OLIGOPEPTIDES.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).

CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.

CC -----
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CC -----

DR EMBL; AE001214; AAC65334.1; -.

DR TIGR; TP0349; -.

DR InterPro; IPR001179; FKBP_PPIase.

DR Pfam; PF00254; FKBP; 1.

DR PROSITE; PS00453; FKBP_PPIASE_1; FALSE_NEG.

DR PROSITE; PS00454; FKBP_PPIASE_2; FALSE_NEG.

DR PROSITE; PS50059; FKBP_PPIASE_3; 1.

KW Isomerase; Rotamase; Complete proteome.

FT DOMAIN 1 95 PPIASE, FKBP-TYPE.

FT DOMAIN 158 176 GLY-RICH.

SQ SEQUENCE 176 AA; 18428 MW; 77F8FE1901E73399 CRC64;

Query Match 42.9%; Score 45; DB 1; Length 176;
Best Local Similarity 57.1%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 GAASGLNGCCRCGA 14

| | | | |

Db 160 GCGSGAGCGSCGA 173

RESULT 9

YXWK_CAEEL

ID YXWK_CAEEL STANDARD; PRT; 266 AA.

AC Q21184; Q20807;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Putative cuticle collagen F55C10.3.

GN F55C10.3.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA White S.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]

RP REVISIONS.

RC STRAIN=BRISTOL N2;

RA Jones S.J.M.;

RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: NEMATODE CUTICLES ARE COMPOSED LARGELY OF COLLAGEN-LIKE

CC PROTEINS. THE CUTICLE FUNCTIONS BOTH AS AN EXOSKELETON AND AS A

CC BARRIER TO PROTECT THE WORM FROM ITS ENVIRONMENT (BY SIMILARITY).

CC -!- SUBUNIT: COLLAGEN POLYPEPTIDE CHAINS ARE COMPLEXED WITHIN THE

CC CUTICLE BY DISULFIDE BONDS AND OTHER TYPES OF COVALENT CROSS-

CC LINKS (BY SIMILARITY).

CC -!- SIMILARITY: TO OTHER COLLAGENS. STRONG, TO OTHER CUTICLE

CC COLLAGENS.

CC -----
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CC -----

DR EMBL; Z74036; CAA98487.1; -.

DR WormPep; F55C10.3; Cell1182.

DR InterPro; IPR000087; Collagen.

DR Pfam; PF01391; Collagen; 2.

KW Hypothetical protein; Cuticle; Connective tissue; Repeat;

KW Collagen; Multigene family.

FT DOMAIN 70 99 TRIPLE-HELICAL REGION.

FT DOMAIN 118 144 TRIPLE-HELICAL REGION.

FT DOMAIN 148 169 TRIPLE-HELICAL REGION.

FT DOMAIN 183 245 TRIPLE-HELICAL REGION.

SQ SEQUENCE 266 AA; 25616 MW; 984556680F1AAF22 CRC64;

Query Match 42.9%; Score 45; DB 1; Length 266;
Best Local Similarity 52.6%; Pred. No. 14;
Matches 10; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

OY 1 GAAS--GLNGCCRCGARGP 17

| : | | | : | | | | |

Db 56 GSASTGGCDACCLPGAAGP 74

RESULT 10

ITB8_HUMAN

ID ITB8_HUMAN STANDARD; PRT; 769 AA.

AC P26012;

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Integrin beta-8 precursor.

GN ITGB8.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RX MEDLINE=92011767; PubMed=1918072;

RA Moyle M., Napier M.A., McLean J.W.;

RT "Cloning and expression of a divergent integrin subunit beta 8.";

RL J. Biol. Chem. 266:19650-19658(1991).

RN [2]

RP SEQUENCE FROM N.A.

RA Tin-Wollam A., Sutterer C., Fronick B.;

RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: INTEGRIN ALPHA-V/BETA-8 IS A RECEPTOR FOR FIBRONECTIN.


```
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. BETA-8
CC ASSOCIATES WITH ALPHA-V.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: PLACENTA, KIDNEY, BRAIN, OVARY, UTERUS, AND IN
CC SEVERAL TRANSFORMED CELLS. TRANSIENTLY EXPRESSED IN 293 HUMAN
CC EMBRYONIC KIDNEY CELLS.
CC -!- SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.
CC -!- SIMILARITY: CONTAINS 1 VWFA-LIKE DOMAIN.
CC -----
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CC -----
CC EMBL; M73780; AAA36034.1; -.
CC EMBL; AC004130; AAC01769.1; -.
CC PIR; A41029; A41029.
CC MIM; 604160; -.
CC InterPro; IPR000561; EGF-like.
CC InterPro; IPR002369; Integrin_B.
CC InterPro; IPR001169; Integrin_beta_C.
CC InterPro; IPR003659; PSI.
CC InterPro; IPR002035; VWFA.
CC Pfam; PF00362; integrin_B; 1.
CC ProDom; PD001811; Integrin_B; 1.
CC SMART; SM00181; EGF; 1.
CC SMART; SM00187; INB; 1.
CC SMART; SM00423; PSI; 1.
CC SMART; SM00327; VWA; 1.
CC PROSITE; PS00243; INTEGRIN_BETA; 2.
CC PROSITE; PS00022; EGF_1; UNKNOWN_1.
CC PROSITE; PS01186; EGF_2; UNKNOWN_1.
CC Integrin; Cell adhesion; Receptor; Transmembrane; Glycoprotein;
CC Repeat; Signal.
CC SIGNAL 1 42 POTENTIAL.
CC CHAIN 43 769 INTEGRIN BETA-8.
CC DOMAIN 43 684 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 685 704 POTENTIAL.
CC DOMAIN 705 769 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 146 384 VWFA-LIKE.
CC DOMAIN 471 629 4 CYSTEINE-RICH TANDEM REPEATS.
CC REPEAT 471 510 I.
CC REPEAT 511 552 II.
CC REPEAT 553 592 III.
CC REPEAT 593 629 IV.
CC DISULFID 47 469 BY SIMILARITY.
CC DISULFID 55 65 BY SIMILARITY.
CC DISULFID 58 94 BY SIMILARITY.
CC DISULFID 68 83 BY SIMILARITY.
CC DISULFID 211 218 BY SIMILARITY.
CC DISULFID 266 307 BY SIMILARITY.
CC DISULFID 407 419 BY SIMILARITY.
CC DISULFID 467 471 BY SIMILARITY.
CC DISULFID 494 499 BY SIMILARITY.
CC DISULFID 526 531 BY SIMILARITY.
CC DISULFID 528 561 BY SIMILARITY.
CC DISULFID 533 546 BY SIMILARITY.
CC DISULFID 567 572 BY SIMILARITY.
CC DISULFID 574 583 BY SIMILARITY.
CC DISULFID 585 593 BY SIMILARITY.
CC DISULFID 607 612 BY SIMILARITY.
CC DISULFID 609 657 BY SIMILARITY.
CC DISULFID 614 624 BY SIMILARITY.
CC DISULFID 627 630 BY SIMILARITY.
CC DISULFID 634 643 BY SIMILARITY.
CC CARBOHYD 233 233 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 421 421 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 431 431 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 456 456 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 466 466 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 648 648 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 769 AA; 85631 MW; F7E3994F92B12A65 CRC64;

Query Match 42.9%; Score 45; DB 1; Length 769;
Best Local Similarity 52.9%; Pred. No. 32;
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2 AASGLNGCCRCGARGPE 18
   |:| | | | | | |
Db 48 ASSNAASCARCLALGPE 64

RESULT 11
MTL_MAIZE
ID MTL_MAIZE STANDARD; PRT; 76 AA.
AC P30571;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Metallothionein-like protein 1.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92008639; PubMed=1915859;
RA de Framond A.J.;
RT "A metallothionein-like gene from maize (Zea mays). Cloning and
   characterization."
RL FEBS Lett. 290:103-106(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Root meristem;
RX MEDLINE=95359405; PubMed=7632917;
RA Chevalier C., Bourgeois E., Pradet A., Raymond P.;
RT "Molecular cloning and characterization of six cDNAs expressed during
   glucose starvation in excised maize (Zea mays L.) root tips."
RL Plant Mol. Biol. 28:473-485(1995).
CC -!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
   RESIDUES THAT BIND VARIOUS HEAVY METALS.
CC -!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 15.
CC -----
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CC -----
CC EMBL; S57628; AAB19992.1; -.
CC EMBL; X82186; CAA57676.1; -.
CC PIR; S17560; S17560.
CC MaizedB; 64922; -.
CC InterPro; IPR000347; Metallothion_15.
CC Pfam; PF01439; Metallothio_2; 1.
CC ProDom; PD001611; Metallothion_15; 1.
KW Metal-binding; Metal-thiolate cluster; Chelation.
SQ SEQUENCE 76 AA; 7486 MW; 94FDC4102262A8BD CRC64;
```

```
Query Match 41.9%; Score 44; DB 1; Length 76;
Best Local Similarity 33.3%; Pred. No. 7.4;
Matches 6; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
   |:| | | | | | |
Db 6 GSSCGGSSCKCGKKYPD 23
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RESULT 12
GRP2_NICSY STANDARD; PRT; 214 AA.
AC P27484;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Glycine-rich protein 2.
GN GRP-2.
OS Nicotiana sylvestris (Wood tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4096;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92003709; PubMed=1912512;
RA Obokata J., Ohme M., Hayashida N.;
RT "Nucleotide sequence of a cDNA clone encoding a putative glycine-rich
RL Plant Mol. Biol. 17:953-955(1991).
CC -!- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.
CC -!- SIMILARITY: CONTAINS 2 C2HC-TYPE ZINC FINGERS.
CC -!- SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
CC -!- CAUTION: Was originally (Ref.1) thought to be a cell wall
CC structural protein.
CC -----
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CC -----
DR EMBL; X60007; CAA42622.1; -.
DR PIR; S17731; KNNT2S.
DR HSSP; P15277; IMJC.
DR InterPro; IPR002059; Cold_shock.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00313; CSD; 1.
DR Pfam; PF00098; zf-CCHC; 2.
DR PRINTS; PR00939; C2HCZNFINGER.
DR PRINTS; PR00050; COLDSHOCK.
DR PRODOM; PD000621; Cold_shock; 1.
DR SMART; SM00357; CSP; 1.
DR SMART; SM00343; Znf_C2HC; 2.
DR PROSITE; PS00352; COLD_SHOCK; 1.
DR PROSITE; PS0158; ZF_CCHC; 2.
KW RNA-binding; Repeat; Zinc-finger.
FT DOMAIN 8 75 CSD.
FT DOMAIN 82 158 GLY-RICH.
FT ZN_FING 157 174 CCHC-TYPE 1.
FT DOMAIN 176 195 GLY-RICH.
FT ZN_FING 194 211 CCHC-TYPE 2.
SQ SEQUENCE 214 AA; 19746 MW; E28DB84538F2A0AA CRC64;

Query Match 41.9%; Score 44; DB 1; Length 214;
Best Local Similarity 43.8%; Pred. No. 16;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARG 16
| : | : | : | : |
Db 151 GSGSGGCGCFKCGESG 166

RESULT 13
Y304_TREPA
ID Y304_TREPA STANDARD; PRT; 1039 AA.
AC O83326;
DT 16-OCT-2001 (Rel. 40, Created)
```

```
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein TP0304.
GN TP0304.
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=NICHOLS;
RX MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R., Winn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
RA McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT Spirochete.";
RL Science 281:375-388(1998).
CC -----
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CC -----
DR EMBL; AE001210; AAC65294.1; -.
DR TIGR; TP0304; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 1039 AA; 115873 MW; E8153EA72D071A5A CRC64;

Query Match 41.9%; Score 44; DB 1; Length 1039;
Best Local Similarity 47.8%; Pred. No. 56;
Matches 11; Conservative 0; Mismatches 6; Indels 6; Gaps 2;

QY 1 GAASGLNG---CCRC---GARGP 17
| | | | | | | | | |
Db 791 GNCCGNNGGQQCCACNGGANGP 813

RESULT 14
CC12_CAEEL STANDARD; PRT; 316 AA.
ID CC12_CAEEL
AC P20630;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Cuticle collagen 12 precursor.
GN COL-12 OR F15H10.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BRISTOL N2;
RX MEDLINE=90172409; PubMed=1689778;
RA Park Y.-S., Kramer J.M.;
RT "Tandemly duplicated Caenorhabditis elegans collagen genes differ in
RT their modes of splicing.";
RL J. Mol. Biol. 211:395-406(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=BRISTOL N2;
RA Berks M.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: NEMATODE CUTICLES ARE COMPOSED LARGELY OF COLLAGEN-LIKE
CC PROTEINS. THE CUTICLE FUNCTIONS BOTH AS AN EXOSKELETON AND AS A
```

```
CC BARRIER TO PROTECT THE WORM FROM ITS ENVIRONMENT.
CC -!- SUBUNIT: COLLAGEN POLYPEPTIDE CHAINS ARE COMPLEXED WITHIN THE
CC CUTICLE BY DISULFIDE BONDS AND OTHER TYPES OF COVALENT CROSS-
CC LINKS.
CC -!- SIMILARITY: TO OTHER COLLAGENS. STRONG, TO OTHER CUTICLE
CC COLLAGENS. THE MATURE COL-12 AND COL-13 ARE IDENTICAL.
CC -----
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CC -----
CC EMBL; X51622; CAA35954.1; -.
CC EMBL; Z73972; CAA98257.1; -.
CC PIR; S08169; S08169.
CC WormPep; F15H10.1; CE05638.
CC InterPro; IPR002486; Col_cuticle_N.
CC InterPro; IPR000087; Collagen.
CC Pfam; PF01391; Collagen; 2.
CC Pfam; PF01484; Col_cuticle_N; 1.
CC Cuticle; Connective tissue; Repeat; Multigene family; Collagen;
KW Signal.
FT SIGNAL 1 36 POTENTIAL.
FT CHAIN 37 316 CUTICLE COLLAGEN 12.
FT DOMAIN 128 157 TRIPLE-HELICAL REGION.
FT DOMAIN 176 202 TRIPLE-HELICAL REGION.
FT DOMAIN 206 235 TRIPLE-HELICAL REGION.
FT DOMAIN 240 266 TRIPLE-HELICAL REGION.
FT DOMAIN 269 304 TRIPLE-HELICAL REGION.
SQ SEQUENCE 316 AA; 30098 MW; 6CA81FF94706D42E CRC64;
```

Query Match 41.4%; Score 43.5; DB 1; Length 316;
Best Local Similarity 52.6%; Pred. No. 26;
Matches 10; Conservative 1; Mismatches 5; Indels 3; Gaps 2;

```
QY 1 GAASGLNGCCRC--GARGP 17
   | :|| | | | | | |
Db 115 GGSSG-GSCSCGSGAAGP 132
```

```
RESULT 15
CC13_CAEEL
ID CC13_CAEEL STANDARD; PRT; 316 AA.
AC P20631;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Cuticle collagen 13 precursor.
GN COL-13 OR F15H10.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=90172409; PubMed=1689778;
RA Park Y.-S., Kramer J.M.;
RT "Tandemly duplicated Caenorhabditis elegans collagen genes differ in
RT their modes of splicing.";
RL J. Mol. Biol. 211:395-406(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Berks M.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: NEMATODE CUTICLES ARE COMPOSED LARGELY OF COLLAGEN-LIKE
CC PROTEINS. THE CUTICLE FUNCTIONS BOTH AS AN EXOSKELETON AND AS A
CC BARRIER TO PROTECT THE WORM FROM ITS ENVIRONMENT.
```

```
CC -!- SUBUNIT: COLLAGEN POLYPEPTIDE CHAINS ARE COMPLEXED WITHIN THE
CC CUTICLE BY DISULFIDE BONDS AND OTHER TYPES OF COVALENT CROSS-
CC LINKS.
CC -!- SIMILARITY: TO OTHER COLLAGENS. STRONG, TO OTHER CUTICLE
CC COLLAGENS. THE MATURE COL-12 AND COL-13 ARE IDENTICAL.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X51623; CAA35955.1; -.
CC EMBL; Z73972; CAA98258.1; -.
CC PIR; S08170; S08170.
CC WormPep; F15H10.2; CE05639.
CC InterPro; IPR002486; Col_cuticle_N.
CC InterPro; IPR000087; Collagen.
CC Pfam; PF01391; Collagen; 2.
CC Pfam; PF01484; Col_cuticle_N; 1.
CC Cuticle; Connective tissue; Repeat; Multigene family; Collagen;
KW Signal.
FT SIGNAL 1 36 POTENTIAL.
FT CHAIN 37 316 CUTICLE COLLAGEN 13.
FT DOMAIN 128 157 TRIPLE-HELICAL REGION.
FT DOMAIN 176 202 TRIPLE-HELICAL REGION.
FT DOMAIN 206 235 TRIPLE-HELICAL REGION.
FT DOMAIN 240 266 TRIPLE-HELICAL REGION.
FT DOMAIN 269 304 TRIPLE-HELICAL REGION.
SQ SEQUENCE 316 AA; 30100 MW; 00C6D08FBC4701AF CRC64;
```

Query Match 41.4%; Score 43.5; DB 1; Length 316;
Best Local Similarity 52.6%; Pred. No. 26;
Matches 10; Conservative 1; Mismatches 5; Indels 3; Gaps 2;

```
QY 1 GAASGLNGCCRC--GARGP 17
   | :|| | | | | | |
Db 115 GGSSG-GSCSCGSGAAGP 132
```

Search completed: July 3, 2002, 11:24:44
Job time: 891 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:24:08 ; Search time 107.89 Seconds
(without alignments)
28.862 Million cell updates/sec

Title: US-09-165-546A-11
Perfect score: 105
Sequence: 1 GAASGLNGCCRCGARGPE 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_19:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archheap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	100.0	142	4 Q9NY13	Q9ny13 homo sapien
2	58	55.2	180	4 Q9Y479	Q9y479 homo sapien
3	58	55.2	210	4 Q9BU80	Q9bu80 homo sapien
4	58	55.2	210	4 Q9UJ89	Q9uj89 homo sapien
5	55	52.4	149	10 Q9FJ67	Q9fj67 arabidopsis
6	51	48.6	172	10 Q94E57	Q94e57 oryza sativ
7	51	48.6	312	5 O18097	O18097 caenorhabdi
8	50	47.6	1561	11 O88286	O88286 mus musculu
9	49	46.7	300	5 Q18620	Q18620 caenorhabdi
10	48	45.7	268	5 Q9V3X2	Q9v3x2 drosophila
11	48	45.7	299	5 Q18302	Q18302 caenorhabdi
12	48	45.7	316	5 Q19111	Q19111 caenorhabdi
13	48	45.7	333	5 Q19050	Q19050 caenorhabdi
14	48	45.7	815	11 Q9JLF6	Q9jlf6 mus musculu
15	47.5	45.2	416	5 O17374	O17374 caenorhabdi
16	47	44.8	236	10 Q9SK78	Q9sk78 arabidopsis

17	47	44.8	270	10 Q93XY5	Q93xy5 arabidopsis
18	47	44.8	281	10 Q9SVU4	Q9svu4 arabidopsis
19	47	44.8	542	10 Q9SZB4	Q9szb4 arabidopsis
20	47	44.8	591	10 Q9LU46	Q9lu46 arabidopsis
21	46	43.8	299	5 Q27318	Q27318 caenorhabdi
22	46	43.8	299	5 Q20805	Q20805 caenorhabdi
23	46	43.8	299	5 Q22393	Q22393 caenorhabdi
24	46	43.8	328	12 Q68387	Q68387 human cytom
25	46	43.8	419	5 Q25599	Q25599 onchocerca
26	46	43.8	1568	4 Q95785	Q95785 homo sapien
27	45.5	43.3	304	5 Q9XUE9	Q9xue9 caenorhabdi
28	45	42.9	123	5 Q9VQM7	Q9vqm7 drosophila
29	45	42.9	196	11 Q9D226	Q9d226 mus musculu
30	45	42.9	284	2 Q9FA10	Q9fa10 acetobacter
31	45	42.9	309	5 O16787	O16787 caenorhabdi
32	45	42.9	439	4 Q9BUG9	Q9bug9 homo sapien
33	45	42.9	528	5 Q9N9K2	Q9n9k2 leishmania
34	45	42.9	590	11 Q91VM4	Q91vm4 mus musculu
35	45	42.9	1225	10 Q94GB9	Q94gb9 oryza sativ
36	44.5	42.4	213	10 Q9SNT0	Q9snt0 oryza sativ
37	44.5	42.4	286	5 Q9U119	Q9u119 leishmania
38	44	41.9	93	15 Q9D204	Q9dz04 human immun
39	44	41.9	125	6 Q95K85	Q95k85 macaca fasc
40	44	41.9	194	5 Q9GNM7	Q9gnm7 oostertagia
41	44	41.9	267	10 Q39589	Q39589 chlamydomon
42	44	41.9	267	10 Q39590	Q39590 chlamydomon
43	44	41.9	267	10 P93108	P93108 chlamydomon
44	44	41.9	267	10 P93109	P93109 chlamydomon
45	44	41.9	268	16 Q9CCN0	Q9ccn0 mycobacteri

ALIGNMENTS

RESULT 1
Q9NY13
ID Q9NY13 PRELIMINARY; PRT; 142 AA.
AC Q9NY13;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TremBLrel. 15, Last annotation update)
DE HYPOTHETICAL 13.9 KDA PROTEIN (FRAGMENT).
GN LAGE-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lethe B.G.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AJ275978; CAB76945.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 142 AA; 13895 MW; 27EBE922AC4ACC7B CRC64;

Query Match 100.0%; Score 105; DB 4; Length 142;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
|||||
Db 41 GAASGLNGCCRCGARGPE 58

RESULT 2
Q9Y479
ID Q9Y479 PRELIMINARY; PRT; 180 AA.
AC Q9Y479;
DT 01-NOV-1999 (TremBLrel. 12, Created)
DT 01-NOV-1999 (TremBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)


```
DE LAGE-1S PROTEIN (CANCER/TESTIS ANTIGEN 2).
GN LAGE1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MELANOMA;
RX MEDLINE=99325550; PubMed=10399963;
RA Aarnoudse C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.;
RT "Interleukin-2-induced, melanoma-specific T cells recognize CAMEL, an
RT unexpected translation product of LAGE-1.";
RL Int. J. Cancer 82:442-448(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Aradhya S., Bardaro T., Galgoczy P., Yamagata T., Esposito T.,
RA Patlan H., Ciccodicola A., Kenwrick S., Platzer M., D'Urso M.,
RA Nelson D.L.;
RT "Multiple pathogenic and benign genomic rearrangements occur at a 35-
RT kb duplication involving the NEMO and the LAGE2 genes.";
RL Hum. Mol. Genet. 0:0-0(2001).
DR EMBL; AJ012834; CAA10194.1; -.
DR EMBL; AF277315; AAL27015.1; -.
SQ SEQUENCE 180 AA; 18236 MW; 9077FAF953543A25 CRC64;

Query Match 55.2%; Score 58; DB 4; Length 180;
Best Local Similarity 61.1%; Pred. No. 0.21;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
   |||| :| | |||| |
Db 67 GAASAQDGRCPGARRPD 84

RESULT 3
Q9BU80
ID Q9BU80 PRELIMINARY; PRT; 210 AA.
AC Q9BU80;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CANCER/TESTIS ANTIGEN 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA, CHORIOCARCINOMA;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBDJ databases.
DR EMBL; BC002833; AAH02833.1; -.
SQ SEQUENCE 210 AA; 21089 MW; 8FB5BF04FB04E8BE CRC64;

Query Match 55.2%; Score 58; DB 4; Length 210;
Best Local Similarity 61.1%; Pred. No. 0.24;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
   |||| :| | |||| |
Db 67 GAASAQDGRCPGARRPD 84

RESULT 4
Q9UJ89
ID Q9UJ89 PRELIMINARY; PRT; 210 AA.
AC Q9UJ89;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
```

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DE LAGE-1L PROTEIN.
GN LAGE-1L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MELANOMA;
RX MEDLINE=99325550; PubMed=10399963;
RA Aarnoudse C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.;
RT "Interleukin-2-induced, melanoma-specific T cells recognize CAMEL, an
RT unexpected translation product of LAGE-1.";
RL Int. J. Cancer 82:442-448(1999).
DR EMBL; AJ012835; CAA10196.1; -.
SQ SEQUENCE 210 AA; 21060 MW; 1DD0B1829735B60A CRC64;

Query Match 55.2%; Score 58; DB 4; Length 210;
Best Local Similarity 61.1%; Pred. No. 0.24;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
   |||| :| | |||| |
Db 67 GAASAQDGRCPGARRPD 84

RESULT 5
Q9FJ67
ID Q9FJ67 PRELIMINARY; PRT; 149 AA.
AC Q9FJ67;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GENOMIC DNA, CHROMOSOME 5, P1 CLONE:MTE17.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=99087489; PubMed=9872454;
RA Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VII.
RT Sequence features of the regions of 1,013,767 bp covered by sixteen
RT physically assigned p1 and TAC clones.";
RL DNA Res. 5:297-308(1998).
DR EMBL; AB015479; BAB08560.1; -.
SQ SEQUENCE 149 AA; 16682 MW; 81F16977DD7B93AA CRC64;

Query Match 52.4%; Score 55; DB 10; Length 149;
Best Local Similarity 56.2%; Pred. No. 0.52;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARG 16
   | :| | |||| |
Db 118 GCGNGCGCIRCGRG 133

RESULT 6
Q94E57
ID Q94E57 PRELIMINARY; PRT; 172 AA.
AC Q94E57;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE OSJNBA0089K24.13 PROTEIN.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
```

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
RT clone:OSJNBa009K24.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003215; BAB62555.1; -.
SQ SEQUENCE 172 AA; 18162 MW; 9EF8EDBFA41112C7 CRC64;

Query Match 48.6%; Score 51; DB 10; Length 172;
Best Local Similarity 57.9%; Pred. No. 2.4;
Matches 11; Conservative 1; Mismatches 3; Indels 4; Gaps 1;

QY 1 GAASGL-----NGCCRCGAR 15
||:| ||| |||||
Db 66 GAGAGARERNGCGRCGAR 84

RESULT 7

O18097 PRELIMINARY; PRT; 312 AA.
AC O18097;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE T21B4.2 PROTEIN.
GN T21B4.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Smye R.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z81124; CAB03369.1; -.
DR InterPro; IPR000087; Collagen.
DR InterPro; IPR002486; Col_cuticle_N.
DR Pfam; PF01484; Col_cuticle_N; 1.
SQ SEQUENCE 312 AA; 28866 MW; 46E942A8D85E904C CRC64;

Query Match 48.6%; Score 51; DB 5; Length 312;
Best Local Similarity 52.6%; Pred. No. 4;
Matches 10; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

QY 1 GAASGLNGCCRC--GARGP 17
| | ||| | |||
Db 111 GGGGGGGCGCGGIGAAGP 129

RESULT 8

O88286 PRELIMINARY; PRT; 1561 AA.
AC O88286;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE WIZL.
GN WIZ OR WIZ.
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Matsumoto K., Ishii N., Yoshida S., Shiosaka S., Wanaka A.,
RA Tohyama M.;
RT "Molecular Cloning and Distinct Developmental Expression Pattern of
RT Spliced Forms of A Novel Zinc Finger Gene wiz in The Cerebellum.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AB012265; BAA32790.1; -.
DR MGD; MGI:1332638; Wiz.
DR InterPro; IPR000822; Znf-C2H2.
DR Pfam; PF00096; zf-C2H2; 10.
DR PRINTS; PR00048; ZINCFINGER.
DR SMART; SM00355; Znf_C2H2; 10.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 8.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 7.
KW DNA-binding; Metal-binding; Nuclear protein; Zinc-finger.
SQ SEQUENCE 1561 AA; 171243 MW; 8A0130A7B5374CF6 CRC64;

Query Match 47.6%; Score 50; DB 11; Length 1561;
Best Local Similarity 52.9%; Pred. No. 23;
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGP 17
| : |||| | || |
Db 326 GDSSGLNTCVHCGFTAP 342

RESULT 9

O18620 PRELIMINARY; PRT; 300 AA.
AC O18620;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE C44C10.1 PROTEIN.
GN C44C10.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Cottage A.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z69787; CAA93642.1; -.
DR InterPro; IPR000087; Collagen.
DR InterPro; IPR002486; Col_cuticle_N.
DR Pfam; PF01391; Collagen; 2.
DR Pfam; PF01484; Col_cuticle_N; 1.
SQ SEQUENCE 300 AA; 28526 MW; 1404CC8AD5581684 CRC64;

Query Match 46.7%; Score 49; DB 5; Length 300;
Best Local Similarity 52.6%; Pred. No. 7.8;
Matches 10; Conservative 1; Mismatches 6; Indels 2; Gaps 1;

QY 1 GAASGLNGCCRCG--ARGP 17
| : | ||| || | ||
Db 97 GSFSSQGGCCGCVSAGP 115

```
RESULT 10
Q9V3X2          PRELIMINARY;          PRT;    268 AA.
AC  Q9V3X2;
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE  BCDNA:LD19727 PROTEIN.
GN  TSP96F OR BCDNA:LD19727 OR CG6120.
OS  Drosophila melanogaster (Fruit fly).
OC  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC  Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC  Ephydroidea; Drosophilidae; Drosophila.
OX  NCBI_TaxID=7227;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=BERKELEY;
RX  MEDLINE=20196006; PubMed=10731132;
RA  Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA  Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA  George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA  Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA  Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA  Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA  Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA  Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA  Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA  Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA  Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA  Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA  de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA  Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA  Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA  Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA  Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA  Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA  Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA  Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA  Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA  Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA  Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA  Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA  Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA  Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA  Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA  Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA  Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA  Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA  Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA  Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA  Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA  Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA  Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA  Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT  "The genome sequence of Drosophila melanogaster.";
RL  Science 287:2185-2195(2000).
RN  [2]
RP  SEQUENCE FROM N.A.
RA  Tsang G., Brokstein P., Frise E., Harvey D., Evans-Holm M.,
RA  Lewis S.E., Suh C., Rubin G.M.;
RT  "Full Length Drosophila melanogaster cDNA sequence.";
RL  Submitted (JUN-1999) to the EMBL/GenBank/DBDJ databases.
DR  EMBL; AE003753; AAF56520.1; -.
DR  EMBL; AF160941; AAD46881.1; -.
DR  FlyBase; FBgn0027865; Tsp96F.
DR  InterPro; IPR000301; Transmem_4.
DR  Pfam; PF00335; transmembrane4; 1.
DR  PRINTS; PR00259; TMFOUR.
SQ  SEQUENCE 268 AA; 29849 MW; 49CFD43591A1B712 CRC64;
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Query Match 45.7%; Score 48; DB 5; Length 268;

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Best Local Similarity 87.5%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GLNGCCRC 12
Db 2 GLNGCCSC 9

RESULT 11
Q18302          PRELIMINARY;          PRT;    299 AA.
ID  Q18302;
AC  Q18302;
DT  01-NOV-1996 (TrEMBLrel. 01, Created)
DT  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  C29F4.1 PROTEIN.
GN  C29F4.1.
OS  Caenorhabditis elegans.
OC  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC  Rhabditidae; Peloderinae; Caenorhabditis.
OX  NCBI_TaxID=6239;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Kershaw J.K.;
RL  Submitted (JAN-1996) to the EMBL/GenBank/DBDJ databases.
RN  [2]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=99069613; PubMed=9851916;
RA  none;
RT  "Genome sequence of the nematode C.elegans: A platform for
RT  investigating biology.";
RL  Science 282:2012-2018(1998).
DR  EMBL; Z68335; CAA92729.1; -.
DR  InterPro; IPR000087; Collagen.
DR  InterPro; IPR002486; Col_cuticle_N.
DR  Pfam; PF01391; Collagen; 2.
DR  Pfam; PF01484; Col_cuticle_N; 1.
DR  SEQUENCE 299 AA; 28680 MW; 3359443F45BB565C CRC64;
SQ  SEQUENCE 299 AA; 28680 MW; 3359443F45BB565C CRC64;

Query Match 45.7%; Score 48; DB 5; Length 299;
Best Local Similarity 57.9%; Pred. No. 11;
Matches 11; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

QY 1 GAAS--GLNGCCRCGARGP 17
Db 89 GAASAGGCDACCLPGAAGP 107

RESULT 12
Q19111          PRELIMINARY;          PRT;    316 AA.
ID  Q19111;
AC  Q19111;
DT  01-NOV-1996 (TrEMBLrel. 01, Created)
DT  01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  F02D10.1 PROTEIN.
GN  F02D10.1.
OS  Caenorhabditis elegans.
OC  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC  Rhabditidae; Peloderinae; Caenorhabditis.
OX  NCBI_TaxID=6239;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Swinburne J.;
RL  Submitted (NOV-1995) to the EMBL/GenBank/DBDJ databases.
RN  [2]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=99069613; PubMed=9851916;
RA  none;
RT  "Genome sequence of the nematode C.elegans: A platform for
RT  investigating biology.";
RL  Science 282:2012-2018(1998).
```


DR EMBL; 267990; CAA91932.1; -.
DR InterPro; IPR000087; Collagen.
DR InterPro; IPR002486; Col_cuticle_N.
DR Pfam; PF01484; Col_cuticle_N; 1.
SQ SEQUENCE 316 AA; 29444 MW; 4D76D5BA07923499 CRC64;

Query Match 45.7%; Score 48; DB 5; Length 316;
Best Local Similarity 47.1%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 9; Gaps 0;

QY 1 GAASGLNGCCRCGARGP 17
| | | | |
Db 108 GGGGGCTGCNPGPPGP 124

RESULT 13
Q19050
ID Q19050 PRELIMINARY; PRT; 333 AA.
AC Q19050;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E03G2.4 PROTEIN.
GN E03G2.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA McMurray A.A.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; 268113; CAA92150.1; -.
DR InterPro; IPR000087; Collagen.
DR InterPro; IPR002486; Col_cuticle_N.
DR Pfam; PF01391; Collagen; 2.
DR Pfam; PF01484; Col_cuticle_N; 1.
SQ SEQUENCE 333 AA; 34388 MW; 0A25985E45C69068 CRC64;

Query Match 45.7%; Score 48; DB 5; Length 333;
Best Local Similarity 47.1%; Pred. No. 12;
Matches 8; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGP 17
| | | | |
Db 130 GSQGGGGCCGCGQSP 146

RESULT 14
Q9JLF6
ID Q9JLF6 PRELIMINARY; PRT; 815 AA.
AC Q9JLF6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE TRANSLUTAMINASE TYPE 1.
GN TGM1 OR TGASE1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20036556; PubMed=10567386;

RA Hiragi T., Sasaki H., Nagafuchi A., Sabe H., Shen S.C., Matsuki M.,
Yamanishi K., Tsukita S.;
RT "transglutaminase type 1 and its cross-linking activity are
concentrated at adherens junctions in simple epithelial cells.";
RL J. Biol. Chem. 274:34148-34154(1999).
DR EMBL; AF186373; AAF35986.1; -.
DR HSSP; P00488; 1GGU.
DR MGD; MGI:98730; Tgml.
DR InterPro; IPR001102; Transglutmnse.
DR InterPro; IPR002931; Transglut_core.
DR Pfam; PF00927; Transglutamin_C; 1.
DR Pfam; PF00868; Transglutamin_N; 1.
DR Pfam; PF01841; Transglut_core; 1.
DR SMART; SM00460; TGC; 1.
DR PROSITE; PS00547; TRANSLUTAMINASES; 1.
SQ SEQUENCE 815 AA; 89795 MW; E4688C6E2E07EA8C CRC64;

Query Match 45.7%; Score 48; DB 11; Length 815;
Best Local Similarity 63.6%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 8 GCCRCGARGPE 18
| | | | | | | |
Db 52 GCCSCGNRGDD 62

RESULT 15
O17374
ID O17374 PRELIMINARY; PRT; 416 AA.
AC O17374;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 39.7 KDA PROTEIN.
GN T13B5.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Maggi L.;
RT "The sequence of C. elegans cosmid T13B5.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026211; AAB71295.1; -.
DR InterPro; IPR000087; Collagen.
DR InterPro; IPR002486; Col_cuticle_N.
DR Pfam; PF01391; Collagen; 2.
DR Pfam; PF01484; Col_cuticle_N; 1.
KW Hypothetical protein.
SQ SEQUENCE 416 AA; 39741 MW; DA62E651CACAF617 CRC64;

Query Match 45.2%; Score 47.5; DB 5; Length 416;
Best Local Similarity 50.0%; Pred. No. 17;
Matches 12; Conservative 1; Mismatches 4; Indels 7; Gaps 2;

QY 1 GAASGLNG-----CCRC--GARGP 17
|||:| | || | || ||
Db 111 GAAAGGGGGGGSCCSCGIGAAGP 134

Search completed: July 3, 2002, 11:24:09
Job time: 916 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:08:49 ; Search time 136.43 Seconds
(without alignments)
14.655 Million cell updates/sec

Title: US-09-165-546A-11

Perfect score: 105

Sequence: 1 GAASGLNGCCRCGARGPE 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
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22:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	100.0	18	21	AA52438 Human tumour antig
2	105	100.0	18	22	AAU01542 HLA-DR53 recognisi
3	105	100.0	18	22	AAB69942 Human NY-ESO-1 HLA
4	105	100.0	180	19	AAW69665 Human NY-ESO-1 pro
5	105	100.0	180	19	AAW62584 Cancer associated
6	105	100.0	180	20	AAW05965 Human cancer antig
7	105	100.0	180	21	AAB03154 Human oesophageal
8	105	100.0	180	21	AAW70862 Human tumour antig
9	105	100.0	180	21	AAW52430 Human tumour antig
10	105	100.0	180	22	AAG67164 Amino acid sequenc
11	105	100.0	180	22	AAE07714 Human NY ESO-1 pro

12	105	100.0	180	22	AAU01535 Human NY-ESO-1 tum
13	105	100.0	180	22	AAB69946 Human NY-ESO-1 pro
14	105	100.0	397	22	AAE13122 NY-ESO-1C-HER-2 me
15	64	61.0	10	20	AAW06012 Human cancer antig
16	63	60.0	10	20	AAW06063 Human cancer antig
17	63	60.0	10	20	AAW06008 Human cancer antig
18	59	56.2	9	20	AAW06044 Human cancer antig
19	58	55.2	180	19	AAW69664 Human LAGE-1 clone
20	58	55.2	180	21	AAW70860 Human LAGE-1 splic
21	58	55.2	210	19	AAW69663 Human LAGE-1 clone
22	58	55.2	210	21	AAW70861 Human LAGE-1 unspl
23	57	54.3	10	20	AAW06060 Human cancer antig
24	57	54.3	10	20	AAW05994 Human cancer antig
25	56	53.3	269	22	ABG03645 Novel human diagno
26	53	50.5	9	20	AAW06047 Human cancer antig
27	51	48.6	532	22	AAM41641 Human polypeptide
28	50	47.6	226	22	AAU21593 Novel human neopla
29	49	46.7	73	22	ABG18126 Novel human diagno
30	48	45.7	90	22	ABB03117 Human musculoskele
31	48	45.7	111	22	ABG19831 Novel human diagno
32	48	45.7	268	22	ABB62086 Drosophila melanog
33	48	45.7	982	19	AAW77288 Zebrafish differen
34	48	45.7	1679	22	AAU07343 1-aminocyclopropan
35	47.5	45.2	248	22	AAU53875 Propionibacterium
36	47	44.8	10	20	AAW06059 Human cancer antig
37	47	44.8	10	20	AAW05993 Human cancer antig
38	47	44.8	62	22	ABG10946 Novel human diagno
39	47	44.8	72	22	AAU49364 Propionibacterium
40	47	44.8	166	21	AAG09880 Arabidopsis thalia
41	47	44.8	166	21	AAG17711 Arabidopsis thalia
42	47	44.8	166	21	AAG50266 Arabidopsis thalia
43	47	44.8	236	21	AAG17710 Arabidopsis thalia
44	47	44.8	236	21	AAG50265 Arabidopsis thalia
45	47	44.8	247	21	AAG09879 Arabidopsis thalia

ALIGNMENTS

RESULT	1
AA52438	
ID	AA52438 standard; Protein; 18 AA.
XX	
AC	AA52438;
XX	
DT	15-FEB-2000 (first entry)
XX	
DE	Human tumour antigen NY-ESO-1 peptide #11.
XX	
KW	Cancer; tumour; antigen; MHC; major histocompatibility complex; Class II;
KW	T-cell; helper; stimulation; proliferation; treatment;
KW	diagnosis; prevention; melanoma; breast cancer; ovarian cancer;
KW	prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer;
KW	lymphoma.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
PN	WO9953938-A1.
XX	
PD	28-OCT-1999.
XX	
PF	24-MAR-1999; 99WO-US06875.
XX	
PR	17-APR-1998; 98US-0062422.
PR	02-OCT-1998; 98US-0165546.
XX	
PA	(LUDW-) LUDWIG INST CANCER RES.
XX	
PI	Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
PI	Gure A, Ritter G;
XX	
DR	WPI; 2000-038483/03.

XX Novel peptides which bind to MHC class I and MHC class II molecules,
PT useful for therapeutic and diagnostic purposes -
XX
XX
PS Claim 4; Page 22; 49pp; English.
XX
CC Peptides #8-#13 (AAAY52435-Y52440) are peptides derived from the human
CC tumour antigen, NY-ESO-1 (AAAY52430) which can bind to MHC(major
CC histocompatibility Class II HLA-DR53 molecules, thereby stimulating
CC proliferation of helper T-cells. cDNA encoding NY-ESO-1 was initially
CC isolated from an oesophagus squamous cell cancer cDNA library. Tissue
CC localisation studies revealed it to be expressed at high levels
CC in normal ovary and testis but not in normal colon, kidney, liver,
CC brain, oesophagus and skin. It was expressed in certain tumours and
CC tumour cell lines with some degree of frequency - these included
CC melanoma specimens and cell lines, and breast and bladder cancer
CC specimens, with expression in other tumour types being sporadic.
CC These NY-ESO-1-derived peptides may be used in methods and
CC compositions used for the treatment, diagnosis and prevention of
CC cancers (such as melanoma, breast cancer, prostate cancer, lung
CC cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer,
CC or lymphoma) and to stimulate the proliferation of T cells.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 105; DB 21; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
| | | | | | | | | | | | | | | |
Db 1 gaasglngccrcgargpe 18

RESULT 2
AAU01542
ID AAU01542 standard; Peptide; 18 AA.
XX
AC AAU01542;
XX
DT 18-JUL-2001 (first entry)
XX
DE HLA-DR53 recognising NY-ESO-1 peptide #4.
XX
KW NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
KW human leukocyte antigen-determining region; disease progression;
KW disease regression; disease onset; body tissue; body fluid; enzyme label;
KW radioactive label; monoclonal antibody.
XX
OS Homo sapiens.
XX
PN WO200123560-A2.
XX
PD 05-APR-2001.
XX
PF 26-SEP-2000; 2000WO-US26411.
XX
PR 29-SEP-1999; 99US-0408036.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Tureci O, Sahin U, Pfreundschuh M;
XX
DR WPI; 2001-266156/27.
XX
PT Polypeptides binding to major histocompatibility complex class II human
PT leukocyte antigen-determining region molecule having amino acid
PT sequence found in tumour rejection antigen precursor used for
PT stimulating proliferation of helper T cells -
XX
PS Example 13; Page 19; 62pp; English.

XX The sequence represents a human NY-ESO-1 tumour rejection antigen
CC precursor fragment which recognises and binds to HLA-DR53. NY-ESO-1 and
CC SSX-2 polypeptides, or fragments of, bind to major histocompatibility
CC complex (MHC) Class II molecules such as human leukocyte
CC antigen-determining region (HLA-DR) molecules and stimulate proliferation
CC of helper T cells. The peptides can be administered to an HLA-DR positive
CC subject in order to stimulate the helper T cells. An MHC Class II
CC HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell or
CC present in free form is useful for this stimulation. The nucleic acid is
CC useful for screening for a cancerous condition, which involves contacting
CC a subject sample to a cell line transfected with the immunoreactive cell
CC (helper T cell), where interaction is indicative of cancer. In addition,
CC a sample from a patient (for example, a body fluid or tissue) can be
CC monitored for the amount of the complex present in the bloodstream. This
CC is useful for determining regression, progression or onset of a cancerous
CC condition. The method involves contacting the sample with a radioactive
CC labelled or enzyme labelled monoclonal antibody which specifically binds
CC with the complex.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 105; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
| | | | | | | | | | | | | | | |
Db 1 gaasglngccrcgargpe 18

RESULT 3
AAB69942
ID AAB69942 standard; Peptide; 18 AA.
XX
AC AAB69942;
XX
DT 27-APR-2001 (first entry)
XX
DE Human NY-ESO-1 HLA-DR53 binding motif #4.
XX
KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW non-small cell lung carcinoma; tumour status determination.
XX
OS Homo sapiens.
XX
PN WO200107917-A1.
XX
PD 01-FEB-2001.
XX
PF 14-JUL-2000; 2000WO-US19220.
XX
PR 23-JUL-1999; 99US-0359503.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.
XX
PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
XX
DR WPI; 2001-182822/18.
XX
PT Method useful for determining the status (e.g. progression, regression
PT or stability of the disease) of a cancerous condition, involves
PT determining the levels of NY-ESO-1 specific antibodies in a sample
PT taken from a patient -
XX
PS Example 16; Page 28; 50pp; English.
XX
CC The present sequence is given in a specification relating to a method
CC for determining the status of a cancerous condition in a patient

CC with a tumour that expresses NY-ESO-1. The method comprises assaying a
CC sample taken from the patient for antibodies that specifically bind to
CC the NY-ESO-1 and comparing the value obtained to a prior value obtained
CC from assay of a prior sample taken from the patient. Any difference
CC between the values is indicative of a change in status of the cancerous
CC condition. The method is useful for determining whether a cancerous
CC condition is progressing, regressing or remaining stable, in particular
CC in patients receiving treatment for a melanoma, adenocarcinoma,
CC non-small cell lung carcinoma or bladder carcinoma.

XX Sequence 18 AA;

Query Match 100.0%; Score 105; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
Db 1 gaasgngccrcgargpe 18
|||||

RESULT 4
AAW69665
ID AAW69665 standard; Protein; 180 AA.

XX AC AAW69665;

XX DT 27-OCT-1998 (first entry)

XX DE Human NY-ESO-1 protein sequence, formerly known as LL-1.2 clone.

XX KW Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour.

XX OS Homo sapiens.

XX PN WO9832855-A1.

XX PD 30-JUL-1998.

XX PF 27-JAN-1998; 98WO-US01445.

XX PR 27-JAN-1997; 97US-0791495.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Boon-Falleur T, De Smet C, Godelaine D, Lethe B;
PI Lucas S;

XX DR WPI; 1998-427951/36.
DR N-PSDB; AAV50348.

XX PT New isolated LAGE-1 tumour associated nucleic acids - used to
PT develop products for the diagnosis and treatment of LAGE-1
PT associated disorders, particularly tumours

XX PS Example 2; Page 57-58; 73pp; English.

XX CC The present sequence represents human NY-ESO-1, formerly known as LL-1.2
CC clone, which is used in an example from the present invention which
CC describes IAGE-1 tumour associated protein (TAP). The present invention
CC also describes: (1) a method for treating a subject with a disorder
CC characterised by expression of a LAGE-1 nucleic acid molecule or an
CC expression product, comprising administering to the subject autologous
CC cytolytic T cells to ameliorate the disorder, where the cytolytic T
CC cells are specific for complexes of an HLA molecule and a LAGE-1 TAP or
CC an immunogenic fragment; (2) a method for treating a subject with a
CC disorder characterised by expression of a LAGE-1 nucleic acid molecule
CC or an expression product, comprising administering a LAGE-1 TAP or an
CC immunogenic fragment to ameliorate the disorder; and (3) a method for
CC selectively enriching a population of T cells with cytolytic T cells
CC specific for a LAGE-1 TAP comprising contacting an isolated population
CC of T cells with an agent presenting a complex of a LAGE TAP or an

CC immunogenic fragment and a HLA presenting molecule to selectively
CC enrich the isolated population of T cells with the cytolytic T cells.
CC The methods and products from the present invention can be used for the
CC diagnosis and treatment of LAGE-1 associated disorders, particularly
CC tumours.

XX Sequence 180 AA;

Query Match 100.0%; Score 105; DB 19; Length 180;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
Db 67 gaasgngccrcgargpe 84
|||||

RESULT 5
AAW62584
ID AAW62584 standard; Protein; 180 AA.

XX AC AAW62584;

XX DT 17-SEP-1998 (first entry)

XX DE Cancer associated antigen NY-ESO-1.

XX KW Cancer associated antigen; NY-ESO-1; regression; progression; onset;
XX cancer; treatment; diagnosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Misc-difference 7 /note= "potential myristoylation site"

FT Misc-difference 9 /note= "potential myristoylation site"

FT Misc-difference 11 /note= "potential phosphorylation site"

FT Misc-difference 98 /note= "potential phosphorylation site"

FT Misc-difference 134 /note= "potential phosphorylation site"

FT Misc-difference 138 /note= "potential phosphorylation site"

XX PN WO9814464-A1.

XX PD 09-APR-1998.

XX PF 15-SEP-1997; 97WO-US16335.

XX PR 03-OCT-1996; 96US-0725182.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Chen Y, Drijfhout JW, Gure A, Jager E, Knuth A;
PI Old LJ, Scanlan M;

XX DR WPI; 1998-286417/25.
DR N-PSDB; AAV38566.

XX PT New isolated cancer associated antigen - is used to develop products
PT for the diagnosis and treatment of cancers and for monitoring cancer
PT therapy

XX PS Claim 8; Fig 3; 49pp; English.

XX CC The present sequence represents a cancer associated antigen. The clone
CC from which the DNA sequence is obtained is designated NY-ESO-1. The
CC specification described a method for determining regression, progression
CC of onset of a cancerous condition, comprising monitoring a sample from a

CC patient with the cancerous condition for a parameter selected from
CC NY-ESO-1 protein, a peptide derived from NY-ESO-1 protein and cytolytic
CC T cells specific for the peptide and an MHC molecule with which it
CC non-covalently complexes. Methods for the treatment of a cancerous
CC condition are also described. The NY-ESO-1 protein and peptides derived
CC from it can be used for diagnosis and treatment of cancers and to monitor
CC the efficacy of a therapeutic regime.

XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 105; DB 19; Length 180;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
| | | | | | | | | | | | | | | | | |
Db 67 gaasglnGCCRCGARGPE 84

RESULT 6
AAY05965
ID AAY05965 standard; Protein; 180 AA.
XX
AC AAY05965;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 ORF1 protein.
XX

KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer antigen; human; leukaemia;
KW non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; ORF1.

XX Homo sapiens.

XX WO9918206-A2.

XX 15-APR-1999.

PF 21-SEP-1998; 98WO-US19609.

PR 08-OCT-1997; 97US-0061428.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Rosenberg SA, Wang RF;

XX WPI; 1999-277270/23.

DR N-PSDB; AAX58599.

XX Cancer antigen NY ES01/CAG-3

PS Claim 4; Fig 3A; 88pp; English.

XX The present sequence represents the ORF1 protein encoded by
CC open reading frame 1 of the human ESO-1/CAG-3 (or CAG-3) gene.
CC CAG-3 is a new and potent tumour antigen capable of eliciting an
CC antigen specific immune response by T cells. Cancer peptides
CC comprising ORF1, ORF2 (see AAY05966), portions of these peptides and
CC their variants (see AAY05965-87), are useful as cancer vaccines that
CC protect the recipient from development of cancer. The invention
CC provides vectors and host cells (also useful as vaccines); a
CC method of diagnosis of cancer or precancer; a transgenic animal;
CC antisense oligonucleotides that inhibit expression of the cancer
CC peptide or tumour antigen; antibodies reacting with the CAG-3
CC cancer peptide, useful in diagnostic and detection assays; and
CC methods for preventing or inhibiting cancer by administering a
CC cancer peptide, with or without an HLA molecule. The cancer

CC peptides form part of, or are derived from, cancers such as primary
CC or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer,
CC liver cancer, leukaemia, uterine cancer, cervical cancer, bladder
CC cancer, kidney cancer and adenocarcinomas such as breast, prostate,
CC ovarian, pancreatic and thyroid cancers. Melanoma is treated by
CC inducing cancer-specific T cells in vitro for subsequent return to
CC a patient.

XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 105; DB 20; Length 180;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
| | | | | | | | | | | | | | | | | |
Db 67 gaasglnGCCRCGARGPE 84

RESULT 7
AAB03154
ID AAB03154 standard; Protein; 180 AA.
XX
AC AAB03154;
XX
DT 23-OCT-2000 (first entry)
XX
DE Human oesophageal cancer-associated antigen NY-ESO-1.
XX

KW Oesophageal cancer associated antigen; NY-ESO-1; human;
KW immunogen; oesophageal carcinoma; melanoma; ovary; testis;
KW transmembrane domain; antibody; diagnostic marker; drug delivery target.
XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 7 /note= "Potential N-myristoylation site"

FT Modified-site 9 /note= "Potential N-myristoylation site"

FT Modified-site 11 /note= "Potential O-phosphorylation site"

FT Modified-site 98 /note= "Potential O-phosphorylation site"

FT Modified-site 134 /note= "Potential O-phosphorylation site"

FT Modified-site 138 /note= "Potential O-phosphorylation site"

FT Domain 152..172 /note= "Potential transmembrane domain"

XX US6069233-A.

XX 30-MAY-2000.

PF 26-JAN-1998; 98US-0013150.

PR 03-OCT-1996; 96US-0725381.

XX (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.
PA (LUDW-) LUDWIG INST CANCER RES.

XX Scanlan M, Gure AO, Chen Y, Tureci O, Sahin U, Pfreundschuh M;
PI Old LJ;

XX WPI; 2000-410880/35.

DR N-PSDB; AAA61483.

XX New isolated esophageal cancer-associated antigen useful as markers for
PT producing antibodies and as targets for identifying abnormal
PT conditions, e.g. infections and cancer -

FT	Peptide	/note= "Peptide presented by MHC Class I HLA-B44"
FT		107..116
FT	Peptide	/note= "Peptide presented by MHC Class I HLA-A24"
FT		110..118
FT	Peptide	/note= "Peptide presented by MHC Class I HLA-B52"
FT		113..121
FT	Peptide	/note= "Peptide presented by MHC Class I HLA-B7"
FT		113..122
FT	Peptide	/note= "Peptide presented by MHC Class I HLA-B7 and HLA-B52"
FT		115..124
FT	Peptide	/note= "Peptide presented by MHC Class I HLA-A3"
FT		118..126
FT	Peptide	/note= "Peptide presented by MHC Class I HLA-B35"
FT		124..133
FT	Peptide	/note= "Peptide presented by MHC Class I HLA-B52"
FT		125..133
FT	Peptide	/note= "Peptide presented by MHC Class I HLA-A24"
FT		138..147
FT	Peptide	/note= "Peptide presented by MHC Class I HLA-B8"
FT		139..147
FT	Peptide	/note= "Peptide presented by MHC Class I HLA-B7"
FT		145..153
FT	Peptide	/note= "Peptide presented by MHC Class I HLA-A24 and HLA-B52"
FT		153..162
FT	Peptide	/note= "Peptide presented by MHC Class I HLA-B52"
FT		154..162
FT	Peptide	/note= "Peptide presented by MHC Class I HLA-B52"
FT		154..163
FT	Peptide	/note= "Peptide presented by MHC Class I HLA-B52"
FT		156..167
FT	Peptide	/note= "Peptide (AAV52434) presented by MHC Class I 158..166
FT	HLA-A2" Peptide	
FT		158..166
FT	Peptide	/note= "Peptide presented by MHC Class I HLA-A3"
FT		159..167
FT	Peptide	/note= "Peptide presented by MHC Class I HLA-A3"
FT		162..170
FT	Peptide	/note= "Peptide presented by MHC Class I HLA-B52"
XX		
XX	W09953938-A1.	
XX		
XX	28-OCT-1999.	
XX		
XX	24-MAR-1999;	99WO-US06875.
XX		
XX	17-APR-1998;	98US-0062422.
XX	02-OCT-1998;	98US-0165546.
XX		
XX	(LUDW-) LUDWIG INST CANCER RES.	
XX		
XX	Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ; Gure A, Ritter G;	
XX		
XX	WPI; 2000-038483/03.	
XX	N-PSDB; AAZ38380.	
XX		
XX	Novel peptides which bind to MHC class I and MHC class II molecules, useful for therapeutic and diagnostic purposes -	
XX		
XX	Claim 30; Fig 3; 49pp; English.	
XX		
XX	This sequence represents a human tumour antigen, NY-ESO-1, the cDNA encoding which was isolated from an oesophagus squamous cell cancer library. Tissue localisation studies revealed it to be expressed at high levels in normal ovary and testis but not in normal colon, kidney, liver, brain, oesophagus and skin. It was expressed in certain tumours and tumour cell lines with some degree of frequency - these included melanoma specimens and cell lines, and breast and bladder cancer specimens, with expression in other tumour types being sporadic. Peptides derived from NY-ESO-1 are bound by both MHC (major histocompatibility complex) Class I and Class II molecules for presentation to T-cells. Peptides AAY52431-Y52434 bind to Class I HLA-A2	

molecules, thereby stimulating proliferation of cytotoxic T-cells, while peptides AAY52435-Y52440 bind to Class II HLA-DR53 molecules, stimulating helper T-cell proliferation. The peptides derived from NY-ESO-1 may be used in methods and compositions used for the treatment, diagnosis and prevention of cancers (such as melanoma, breast cancer, prostate cancer, lung cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer, or lymphoma) and to stimulate the proliferation of T cells.

XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 105; DB 21; Length 180;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAASGLNGCCRCGARGPE 18
 |
Db 67 gaasglngccrcgargpe 84

RESULT 10
AAG67164

ID AAG67164 standard; Protein; 180 AA.

XX AAG67164;

DT 13-NOV-2001 (first entry)

DE Amino acid sequence of cancer testis tumour antigen NY-ESO-1.
XX
KW Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;
KW HLA; HLA binding peptide; major histocompatibility complex; MHC;
KW tumour; cancer; testis tumour.
XX
OS Homo sapiens.
XX
PN WO200162917-A1.
PD 30-AUG-2001.
XX
PF 22-JAN-2001; 2001WO-US02126.
XX
PR 22-FEB-2000; 2000US-0510635.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Lethe B, Boon-Falleur T;
XX
DR WPI; 2001-550091/61.
DR N-PSDB; AAH75118.
XX
PT Genomic sequences of tumour associated antigen EY-ESO-1 (LAGE-2) useful
PT for diagnosing testicular tumours -
XX
PS Example 5; Fig 3; 50pp; English.
XX
CC The present sequence represents cancer testis tumour antigen NY-ESO-1
CC (also called LAGE-2). NY-ESO-1 is a molecule that is processed to at
CC least one human leukocyte antigen (HLA) binding peptide, which binds
CC to Class I and Class II major histocompatibility complex (MHC).
CC NY-ESO-1 is expressed in tumour mRNA and in testis, but not normal
CC colon, kidney, liver or brain tissue. The presence or level of expression
CC of NY-ESO-1 may be assayed for the diagnosis of cancer, especially
CC testis tumours.
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 105; DB 22; Length 180;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GAASGLNGCCRCGARGPE 18

CC onset of a cancerous condition. The method involves contacting the sample
CC with a radioactive labelled or enzyme labelled monoclonal antibody which
CC specifically binds with the complex.

XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 105; DB 22; Length 180;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
Db 67 gaasglnccrcgargpe 84
|||||

RESULT 13
AAB69946
ID AAB69946 standard; Protein; 180 AA.
XX
AC AAB69946;
XX
DT 27-APR-2001 (first entry)
XX
DE Human NY-ESO-1 protein.
XX
KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW non-small cell lung carcinoma; tumour status determination.

XX Homo sapiens.

XX WO200107917-A1.

XX 01-FEB-2001.

XX 14-JUL-2000; 2000WO-US19220.

XX 23-JUL-1999; 99US-0359503.

XX (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.

PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;

XX WPI; 2001-182822/18.
DR N-PSDB; AAF58634.

XX Method useful for determining the status (e.g. progression, regression
PT or stability of the disease) of a cancerous condition, involves
PT determining the levels of NY-ESO-1 specific antibodies in a sample
PT taken from a patient -

XX Example 5; Fig 3; 50pp; English.

XX The present sequence is human NY-ESO-1 protein. It is provided in a
CC specification relating to a method for determining the status of a
CC cancerous condition in a patient with a tumour that expresses NY-ESO-1.
CC The method comprises assaying a sample taken from the patient for
CC antibodies that specifically bind to the NY-ESO-1 and comparing the
CC value obtained to a prior value obtained from assay of a prior sample
CC taken from the patient. Any difference between the values is indicative
CC of a change in status of the cancerous condition. The method is useful
CC for determining whether a cancerous condition is progressing, regressing
CC or remaining stable, in particular in patients receiving treatment for a
CC melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder
CC carcinoma.

XX Sequence 180 AA;

Query Match 100.0%; Score 105; DB 22; Length 180;

Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
Db 67 gaasglnccrcgargpe 84
|||||

RESULT 14
AAE13122
ID AAE13122 standard; Protein; 397 AA.

XX AAE13122;

XX 28-JAN-2002 (first entry)

XX NY-ESO-IC-HER-2 membrane distal intracellular domain fusion protein.
DE
XX Immunostimulatory fusion protein; IFP; antigen component; therapy;
KW immunostimulatory component; T-cell mediated immune response; DC;
KW dendritic cell; colon cancer; breast carcinoma; ovarian cancer;
KW human; HER-2 membrane distal intracellular domain; NY-ESO-IC;
KW autoimmunogenic cancer/testis antigen.

XX Homo sapiens.

XX WO200174855-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10515.

XX 30-MAR-2000; 2000US-193504P.

XX (DEND-) DENDREON CORP.

XX Laus R, Vidovic D, Graddis T;

XX WPI; 2001-662965/76.
DR N-PSDB; AAD21573.

XX An immunostimulatory fusion protein comprising the intracellular domain
PT of HER-2 and an antigen elicits an immune response to the antigen and
PT is useful for the treatment of associated cancer associated -

XX Disclosure; Page 54-55; 59pp; English.

XX The invention relates to immunostimulatory fusion proteins (IFP) and
CC nucleic acid molecules encoding such proteins. The IFPs comprise a
CC polypeptide antigen component and an immunostimulatory component derived
CC from the intracellular domain of HER-2 protein which is effective to
CC elicit a protective dendritic cell (DC)-induced T-cell mediated cellular
CC immune response to the antigen. IFP or superactivated dendritic cells
CC are used to treat cancer e.g. breast carcinoma, ovarian and colon cancer
CC associated with a particularly antigen. The present sequence is a
CC fusion protein which comprises human autoimmunogenic
CC cancer/testis antigen, NY-ESO-IC and mature human HER-2 membrane distal
CC intracellular domain.

XX Sequence 397 AA;

Query Match 100.0%; Score 105; DB 22; Length 397;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
Db 67 gaasglnccrcgargpe 84
|||||

RESULT 15
AAY06012

ID AAY06012 standard; Peptide; 10 AA.
XX
AC AAY06012;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; human leukocyte antigen; HLA.
XX
OS Homo sapiens.
XX
PN W09918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US19609.
XX
PR 08-OCT-1997; 97US-0061428.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rosenberg SA, Wang RF;
XX
DR WPI; 1999-277270/23.
XX
PT Cancer antigen NY ESO1/CAG-3
XX
PS Example 10; Page 42; 88pp; English.
XX
CC This peptide was identified as an HLA peptide motif following a
CC screen for epitopes from the coding region of human ESO-1/CAG-3
CC ORF1 (see AAX58599). 30 Epitopes (see AAY05988-Y06017) were identified.
CC The present peptide (ranked 25) corresponds to amino acid residues
CC 71-80 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent
CC tumour antigen capable of eliciting an antigen specific immune
CC response by T cells. Cancer peptides (see AAY05967-87) derived from
CC CAG-3, portions of CAG-3 and their variants, are useful as cancer
CC vaccines. A claimed method of preventing or inhibiting cancer
CC involves administering a cancer peptide, with or without an HLA
CC molecule. The cancer peptides form part of, or are derived
CC from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer and
CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
CC thyroid cancers.
XX
SQ Sequence 10 AA;

Query Match 61.0%; Score 64; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GLNGCCRCGA 14
| | | | | | | | | |
Db 1 glngccrcga 10

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:21:01 ; Search time 599.92 Seconds
(without alignments)
10.561 Million cell updates/sec

Title: US-09-165-546A-11
Perfect score: 105
Sequence: 1 GAASGLNGCCRCGARGPE 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :				Pending_Patents_AA_Main:*	
	1:	/cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*			
	2:	/cgn2_6/ptodata/2/paa/US06_COMB.pep:*			
	3:	/cgn2_6/ptodata/2/paa/US07_COMB.pep:*			
	4:	/cgn2_6/ptodata/2/paa/US080_COMB.pep:*			
	5:	/cgn2_6/ptodata/2/paa/US081_COMB.pep:*			
	6:	/cgn2_6/ptodata/2/paa/US082_COMB.pep:*			
	7:	/cgn2_6/ptodata/2/paa/US083_COMB.pep:*			
	8:	/cgn2_6/ptodata/2/paa/US084_COMB.pep:*			
	9:	/cgn2_6/ptodata/2/paa/US085_COMB.pep:*			
	10:	/cgn2_6/ptodata/2/paa/US086_COMB.pep:*			
	11:	/cgn2_6/ptodata/2/paa/US087_COMB.pep:*			
	12:	/cgn2_6/ptodata/2/paa/US088_COMB.pep:*			
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	20:	/cgn2_6/ptodata/2/paa/US096_COMB.pep:*			
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	22:	/cgn2_6/ptodata/2/paa/US098_COMB.pep:*			
	23:	/cgn2_6/ptodata/2/paa/US099_COMB.pep:*			
	24:	/cgn2_6/ptodata/2/paa/US100_COMB.pep:*			
	25:	/cgn2_6/ptodata/2/paa/US101_COMB.pep:*			
	26:	/cgn2_6/ptodata/2/paa/US60_COMB.pep:*			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	105	100.0	18	15	US-09-165-546A-11
2	105	100.0	18	18	US-09-408-036B-10
3	105	100.0	180	11	US-08-791-495-9
4	105	100.0	180	17	US-09-341-829A-9
5	105	100.0	180	17	US-09-392-714-25
6	105	100.0	180	19	US-09-529-206-4
7	105	100.0	180	19	US-09-529-206A-3
					Sequence 11, Appl
					Sequence 10, Appl
					Sequence 9, Appl
					Sequence 25, Appl
					Sequence 4, Appl
					Sequence 3, Appl

8	105	100.0	180	19	US-09-529-206B-3	Sequence 3, Appli
9	105	100.0	180	19	US-09-561-571-3	Sequence 3, Appli
10	105	100.0	180	21	US-09-751-798-8	Sequence 8, Appli
11	105	100.0	180	24	US-10-005-905-3	Sequence 3, Appli
12	105	100.0	180	24	US-10-023-182-8	Sequence 8, Appli
13	105	100.0	180	24	US-10-026-066-3	Sequence 3, Appli
14	105	100.0	180	26	US-60-336-968-11	Sequence 11, Appl
15	105	100.0	397	22	US-09-821-883-27	Sequence 27, Appl
16	63	60.0	10	19	US-09-529-206-24	Sequence 24, Appl
17	63	60.0	10	19	US-09-529-206A-24	Sequence 24, Appl
18	63	60.0	10	19	US-09-529-206A-122	Sequence 122, App
19	63	60.0	10	19	US-09-529-206B-24	Sequence 24, Appl
20	63	60.0	10	19	US-09-529-206B-122	Sequence 122, App
21	59	56.2	9	19	US-09-529-206-81	Sequence 81, Appl
22	59	56.2	9	19	US-09-529-206A-81	Sequence 81, Appl
23	59	56.2	9	19	US-09-529-206B-81	Sequence 81, Appl
24	58	55.2	180	11	US-08-791-495-7	Sequence 7, Appli
25	58	55.2	180	17	US-09-341-829A-7	Sequence 7, Appli
26	58	55.2	210	11	US-08-791-495-5	Sequence 5, Appli
27	58	55.2	210	17	US-09-341-829A-5	Sequence 5, Appli
28	57	54.3	10	19	US-09-529-206-21	Sequence 21, Appl
29	57	54.3	10	19	US-09-529-206A-21	Sequence 21, Appl
30	57	54.3	10	19	US-09-529-206A-119	Sequence 119, App
31	57	54.3	10	19	US-09-529-206B-21	Sequence 21, Appl
32	57	54.3	10	19	US-09-529-206B-119	Sequence 119, App
33	56	53.3	269	1	PCT-US01-08631-34004	Sequence 34004, A
34	54	51.4	51	22	US-09-832-659-8	Sequence 8, Appli
35	54	51.4	177	16	US-09-252-991A-28690	Sequence 28690, A
36	53.5	51.0	113	21	US-09-733-089-23866	Sequence 23866, A
37	53.5	51.0	113	22	US-09-816-660-23866	Sequence 23866, A
38	53	50.5	9	19	US-09-529-206-83	Sequence 83, Appl
39	53	50.5	9	19	US-09-529-206A-83	Sequence 83, Appl
40	53	50.5	9	19	US-09-529-206B-83	Sequence 83, Appl
41	53	50.5	606	26	US-60-187-409-38	Sequence 38, Appl
42	53	50.5	1666	24	US-10-073-912-12	Sequence 12, Appl
43	53	50.5	3518	19	US-09-522-097B-2	Sequence 2, Appli
44	53	50.5	11221	21	US-09-778-963-3	Sequence 3, Appli
45	53	50.5	18636	24	US-10-073-912-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-09-165-546A-11
; Sequence 11, Application US/09165546A
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao,
; Canlan, Matt; Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO
; AMINO ACID SEQUENCES OF NY-ESO-1, WHICH BIND TO
; MHC CLASS I AND MHC CLASS II MOLECULES, AND
; USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,546A
; FILING DATE: 02-Oct-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998


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; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-165-546A-11

Query Match 100.0%; Score 105; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.4e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
| | | | | | | | | | | | | | | |
Db 1 GAASGLNGCCRCGARGPE 18

RESULT 2
US-09-408-036B-10
; Sequence 10, Application US/09408036B
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Isolated Peptides Which Bind to MHC Class II Molecules and Uses T
; FILE REFERENCE: LUD 5624
; CURRENT APPLICATION NUMBER: US/09/408,036B
; CURRENT FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/165,546
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-408-036B-10

Query Match 100.0%; Score 105; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.4e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
| | | | | | | | | | | | | | | |
Db 1 GAASGLNGCCRCGARGPE 18

RESULT 3
US-08-791-495-9
; Sequence 9, Application US/08791495
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
```

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; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-9

Query Match 100.0%; Score 105; DB 11; Length 180;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
| | | | | | | | | | | | | | | |
Db 67 GAASGLNGCCRCGARGPE 84

RESULT 4
US-09-341-829A-9
; Sequence 9, Application US/09341829A
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-341-829A-9

Query Match 100.0%; Score 105; DB 17; Length 180;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
| | | | | | | | | | | | | | | |
Db 67 GAASGLNGCCRCGARGPE 84
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RESULT 5
US-09-392-714-25
; Sequence 25, Application US/09392714A
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Gure, Ali O.
; APPLICANT: Williamson, Barbara
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Cancer Associated Antigens and Uses
; FILE REFERENCE: L0461/7062
; CURRENT APPLICATION NUMBER: US/09/392,714A
; CURRENT FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: PCT/US98/14679
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-392-714-25

Query Match      100.0%; Score 105; DB 17; Length 180;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
   |||||
Db 67 GAASGLNGCCRCGARGPE 84

RESULT 6
US-09-529-206-4
; Sequence 4, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-4

Query Match      100.0%; Score 105; DB 19; Length 180;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
   |||||
Db 67 GAASGLNGCCRCGARGPE 84

RESULT 7
US-09-529-206A-3
; Sequence 3, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
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; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206A-3

Query Match      100.0%; Score 105; DB 19; Length 180;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
   |||||
Db 67 GAASGLNGCCRCGARGPE 84

RESULT 8
US-09-529-206B-3
; Sequence 3, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-3

Query Match      100.0%; Score 105; DB 19; Length 180;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
   |||||
Db 67 GAASGLNGCCRCGARGPE 84

RESULT 9
US-09-561-571-3
; Sequence 3, Application US/09561571
; GENERAL INFORMATION:
; APPLICANT: CTL Immunotherapies Corp.
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; TITLE OF INVENTION: EPITOPE CLUSTERS
; FILE REFERENCE: CTIMM.010A
; CURRENT APPLICATION NUMBER: US/09/561,571
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
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; ORGANISM: homo sapiens
US-09-561-571-3

Query Match      100.0%; Score 105; DB 19; Length 180;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
   |||||
Db 67 GAASGLNGCCRCGARGPE 84

RESULT 10
US-09-751-798-8
; Sequence 8, Application US/09751798
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
; APPLICANT: Knuth, Alexander; Old, Lloyd J.
; TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
; TITLE OF INVENTION: Associated Proteins, Uses Thereof,
; TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
; TITLE OF INVENTION: Binding Peptides Derived Therefrom
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09751,798
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
US-09-751-798-8

Query Match      100.0%; Score 105; DB 21; Length 180;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
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Db 67 GAASGLNGCCRCGARGPE 84

RESULT 11
US-10-005-905-3
; Sequence 3, Application US/10005905
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; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; TITLE OF INVENTION: EPTOPE SYNCHRONIZATION IN ANTIGEN
; TITLE OF INVENTION: PRESENTING CELLS
; FILE REFERENCE: CTLIMM.021cpl
; CURRENT APPLICATION NUMBER: US/10/005,905
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 09/561,074
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/560,465
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,572
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,571
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US01/13806
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-005-905-3

Query Match      100.0%; Score 105; DB 24; Length 180;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
   |||||
Db 67 GAASGLNGCCRCGARGPE 84

RESULT 12
US-10-023-182-8
; Sequence 8, Application US/10023182
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; Chen, Yao-tseng; Scanlan, Matthew;
; Knuth, Alexander; Old, Lloyd J.
; TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
; Associated Proteins, Uses Thereof,
; Truncated Forms of NY-ESO-1, and HLA
; Binding Peptides Derived Therefrom
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/023,182
; FILING DATE: 17-Dec-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/751,798
; FILING DATE: December 29, 2000
; APPLICATION NUMBER: 09/062,422
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
```



```

; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-023-182-8

Query Match      100.0%; Score 105; DB 24; Length 180;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
Db 67 GAASGLNGCCRCGARGPE 84

RESULT 13
US-10-026-066-3
; Sequence 3, Application US/10026066
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; TITLE OF INVENTION: EPITOPE SYNCHRONIZATION IN ANTIGEN
; TITLE OF INVENTION: PRESENTING CELLS
; FILE REFERENCE: CTIMM.21CPIC
; CURRENT APPLICATION NUMBER: US/10/026,066
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 09/561,074
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/560,465
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,572
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,571
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US01/13806
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-026-066-3

Query Match      100.0%; Score 105; DB 24; Length 180;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
Db 67 GAASGLNGCCRCGARGPE 84

RESULT 14
US-60-336-968-11
; Sequence 11, Application US/60336968
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: CTIMM.022PR
; CURRENT APPLICATION NUMBER: US/60/336,968
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; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-336-968-11

Query Match      100.0%; Score 105; DB 26; Length 180;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
Db 67 GAASGLNGCCRCGARGPE 84

RESULT 15
US-09-821-883-27
; Sequence 27, Application US/09821883
; GENERAL INFORMATION:
; APPLICANT: Laus, Reiner
; APPLICANT: Vidovic, Damir
; APPLICANT: Graddis, Thomas
; TITLE OF INVENTION: Compositions and Methods for Dendritic
; TITLE OF INVENTION: Cell-Based Immunotherapy
; FILE REFERENCE: 7636-0022.30
; CURRENT APPLICATION NUMBER: US/09/821,883
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/193,504
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: NY-ESO-IC tumor antigen
US-09-821-883-27

Query Match      100.0%; Score 105; DB 22; Length 397;
Best Local Similarity 100.0%; Pred. No. 7.3e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
Db 67 GAASGLNGCCRCGARGPE 84

Search completed: July 3, 2002, 11:21:01
Job time: 888 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:22:12 ; Search time 64.42 Seconds
(without alignments)
28.270 Million cell updates/sec

Title: US-09-165-546A-11
Perfect score: 105
Sequence: 1 GAASGLNGCCRCGARGPE 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 308740 seqs, 101176262 residues

Total number of hits satisfying chosen parameters: 308740

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
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2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
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7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	100.0	180	1	PCT-US02-13994-30
2	105	100.0	180	5	US-09-807-512-8
3	105	100.0	180	6	US-10-117-937-74
4	58	55.2	180	5	US-09-807-512-4
5	58	55.2	180	6	US-10-117-937-75
6	58	55.2	180	6	US-10-146-473-69
7	58	55.2	210	5	US-09-807-512-6
8	58	55.2	210	6	US-10-117-937-76
9	58	55.2	210	6	US-10-157-031-88
10	57	54.3	2933	6	US-10-123-155-345
11	57	54.3	2933	6	US-10-137-871-345
12	57	54.3	2933	6	US-10-141-761-345
13	57	54.3	2933	6	US-10-140-864-345
14	57	54.3	2933	6	US-10-140-923-345
15	57	54.3	2933	6	US-10-141-756-345
16	57	54.3	2933	6	US-10-141-759-345
17	57	54.3	2933	6	US-10-140-472-345
18	57	54.3	2933	6	US-10-140-885-345
19	57	54.3	2933	6	US-10-142-885-345
20	57	54.3	2933	6	US-10-146-731-345
21	57	54.3	2933	6	US-10-142-426-345
22	57	54.3	2933	6	US-10-123-155-467
23	56.5	53.8	2475	6	US-10-123-155-467
24	56.5	53.8	2475	6	US-10-137-871-467
25	56.5	53.8	2475	6	US-10-141-761-467
26	56.5	53.8	2475	6	US-10-140-864-467

27	56.5	53.8	2475	6	US-10-140-923-467	Sequence 467, App
28	56.5	53.8	2475	6	US-10-141-756-467	Sequence 467, App
29	56.5	53.8	2475	6	US-10-141-759-467	Sequence 467, App
30	56.5	53.8	2475	6	US-10-140-472-467	Sequence 467, App
31	56.5	53.8	2475	6	US-10-140-805-467	Sequence 467, App
32	56.5	53.8	2475	6	US-10-142-885-467	Sequence 467, App
33	56.5	53.8	2475	6	US-10-146-731-467	Sequence 467, App
34	56.5	53.8	2475	6	US-10-142-426-467	Sequence 467, App
35	56.5	53.8	2475	6	US-10-158-790-467	Sequence 467, App
36	56	53.3	2477	6	US-10-123-155-331	Sequence 331, App
37	56	53.3	2477	6	US-10-137-871-331	Sequence 331, App
38	56	53.3	2477	6	US-10-141-761-331	Sequence 331, App
39	56	53.3	2477	6	US-10-140-864-331	Sequence 331, App
40	56	53.3	2477	6	US-10-140-923-331	Sequence 331, App
41	56	53.3	2477	6	US-10-141-756-331	Sequence 331, App
42	56	53.3	2477	6	US-10-141-759-331	Sequence 331, App
43	56	53.3	2477	6	US-10-140-472-331	Sequence 331, App
44	56	53.3	2477	6	US-10-140-805-331	Sequence 331, App
45	56	53.3	2477	6	US-10-142-885-331	Sequence 331, App

ALIGNMENTS

RESULT 1
PCT-US02-13994-30
; Sequence 30, Application PC/TUS0213994
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research
; APPLICANT: Cornell Research Foundation, Inc.
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd
; APPLICANT: Scanlan, Matthew
; APPLICANT: Stockert, Elisabeth
; TITLE OF INVENTION: COLON CANCER ANTIGEN PANEL
; FILE REFERENCE: L00461/70105WO(JRV)
; CURRENT APPLICATION NUMBER: PCT/US02/13994
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US 09/849,602
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-13994-30

Query Match 100.0%; Score 105; DB 1; Length 180;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
Db 67 GAASGLNGCCRCGARGPE 84
|||||

RESULT 2
US-09-807-512-8
; Sequence 8, Application US/09807512
; GENERAL INFORMATION:
; APPLICANT: Schrier, Peter I.
; APPLICANT: Aarnoudse, Corlien
; APPLICANT: Heider, Karl-Heinz
; APPLICANT: Klade, Christoph
; TITLE OF INVENTION: Camel, An Alternative Translation Product of the Tumor
; TITLE OF INVENTION: Antigen-Lage 1
; FILE REFERENCE: 0652.220000
; CURRENT APPLICATION NUMBER: US/09/807,512
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: PCT/EP99/07832
; PRIOR FILING DATE: 1999-10-15

; PRIOR APPLICATION NUMBER: EP 98119583.7
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-807-512-8

Query Match 100.0%; Score 105; DB 5; Length 180;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
| | | | | | | | | | | | | | | | | | | | | |
Db 67 GAASGLNGCCRCGARGPE 84

RESULT 3
US-10-117-937-74
; Sequence 74, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLLMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-74

Query Match 100.0%; Score 105; DB 6; Length 180;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
| | | | | | | | | | | | | | | | | | | | | |
Db 67 GAASGLNGCCRCGARGPE 84

RESULT 4
US-09-807-512-4
; Sequence 4, Application US/09807512
; GENERAL INFORMATION:
; APPLICANT: Schrier, Peter I.
; APPLICANT: Aarnoudse, Corlien
; APPLICANT: Heider, Karl-Heinz
; APPLICANT: Klade, Christoph
; TITLE OF INVENTION: Camel, An Alternative Translation Product of the Tumor
; TITLE OF INVENTION: Antigen-Lage 1
; FILE REFERENCE: 0652.2200000
; CURRENT APPLICATION NUMBER: US/09/807,512
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: PCT/EP99/07832
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: EP 98119583.7

; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-807-512-4

Query Match 55.2%; Score 58; DB 5; Length 180;
Best Local Similarity 61.1%; Pred. No. 1.1;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
| | | | : | | | | | :
Db 67 GAASAQDGRCPGARRPD 84

RESULT 5
US-10-117-937-75
; Sequence 75, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLLMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-75

Query Match 55.2%; Score 58; DB 6; Length 180;
Best Local Similarity 61.1%; Pred. No. 1.1;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
| | | | : | | | | | :
Db 67 GAASAQDGRCPGARRPD 84

RESULT 6
US-10-146-473-69
; Sequence 59, Application US/10146473
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Gout, Ivan
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Gure, Ali
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd
; TITLE OF INVENTION: Breast Cancer Antigens
; FILE REFERENCE: L00461/70130(JRV)
; CURRENT APPLICATION NUMBER: US/10/146,473
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/291,150
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 82

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 69
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-473-69

Query Match 55.2%; Score 58; DB 6; Length 180;
Best Local Similarity 61.1%; Pred. No. 1.1;
Matches 11; Conservative 2; Mismatches 5; Indels 5; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
|||| :| | |||| |:
Db 67 GAASAQDGRCPGARRPD 84

RESULT 7

US-09-807-512-6
; Sequence 6, Application US/09807512
; GENERAL INFORMATION:
; APPLICANT: Schrier, Peter I.
; APPLICANT: Aarnoudse, Corlien
; APPLICANT: Heider, Karl-Heinz
; APPLICANT: Klade, Christoph
; TITLE OF INVENTION: Camel, An Alternative Translation Product of the Tumor
; TITLE OF INVENTION: Antigen-Lage 1
; FILE REFERENCE: 0652.2200000
; CURRENT APPLICATION NUMBER: US/09/807,512
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: PCT/EP99/07832
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: EP 98119583.7
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 6
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-807-512-6

Query Match 55.2%; Score 58; DB 5; Length 210;
Best Local Similarity 61.1%; Pred. No. 1.2;
Matches 11; Conservative 2; Mismatches 5; Indels 5; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
|||| :| | |||| |:
Db 67 GAASAQDGRCPGARRPD 84

RESULT 8

US-10-117-937-76
; Sequence 76, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 76
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-76

Query Match 55.2%; Score 58; DB 6; Length 210;
Best Local Similarity 61.1%; Pred. No. 1.2;
Matches 11; Conservative 2; Mismatches 5; Indels 5; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
|||| :| | |||| |:
Db 67 GAASAQDGRCPGARRPD 84

RESULT 9

US-10-157-031-88
; Sequence 88, Application US/10157031
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobashev, A. V.
; APPLICANT: Krukovskaya, L. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequenc
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157,031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-031-88

Query Match 55.2%; Score 58; DB 6; Length 210;
Best Local Similarity 61.1%; Pred. No. 1.2;
Matches 11; Conservative 2; Mismatches 5; Indels 5; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
|||| :| | |||| |:
Db 67 GAASAQDGRCPGARRPD 84

RESULT 10

US-10-123-155-345
; Sequence 345, Application US/10123155
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC30
; CURRENT APPLICATION NUMBER: US/10/123,155
; CURRENT FILING DATE: 2002-04-15

; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 345
; LENGTH: 2933
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-123-155-345

Query Match 54.3%; Score 57; DB 6; Length 2933;
Best Local Similarity 56.2%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARG 16
|| | ||| || |

Db 2296 gagggaggcctcgtgg 2311

RESULT 11

US-10-137-871-345
; Sequence 345, Application US/10137871
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C153
; CURRENT APPLICATION NUMBER: US/10/137,871
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 345
; LENGTH: 2933
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-137-871-345

Query Match 54.3%; Score 57; DB 6; Length 2933;
Best Local Similarity 56.2%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARG 16
|| | ||| || |

Db 2296 gagggaggcctcgtgg 2311

RESULT 12

US-10-141-761-345
; Sequence 345, Application US/10141761
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C198
; CURRENT APPLICATION NUMBER: US/10/141,761
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 345
; LENGTH: 2933
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-141-761-345

Query Match 54.3%; Score 57; DB 6; Length 2933;
Best Local Similarity 56.2%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARG 16
|| | ||| || |

Db 2296 gagggaggcctcgtgg 2311

RESULT 13

US-10-140-864-345
; Sequence 345, Application US/10140864
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C184
; CURRENT APPLICATION NUMBER: US/10/140,864
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 345
; LENGTH: 2933
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-864-345

Query Match 54.3%; Score 57; DB 6; Length 2933;
Best Local Similarity 56.2%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARG 16

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; CURRENT FILING DATE: 2002-05-08
; Prior Applioication removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 345
; LENGTH: 2933
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-141-756-345

Query Match      54.3%; Score 57; DB 6; Length 2933;
Best Local Similarity 56.2%; Pred. No. 16;
Matches      9; Conservative      0; Mismatches      7; Indels      0; Gaps      0;

Qy      1 GAASGLNGCCRCGARG 16
      || | ||| || |
Db      2296 gagggaggcctcgtgg 2311

Search completed: July 3, 2002, 11:22:13
Job time: 945 sec
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Db      2296 gagggaggcctcgtgg 2311

RESULT 14
US-10-140-923-345
; Sequence 345, Application US/10140923
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RIC188
; CURRENT APPLICATION NUMBER: US/10/140,923
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 345
; LENGTH: 2933
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-923-345

Query Match      54.3%; Score 57; DB 6; Length 2933;
Best Local Similarity 56.2%; Pred. No. 16;
Matches      9; Conservative      0; Mismatches      7; Indels      0; Gaps      0;

QY      1 GAASGLNGCCRCGARG 16
      || | ||| || |
Db      2296 gagggaggcctcgtgg 2311

RESULT 15
US-10-141-756-345
; Sequence 345, Application US/10141756
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RIC200
; CURRENT APPLICATION NUMBER: US/10/141,756
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:09:47 ; Search time 49.27 Seconds
(without alignments)
8.923 Million cell updates/sec

Title: US-09-165-546A-11
Perfect score: 105
Sequence: 1 GAASGLNGCCRCGARGPE 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA: *
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep: *
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep: *
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep: *
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep: *
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep: *
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	105	100.0	18	4 US-09-359-503-11	Sequence 11, Appl
2	105	100.0	180	2 US-08-791-495-9	Sequence 9, Appli
3	105	100.0	180	4 US-08-937-263B-8	Sequence 8, Appli
4	58	55.2	180	2 US-08-791-495-7	Sequence 7, Appli
5	58	55.2	210	2 US-08-791-495-5	Sequence 5, Appli
6	48	45.7	1345	2 US-08-977-767-3	Sequence 3, Appli
7	48	45.7	1417	4 US-08-900-230-3	Sequence 37, Appl
8	46.5	44.3	1400	4 US-08-630-915A-37	Sequence 7, Appli
9	46	43.8	45	4 US-08-900-230-7	Sequence 112, App
10	46	43.8	143	4 US-08-990-823-112	Sequence 9, Appli
11	46	43.8	328	1 US-08-414-926A-9	Sequence 9, Appli
12	46	43.8	328	2 US-08-926-922-9	Sequence 9, Appli
13	46	43.8	328	3 US-09-253-682-9	Sequence 9, Appli
14	46	43.8	328	4 US-09-527-657-9	Sequence 9, Appli
15	45	42.9	769	1 US-08-454-455-6	Sequence 6, Appli
16	45	42.9	3788	4 US-09-336-447A-76	Sequence 76, Appl
17	44	41.9	76	1 US-08-322-962-4	Sequence 4, Appli
18	44	41.9	76	3 US-08-450-653-4	Sequence 4, Appli
19	44	41.9	801	1 US-07-906-349A-6	Sequence 6, Appli
20	43	41.0	25	4 US-08-900-230-28	Sequence 28, Appl
21	43	41.0	25	4 US-08-900-230-41	Sequence 41, Appl
22	43	41.0	40	4 US-08-900-230-49	Sequence 49, Appl
23	43	41.0	45	1 US-08-451-947-99	Sequence 99, Appl
24	43	41.0	45	1 US-08-451-947-100	Sequence 100, App
25	43	41.0	45	2 US-08-424-826A-11	Sequence 11, Appl
26	43	41.0	45	2 US-08-424-826A-12	Sequence 12, Appl
27	43	41.0	45	3 US-08-928-694-99	Sequence 99, Appl

28	43	41.0	45	3 US-08-928-694-100	Sequence 100, App
29	43	41.0	45	4 US-08-900-230-51	Sequence 51, Appl
30	43	41.0	45	5 PCT-US91-06950-99	Sequence 99, Appl
31	43	41.0	45	5 PCT-US91-06950-100	Sequence 100, App
32	43	41.0	50	4 US-08-900-230-58	Sequence 58, Appl
33	43	41.0	162	4 US-09-227-357-436	Sequence 436, App
34	42.5	40.5	45	4 US-08-900-230-11	Sequence 11, Appl
35	42	40.0	10	2 US-08-753-781-13	Sequence 13, Appl
36	41	39.0	45	4 US-08-900-230-16	Sequence 16, Appl
37	41	39.0	45	4 US-08-900-230-53	Sequence 53, Appl
38	41	39.0	75	3 US-08-482-085B-72	Sequence 72, Appl
39	41	39.0	115	4 US-09-247-155-124	Sequence 124, App
40	41	39.0	269	2 US-08-460-309-14	Sequence 14, Appl
41	41	39.0	269	2 US-08-125-077-14	Sequence 14, Appl
42	41	39.0	384	3 US-08-852-824-4	Sequence 4, Appli
43	41	39.0	626	6 5268290-2	Patent No. 5268290
44	41	39.0	921	1 US-07-872-644-39	Sequence 39, Appl
45	41	39.0	921	1 US-08-297-494-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1
US-09-359-503-11
; Sequence 11, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid

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; TOPOLOGY: linear
US-09-359-503-11

Query Match 100.0%; Score 105; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
   |||
Db 1 GAASGLNGCCRCGARGPE 18

RESULT 2
US-08-791-495-9
; Sequence 9, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth , Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-9

Query Match 100.0%; Score 105; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 8.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
   |||
Db 67 GAASGLNGCCRCGARGPE 84

RESULT 3
US-08-937-263B-8
; Sequence 8, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
; APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;

; APPLICANT: Alexander, Knuth; Drijfhout, Jan W.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
; TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
; TITLE OF INVENTION: ITSELF, AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,263B
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sinn, Eric, Patent Agent
; REGISTRATION NUMBER: 40,177
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
US-08-937-263B-8

Query Match 100.0%; Score 105; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 8.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
   |||
Db 67 GAASGLNGCCRCGARGPE 84

RESULT 4
US-08-791-495-7
; Sequence 7, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth , Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-9
```

; FILING DATE: 435
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-7

Query Match 55.2%; Score 58; DB 2; Length 180;
Best Local Similarity 61.1%; Pred. No. 0.88;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GAASGLNGCCRCGARGPE 18
||| :| | ||| |:
Db 67 GAASAQDGRPCGARRPD 84

RESULT 5
US-08-791-495-5
; Sequence 5, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-5

Query Match 55.2%; Score 58; DB 2; Length 210;
Best Local Similarity 61.1%; Pred. No. 1;

Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Qy 1 GAASGLNGCCRCGARGPE 18
||| :| | ||| |:
Db 67 GAASAQDGRPCGARRPD 84
RESULT 6
US-08-977-767-3
; Sequence 3, Application US/08977767
; Patent No. 5972684
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Yue, Henry
; APPLICANT: Greenwald, Sara
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: CARBONIC ANHYDRASE VIII
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,767
; FILING DATE: Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0423 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1345 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1532042
US-08-977-767-3

Query Match 45.7%; Score 48; DB 2; Length 1345;
Best Local Similarity 50.0%; Pred. No. 97;
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GAASGLNGCCRCGARG 16
|| :| | ||| |:
Db 511 GAGAGAAGCCTCCGTG 526

RESULT 7
US-08-900-230-3
; Sequence 3, Application US/08900230
; Patent No. 6329197
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A.
; TITLE OF INVENTION: DNA ENCODING GALANN GALR3 RECEPTORS AND

;; TITLE OF INVENTION: USES THEREOF
;; NUMBER OF SEQUENCES: 59
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Cooper & Dunham LLP
;; STREET: 1185 Avenue of The Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 11036
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/900,230
;; FILING DATE: 23-JUL-1997
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: White, John P.
;; REGISTRATION NUMBER: 28,678
;; REFERENCE/DOCKET NUMBER: 52241-C/JPW/ADM
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-278-0400
;; TELEFAX: 212-391-0525
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1417 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE:
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
US-08-900-230-3

Query Match 45.7%; Score 48; DB 4; Length 1417;
Best Local Similarity 53.8%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCG 13
| | | | |
Db 891 GCGGTGCGCGCG 903

RESULT 8
US-08-630-915A-37
; Sequence 37, Application US/08630915A
; Patent No. 6309820
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. 6309820h
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; TITLE OF INVENTION: USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/630,915A
;; FILING DATE: 03-APR-1996
;; CLASSIFICATION: 536
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Misrock, S. Leslie
;; REGISTRATION NUMBER: 18,872
;; REFERENCE/DOCKET NUMBER: 1101-174
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-8864/9741
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 37:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1400 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
US-08-630-915A-37

Query Match 44.3%; Score 46.5; DB 4; Length 1400;
Best Local Similarity 47.4%; Pred. No. 1.6e+02;
Matches 9; Conservative 1; Mismatches 6; Indels 3; Gaps 1;

QY 1 GAASGLNGC---CRCGARG 16
| | : | | | | | | | |
Db 1078 GAGAGCTGCAAGCACGTGG 1096

RESULT 9
US-08-900-230-7
; Sequence 7, Application US/08900230
; Patent No. 6329197
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A.
; TITLE OF INVENTION: DNA ENCODING GALANN GALR3 RECEPTORS AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of The Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/900,230
; FILING DATE: 23-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 52241-C/JPW/ADM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-900-230-7

Query Match 43.8%; Score 46; DB 4; Length 45;
Best Local Similarity 53.3%; Pred. No. 8-9;
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 AASGLNGCCRCGARG 16
| | | | |
Db 28 ACGTGCCACGAGG 42

RESULT 10
US-08-990-823-112
; Sequence 112, Application US/08990823D
; Patent No. 6228371
; GENERAL INFORMATION:
; APPLICANT: Nano, Francis
; TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
; TITLE OF INVENTION: immunostimulatory Peptides
; FILE REFERENCE: 49086
; CURRENT APPLICATION NUMBER: US/08/990,823D
; CURRENT FILING DATE: 1997-12-15
; EARLIER APPLICATION NUMBER: US 96/10375
; EARLIER FILING DATE: 1996-06-14
; EARLIER APPLICATION NUMBER: 60/000,254
; EARLIER FILING DATE: 1995-06-15
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 112
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-08-990-823-112

Query Match 43.8%; Score 46; DB 4; Length 143;
Best Local Similarity 45.0%; Pred. No. 24;
Matches 9; Conservative 0; Mismatches 7; Indels 4; Gaps 1;

QY 1 GAASGLN---GCCRCGARG 16
| | | | |
Db 34 GCAGGAGCCCGCCACGTTG 53

RESULT 11
US-08-414-926A-9
; Sequence 9, Application US/08414926A
; Patent No. 5721354
; GENERAL INFORMATION:
; APPLICANT: Spaete, Richard
; APPLICANT: Cha, Tai-An
; TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,926A
; FILING DATE: March 31, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: AVIR-011/OOUS
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-494-7622
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: tol.03
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..328
; OTHER INFORMATION: /label= UL135
US-08-414-926A-9

Query Match 43.8%; Score 46; DB 1; Length 328;
Best Local Similarity 50.0%; Pred. No. 51;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
| | | | |
Db 66 GAASDKRGACACCCYRNP 83

RESULT 12
US-08-926-922-9
; Sequence 9, Application US/08926922
; Patent No. 5925751
; GENERAL INFORMATION:
; APPLICANT: Spaete, Richard
; APPLICANT: Cha, Tai-An
; TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Luann Cserr Attorney at Law
; STREET: 750 Arimo Avenue
; CITY: Oakland
; STATE: CA
; COUNTRY: USA
; ZIP: 94610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,922
; FILING DATE: September 10, 1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: AVIR 11A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-834-1448
; TELEFAX: 510-839-7810
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: tol.03
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..328
; OTHER INFORMATION: /label= UL135
US-08-926-922-9

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,455
FILING DATE: 30-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/193989
FILING DATE: 09-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004142
FILING DATE: 13-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/670607
FILING DATE: 14-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: P0699C2D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 769 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-454-455-6

Query Match 42.9%; Score 45; DB 1; Length 769;
Best Local Similarity 52.9%; Pred. No. 1.4e+02;
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2 AASGLNGCCRCGARGPE 18
|:| | | | | | | |
Db 48 ASSNAASCARCLALGPE 64

Search completed: July 3, 2002, 11:09:47
Job time: 269 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:10:56 ; Search time 61.47 Seconds
(without alignments)
28.137 Million cell updates/sec

Title: US-09-165-546A-12
Perfect score: 91
Sequence: 1 SRLLEFYLAMPFATPMEA 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	48	52.7	692	2 S56849	probable membrane
2	47	51.6	426	2 C83103	hypothetical prote
3	47	51.6	1249	2 C83358	probable non-ribos
4	44	48.4	230	1 S22406	hydrogenase (EC 1.
5	42	46.2	264	2 D81253	probable peptide A
6	41.5	45.6	475	2 D84593	hypothetical prote
7	41	45.1	266	2 C95288	probable ABC trans
8	41	45.1	417	2 S76137	hypothetical prote
9	40	44.0	250	2 S47343	capsid assembly pr
10	40	44.0	318	1 DEBSLM	L-lactate dehydrog
11	40	44.0	993	2 JQ0488	afSR protein - Str
12	39.5	43.4	1108	2 JC4037	alpha-mannosidase
13	39	42.9	55	2 A42824	triacylglycerol li
14	39	42.9	80	2 T17805	hypothetical prote
15	39	42.9	160	2 S77324	hypothetical prote
16	39	42.9	403	2 F83092	probable cytochrom
17	39	42.9	454	2 G70797	hypothetical prote
18	39	42.9	459	2 T04808	hypothetical prote
19	39	42.9	521	2 F87317	hypothetical prote
20	39	42.9	562	2 S27782	esterase precursor
21	39	42.9	562	2 S27800	elastase precursor
22	39	42.9	570	2 T32061	gut-specific carbo
23	39	42.9	669	2 D96006	probable cytochrom
24	39	42.9	741	2 T37949	hypothetical PSU1-
25	38.5	42.3	161	2 H71959	hypothetical prote
26	38.5	42.3	298	2 G81708	enoyl-(acyl-carrie
27	38	41.8	124	2 C75359	hypothetical prote
28	38	41.8	131	1 WMBP14	gene 14 protein -
29	38	41.8	131	1 WMBP29	gene 14 protein -

30	38	41.8	143	2	H87028	probable membrane
31	38	41.8	160	1	WMLV17	plastoquinol--plas
32	38	41.8	160	1	WMKL17	plastoquinol--plas
33	38	41.8	160	1	S05340	plastoquinol--plas
34	38	41.8	160	1	S04089	plastoquinol--plas
35	38	41.8	160	1	S16918	plastoquinol--plas
36	38	41.8	160	1	B30807	plastoquinol--plas
37	38	41.8	160	2	T07264	plastoquinol--plas
38	38	41.8	160	2	S22472	plastoquinol--plas
39	38	41.8	160	2	AG2233	plastoquinol--plas
40	38	41.8	178	2	T14835	plastoquinol--plas
41	38	41.8	180	2	T07514	plastoquinol--plas
42	38	41.8	268	2	AE3137	hypothetical prote
43	38	41.8	279	2	D71123	probable sugar tra
44	38	41.8	308	2	G98150	dipeptide transpor
45	38	41.8	311	2	F72502	hypothetical prote

ALIGNMENTS

RESULT 1

S56849

probable membrane protein YJL073w - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein HRC558; hypothetical protein J1083

C:Species: Saccharomyces cerevisiae

C>Date: 05-May-1995 #sequence_revision 08-Sep-1995 #text_change 21-Jul-2000

C:Accession: S56849; S56847; S50798; S47117; S57736

R:Rose, M.; Koetter, P.; Entian, K.D.

submitted to the Protein Sequence Database, September 1995

A:Reference number: S56848

A:Accession: S56849

A:Molecule type: DNA

A:Residues: 1-692 <ROS>

A:Cross-references: EMBL:249348; NID:gl008228; PID:gl008229; MIPS:YJL073w

R:Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.

submitted to the Protein Sequence Database, September 1995

A:Reference number: S56835

A:Accession: S56847

A:Molecule type: DNA

A:Residues: 135-692 <POH>

A:Cross-references: EMBL:249348; MIPS:YJL073w

R:Vandenbol, M.; Durand, P.; Dion, C.; Portetelle, D.; Hilger, F.

Yeast 11, 57-60, 1995

A>Title: Sequence of a 17.1 kb DNA fragment from chromosome X of Saccharomyces cerevi

A:Reference number: S50798; MUID:95282514

A:Accession: S50798

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 135-692 <VAN>

A:Cross-references: EMBL:234288; NID:g498992; PIDN:CAA84049.1; PID:g498993

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994

R:Vandenbol, M.; Durand, P.; Dion, C.; Portetelle, D.; Hilger, F.

submitted to the EMBL Data Library, June 1994

A:Description: Sequence analysis of a 17.1 kb DNA fragment from chromosome X of Sacch

A:Reference number: S47117

A:Accession: S47117

A:Molecule type: DNA

A:Residues: 135-692 <VAW>

A:Cross-references: EMBL:234288; NID:g498992; PID:g498993

R:Sor, F.J.

submitted to the EMBL Data Library, June 1995

A:Reference number: S57731

A:Accession: S57736

A:Molecule type: DNA

A:Residues: 1-692 <SOR>

A:Cross-references: EMBL:X88851; NID:g895892; PID:g895898

C:Genetics:

A:Gene: SGD:JEM1

A:Cross-references: SGD:S0003609; MIPS:YJL073w

A:Map position: 10L

C:Superfamily: dnaJ amino-terminal homology

C:Keywords: transmembrane protein

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Accession: D84593
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-475 <STO>
A;Cross-references: GB:AE002093; NID:g4454469; PIDN:AAD20916.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g20790
A;Map position: 2

Query Match 45.6%; Score 41.5; DB 2; Length 475;
Best Local Similarity 45.8%; Pred. No. 23;
Matches 11; Conservative 3; Mismatches 3; Indels 7; Gaps 1;

QY 1 SRLLEFYL-----AMPFATPME 17
||||: | |||| ||::
Db 111 SRLDRDLLRNFATAMPFGTPLD 134

RESULT 7
C95288
probable ABC transporter, permease SMA0396 [imported] - Sinorhizobium meliloti (strain 1
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: C95288
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot
A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: C95288
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-266 <KUR>
A;Cross-references: GB:AE006469; PIDN:AAK64869.1; PID:g14523285; GSPDB:GN00165
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Welis, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: SMA0396
A;Genome: plasmid

Query Match 45.1%; Score 41; DB 2; Length 266;
Best Local Similarity 37.5%; Pred. No. 15;
Matches 6; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 SRLLEFYLAMPFATPM 16
:|::||::|||:
Db 98 ARSIQIYLLLPFTIPL 113

RESULT 8
S76137
hypothetical protein - Synecocystis sp. (strain PCC 6803)
C;Species: Synecocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: S76137
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecchocys
s.
A;Reference number: S74322; MUID:97061201
A;Accession: S76137
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-417 <KAN>
A;Cross-references: EMBL:D90914; GB:AB001339; NID:g1653477; PIDN:BAA18396.1; PID:d101
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 45.1%; Score 41; DB 2; Length 417;
Best Local Similarity 60.0%; Pred. No. 25;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 LEFYLAMPFATPMEA 18
|| ||| | |::||
Db 276 LEQYLAQPDLLPLEA 290

RESULT 9
S47343
capsid assembly protein - suid herpesvirus 1
C;Species: suid herpesvirus 1
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 08-Oct-1999
C;Accession: S47343
R;Kaliman, A.V.; Boldogkoi, Z.S.; Fodor, I.
submitted to the EMBL Data Library, August 1994
A;Description: The nucleotide sequence of Pseudorabies virus DNA fragment, encoding c
logues) and part of HSV-1 UL37 gene homologue.
A;Reference number: S47343
A;Accession: S47343
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-250 <KAL>
A;Cross-references: EMBL:X80797; NID:g525261; PIDN:CAA56773.1; PID:g525262
A;Note: the source is designated as pseudorabies virus

Query Match 44.0%; Score 40; DB 2; Length 250;
Best Local Similarity 53.3%; Pred. No. 22;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 SRLLEFYLAMPFATP 15
||:||||::| ||
Db 21 SRILEFFMAAGRETP 35

RESULT 10
DEBSLM
L-lactate dehydrogenase (EC 1.1.1.27) - Bacillus megaterium
C;Species: Bacillus megaterium
C;Date: 03-Aug-1984 #sequence_revision 30-Sep-1991 #text_change 11-Jun-1999
C;Accession: S00133; S01472; A00354
R;Waldvogel, S.; Weber, H.; Zuber, H.
Biol. Chem. Hoppe-Seyler 368, 1391-1399, 1987
A;Title: Structure and function of L-lactate dehydrogenases from thermophilic and mes
megaterium. Preparation and properties of a hybrid lactate dehydrogenase comprising
A;Reference number: S00133; MUID:88107005
A;Accession: S00133
A;Molecule type: DNA
A;Residues: 1-318 <WAL>
A;Cross-references: EMBL:M22305; NID:g143135; PIDN:AAA22566.1; PID:g143136
R;Stangl, D.; Wiederkehr, F.; Suter, F.; Zuber, H.
Biol. Chem. Hoppe-Seyler 368, 1157-1166, 1987
A;Title: Structure and function of L-lactate dehydrogenases from thermophilic and mes
terium.
A;Reference number: S01472; MUID:88050100
A;Accession: S01472
A;Molecule type: protein
A;Residues: 1-318 <STA>
C;Comment: This enzyme is activated by fructose-1,6-diphosphate.
C;Function:

A;Accession: S77324
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-160 <KAN>
A;Cross-references: EMBL:D90906; GB:AB001339; NID:g1652492; PIDN:BAA17427.1; PID:d101816
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 42.9%; Score 39; DB 2; Length 160;
Best Local Similarity 58.3%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 LLEFYLAMPFAT 14
||| |
Db 50 LLQFYQQPFAS 61

Search completed: July 3, 2002, 11:10:57
Job time: 319 sec

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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:24:44 ; Search time 29.65 Seconds
(without alignments)
23.506 Million cell updates/sec

Title: US-09-165-546A-12

Perfect score: 91

Sequence: 1 SRLLFFYLAMPFATPMEA 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	91	100.0	180	1 CTAG_HUMAN	P78358 homo sapien
2	67	73.6	210	1 LAG1_HUMAN	O75638 homo sapien
3	48	52.7	692	1 YJH3_YEAST	P40358 saccharomyc
4	44	48.4	230	1 CYBH_WOLSU	P31875 wolinnella s
5	40	44.0	318	1 LDH_BACME	P00345 bacillus me
6	40	44.0	993	1 AFSR_STRCO	P25941 streptomyce
7	39.5	43.4	1108	1 MAN2_DROME	Q24451 drosophila
8	39	42.9	454	1 Y1D4_MYCTU	O69701 mycobacteri
9	39	42.9	562	1 EST1_CAEBR	Q04456 caenorhabdi
10	39	42.9	562	1 EST1_CAEBL	Q04457 caenorhabdi
11	38	41.8	131	1 VG14_BPPH2	P11188 bacterioph
12	38	41.8	131	1 VG14_BPPZA	P07539 bacterioph
13	38	41.8	160	1 PETD_CHLEU	P11093 chlamydomon
14	38	41.8	160	1 PETD_CHLPR	P13348 chlorella p
15	38	41.8	160	1 PETD_CHLRE	P23230 chlamydomon
16	38	41.8	160	1 PETD_CHLVU	P56322 chlorella v
17	38	41.8	160	1 PETD_MARPO	P06250 marchantia
18	38	41.8	160	1 PETD_MESVI	Q9muv2 mesostigma
19	38	41.8	160	1 PETD_NEPOL	Q9tl32 nephroselm
20	38	41.8	160	1 PETD_NOSSP	P12117 nostoc sp.
21	38	41.8	160	1 PETD_PROHO	P28059 prochloroth
22	38	41.8	160	1 PETD_SCEOB	P19586 scenedesmus
23	38	41.8	161	1 PETD_CYACA	Q9tlz8 cyanidium c
24	38	41.8	177	1 PETD_PICAB	O47044 picea abies
25	38	41.8	180	1 PETD_PINTH	P52770 pinus thunb
26	38	41.8	597	1 BAL_BOVIN	P30122 bos taurus
27	38	41.8	599	1 BAL_MOUSE	Q64285 mus musculu
28	38	41.8	612	1 BAL_RAT	P07882 rattus norv
29	38	41.8	658	1 SQHC_BRAJA	P54924 bradyrhizob
30	38	41.8	910	1 HUL5_YEAST	P53119 saccharomyc
31	38	41.8	1238	1 YN13_YEAST	P53840 saccharomyc
32	37.5	41.2	1143	1 DP2L_ARCFU	O28552 archaeoglob
33	37	40.7	106	1 PETD_HORVU	P12361 hordeum vul

RESULT 1

ID	CTAG_HUMAN	STANDARD;	PRT;	180 AA.
AC	P78358;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Autoimmunogenic cancer/testis antigen NY-ESO-1.			
GN	CTAG.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97203161; PubMed=9050879;			
RA	Chen Y.-T., Scanlan M.J., Sahin U., Tuereci O., Gure A.O., Tsang S.,			
RA	Williamson B., Stockert E., Pfreundschuh M., Old L.J.;			
RT	"A testicular antigen aberrantly expressed in human cancers detected			
RT	by autologous antibody screening."			
RL	Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Melanoma;			
RX	MEDLINE=98289662; PubMed=9626360;			
RA	Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,			
RA	de Plaen E., Boon T.;			
RT	"LAGE-1 a new gene with tumor specificity."			
RL	Int. J. Cancer 76:903-908(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98430682; PubMed=9759882;			
RA	Wang R.-F., Johnston S.L., Zeng G., Topalian S.L.,			
RA	Schwartzentruber D.J., Rosenberg S.A.;			
RT	"A breast and melanoma-shared tumor antigen: T cell responses to			
RT	antigenic peptides translated from different open reading frames.";			
RL	J. Immunol. 161:3596-3606(1998).			
CC	-I- TISSUE SPECIFICITY: EXPRESSED IN TESTIS AND OVARY AND IN A WIDE			
CC	VARIETY OF CANCERS. DETECTED IN UTERINE MYOMETRIUM.			
CC	-I- SIMILARITY: STRONG, TO LAGE-1.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	-----			
DR	EMBL; U87459; AAB49693.1; -			
DR	EMBL; AJ003149; CAA05908.1; -			
DR	EMBL; AF038567; AAD05202.1; -			
DR	MIM; 300156; -			
KW	Transmembrane; Antigen.			
FT	DOMAIN 5 82			
FT	TRANSMEM 156 172			
FT	GLY-RICH.			
FT	POTENTIAL.			

Q37895 bacterioph
P06527 pisum sativ
P56774 arabidopsis
O78415 guillardia
P05643 zea mays (m
P12118 oryza sativ
P00166 spinacia ol
Q54710 synechococc
P27589 synechocyst
P06249 nicotiana t
P12119 triticum ae
O15264 homo sapien

ALIGNMENTS

RESULT 4
CYBH_WOLSU STANDARD; PRT; 230 AA.
AC P31875;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Quinone-reactive Ni/Fe-hydrogenase B-type cytochrome subunit.
GN HYDC.
OS Wolinella succinogenes.
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Wolinella.
OX NCBI_TaxID=844;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-25.
RX MEDLINE=92267032; PubMed=1587288;
RA Dross F., Geisler V., Lenger R., Theis F., Krafft T.,
RA Fahrenholz F., Kojro E., Duchene A., Tripiet D., Juvenal K.,
RA Kroeger A.;
RT "The quinone-reactive Ni/Fe-hydrogenase of Wolinella succinogenes.";
RL Eur. J. Biochem. 206:93-102(1992).
RN [2]
RP ERRATUM.
RX MEDLINE=93307313; PubMed=8319698;
RA Dross F., Geisler V., Lenger R., Theis F., Krafft T.,
RA Fahrenholz F., Kojro E., Duchene A., Tripiet D., Juvenal K.,
RA Kroeger A.;
RL Eur. J. Biochem. 214:949-950(1993).
CC -!- FUNCTION: B-TYPE CYTOCHROME THAT INTERACTS WITH QUINONES AND
CC ANCHOR THE HYDROGENASE TO THE MEMBRANE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE HUPC/HYAC/HYDC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X65189; CAA46304.1; -.
DR PIR; S22406; S22406.
DR InterPro; IPR000516; Ni_hydr_CytB.
DR Pfam; PF01292; Ni_hydr_CytB; 1.
DR PRINTS; PR00161; NIHGNASECYTB.
DR ProDom; PD005374; Ni_hydr_CytB; 1.
DR PROSITE; PS00882; NI_HGENASE_CYTB_1; 1.
DR PROSITE; PS00883; NI_HGENASE_CYTB_2; 1.
KW Transmembrane; Electron transport; Heme.
FT TRANSMEM 23 43 POTENTIAL.
FT TRANSMEM 67 87 POTENTIAL.
FT TRANSMEM 134 153 POTENTIAL.
FT TRANSMEM 188 205 POTENTIAL.
SQ SEQUENCE 230 AA; 26829 MW; CA823C6F3896D51E CRC64;

Query Match 48.4%; Score 44; DB 1; Length 230;
Best Local Similarity 58.3%; Pred. No. 3;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 FYLAMPFATPME 17
Db 40 FYIAYPFLTPIK 51
||| ||| |||:

RESULT 5
LDH_BACME STANDARD; PRT; 318 AA.
ID LDH_BACME
AC P00345;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE L-lactate dehydrogenase (EC 1.1.1.27) (L-LDH).
GN LDH.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=DSM 090;
RA MEDLINE=88107005; PubMed=3122782;
RA Waldvogel S., Weber H., Zuber H.;
RT "Structure and function of L-lactate dehydrogenases from thermophilic
RT and mesophilic bacteria. VII. Nucleotide sequence of the lactate
RT dehydrogenase gene from the mesophilic bacterium Bacillus megaterium.
RT Preparation and properties of a hybrid lactate dehydrogenase
RT comprising moieties of the B. megaterium and B. stearothermophilus
RT enzymes.";
RL Biol. Chem. Hoppe-Seyler 368:1391-1399(1987).
RN [2]
RP SEQUENCE.
RX MEDLINE=88050100; PubMed=3118900;
RA Stangl D., Wiederkehr F., Suter F., Zuber H.;
RT "Structure and function of L-lactate dehydrogenases from thermophilic
RT and mesophilic bacteria. V. The complete amino-acid sequence of the
RT mesophilic L-lactate dehydrogenase from Bacillus megaterium.";
RL Biol. Chem. Hoppe-Seyler 368:1157-1166(1987).
RN [3]
RP PRELIMINARY SEQUENCE.
RA Wiederkehr F.;
RL Thesis (1982), ETH Zurich, Switzerland.
CC -!- CATALYTIC ACTIVITY: (S)-lactate + NAD(+) = pyruvate + NADH.
CC -!- PATHWAY: Anaerobic glycolysis; final step.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE LDH FAMILY.
CC -----
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CC -----
CC EMBL; M22305; AAA22566.1; -.
DR PIR; S00133; DEBSLM.
DR HSSP; P00344; 1LDB.
DR InterPro; IPR001557; L_LDH.
DR InterPro; IPR000205; NAD_binding.
DR InterPro; IPR001236; ldh.
DR Pfam; PF00056; ldh; 1.
DR Pfam; PF02866; ldh_C; 1.
DR PRINTS; PR00086; LLDHDRGNASE.
DR PROSITE; PS00064; L_LDH; 1.
KW Oxidoreductase; NAD; Glycolysis.
FT ACT_SITE 181 181 BY SIMILARITY.
SQ SEQUENCE 318 AA; 35035 MW; 17122190576E1485 CRC64;

Query Match 44.0%; Score 40; DB 1; Length 318;
Best Local Similarity 87.5%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 10 MPFATPME 17
Db 58 MPFATPMK 65
|||||:

RESULT 6
AFSR_STRCO STANDARD; PRT; 993 AA.
ID AFSR_STRCO
AC P25941; P08467; Q9L000;

DT 01-AUG-1988 (Rel. 08, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Regulatory protein afsR.
GN AFSR OR AFSB OR SCD6.04C.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=91071605; PubMed=2253887;
RA Horinouchi S., Kito M., Nishiyama M., Furuya K., Hong S.-K.,
RA Miyake K., Beppu T.;
RT "Primary structure of AfsR, a global regulatory protein for secondary
RT metabolite formation in Streptomyces coelicolor A3(2).";
RL Gene 95:49-56(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Oliver K., Harris D., Cerdeno A.M., Parkhill J., Barrell B.G.,
RA Rajandream M.A.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 751-993 FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=87008389; PubMed=2428809;
RA Horinouchi S., Suzuki H., Beppu T.;
RT "Nucleotide sequence of afsB, a pleiotropic gene involved in
RT secondary metabolism in Streptomyces coelicolor A3(2) and
RT 'Streptomyces lividans'.";
RL J. Bacteriol. 168:257-269(1986).
CC -!- FUNCTION: GLOBAL REGULATORY PROTEIN FOR SECONDARY METABOLITE
CC FORMATION.
CC -!- PTM: PHOSPHORYLATED BY AFSK.
CC -!- MISCELLANEOUS: THE N-TERMINAL AND THE C-TERMINAL REGIONS ARE
CC INDEPENDENTLY CAPABLE OF DIRECTING ACTINORHODIN PRODUCTION.
CC -!- SIMILARITY: BELONGS TO THE AFSR/DNRI/REDD FAMILY OF REGULATORS.
CC -!- SIMILARITY: CONTAINS 3 TPR REPEATS.
CC -----
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CC -----
DR EMBL; D90155; BAA14186.1; -.
DR EMBL; AL353815; CAB88433.1; -.
DR EMBL; M16011; AAA26694.1; -.
DR PIR; JQ0488; JQ0488.
DR PIR; A25037; A25037.
DR InterPro; IPR001440; TPR.
DR Pfam; PF00515; TPR; 3.
DR SMART; SM00028; TPR; 3.
KW Transcription regulation; ATP-binding; DNA-binding; Activator;
KW Antibiotic biosynthesis; Pigment; Phosphorylation; TPR repeat;
KW Repeat.
FT REPEAT 823 856 TPR 1.
FT REPEAT 863 896 TPR 2.
FT REPEAT 942 975 TPR 3.
FT NP_BIND 330 337 ATP (POTENTIAL).
FT DNA_BIND 796 811 H-T-H MOTIF (BY SIMILARITY).
FT DNA_BIND 974 988 H-T-H MOTIF (BY SIMILARITY).
FT CONFLICT 256 256 Q -> R (IN REF. 1).
FT CONFLICT 318 318 A -> P (IN REF. 1).
FT CONFLICT 751 766 DVLLVSGRIEHAEEA -> MCSWCPVASSMPKRKH (IN
FT REF. 3).
SQ SEQUENCE 993 AA; 105714 MW; 8793CF27CEA7254C CRC64;

Query Match 44.0%; Score 40; DB 1; Length 993;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLLEFYLA 9
| | | | : | | | |
Db 632 SRLLEFYLA 640

RESULT 7
MAN2_DROME STANDARD; PRT; 1108 AA.
ID MAN2_DROME
AC Q24451;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-mannosidase II (EC 3.2.1.114) (Mannosyl-oligosaccharide
DE 1,3-1,6-alpha-mannosidase) (MAN II) (Golgi alpha-mannosidase II)
DE (AMAN II).
GN ALPHA-MAN-II OR GMII.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95196999; PubMed=7890162;
RA Foster J.M., Yudkin B., Lockyer A.E., Roberts D.B.;
RT "Cloning and sequence analysis of GMII, a Drosophila melanogaster
RT homologue of the cDNA encoding murine Golgi alpha-mannosidase II.";
RL Gene 154:183-186(1995).
CC -!- FUNCTION: CATALYZES THE FIRST COMMITTED STEP IN THE BIOSYNTHESIS
CC OF COMPLEX N-GLYCANS. IT CONTROLS CONVERSION OF HIGH MANNOSE TO
CC COMPLEX N-GLYCANS; THE FINAL HYDROLYTIC STEP IN THE N-GLYCAN
CC MATURATION PATHWAY (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: Hydrolysis of the terminal 1,3- and 1,6-linked
CC alpha-D-mannose residues in the mannosyl-oligosaccharide
CC Man(5)(GlcNAc)(3).
CC -!- PATHWAY: GLYCOSYLATION.
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Golgi (By
CC similarity).
CC -!- SIMILARITY: BELONGS TO FAMILY 38 OF GLYCOSYL HYDROLASES.
CC -----
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CC -----
DR EMBL; X77652; CAA54732.1; -.
DR FlyBase; FBgn0011740; Alpha-Man-II.
DR InterPro; IPR000602; Glyco_hydro_38.
DR Pfam; PF01074; Glyco_hydro_38; 1.
KW Hydrolase; Glycosidase; Transmembrane; Signal-anchor; Golgi stack.
FT DOMAIN 1 9 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 10 30 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 31 1108 LUMENAL (POTENTIAL).
SQ SEQUENCE 1108 AA; 126719 MW; 5DC157FA211A8E12 CRC64;

Query Match 43.4%; Score 39.5; DB 1; Length 1108;
Best Local Similarity 33.3%; Pred. No. 77;
Matches 8; Conservative 7; Mismatches 2; Indels 7; Gaps 1;

QY 2 RLLEFYLA MPFAT-----PMEA 18
: | : | | : | | : | : | |
Db 630 QLVDVYSSPFVSVTDLANNPVEA 653

```
RESULT 8
YIDA_MYCTU
ID Y1D4_MYCTU STANDARD; PRT; 454 AA.
AC O69701;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 49.3 kDa protein RV3734c.
GN RV3734C OR MT3839 OR MTV025.082C.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaiia F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE UPF0089 FAMILY.
CC -----
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CC -----
DR EMBL; AL022121; CAA18056.1; -.
DR EMBL; AE007180; AAK48206.1; -.
DR TIGR; MT3839; -.
DR TubercuList; Rv3734c; -.
DR InterPro; IPR004255; UPF0089.
DR Pfam; PF03007; UPF0089; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 454 AA; 49303 MW; 11CD02FA1BEB6ACB CRC64;
Query Match 42.9%; Score 39; DB 1; Length 454;
Best Local Similarity 61.5%; Pred. No. 39;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 3 LLEFYLAMPFATP 15
| | | | |
Db 211 LLEQLTLPPAAP 223
RESULT 9
EST1_CAEBR
ID EST1_CAEBR STANDARD; PRT; 562 AA.
AC Q04456;
```

```
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE GUT esterase precursor (EC 3.1.1.1) (NON-specific carboxylesterase).
GN GES-1.
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93188021; PubMed=8445654;
RA Kennedy B.P., Aamodt E.J., Allen F.L., Chung M.A., Heschl M.F.P.,
RA McGhee J.D.;
RT "The gut esterase gene (ges-1) from the nematodes Caenorhabditis
RT elegans and Caenorhabditis briggsae.";
RL J. Mol. Biol. 229:890-908(1993).
CC -!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
CC carboxylic anion.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- TISSUE SPECIFICITY: EXPRESSED ONLY IN THE INTESTINE.
CC -!- DEVELOPMENTAL STAGE: APPEARS IN MID-PROLIFERATION PHASE WHEN
CC THE DEVELOPING GUT HAS FOUR TO EIGHT CELLS.
CC -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
CC -----
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CC -----
DR EMBL; M96144; AAA28056.1; -.
DR PIR; S27782; S27782.
DR HSSP; P37967; 1QE3.
DR InterPro; IPR002018; Carboxylesterase_B.
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR000379; Est_lip_thioest_actsite.
DR Pfam; PF00135; Coesterase; 2.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase; Serine esterase; Signal; Endoplasmic reticulum.
FT SIGNAL 1 16
FT CHAIN 17 562 GUT ESTERASE.
FT ACT_SITE 199 199 BY SIMILARITY.
FT ACT_SITE 451 451 BY SIMILARITY.
FT DISULFID 75 93 BY SIMILARITY.
FT DISULFID 251 259 BY SIMILARITY.
FT SITE 559 562 PREVENT SECRETION FROM ER.
SQ SEQUENCE 562 AA; 63819 MW; 7FA312F3B2587E53 CRC64;
Query Match 42.9%; Score 39; DB 1; Length 562;
Best Local Similarity 63.6%; Pred. No. 48;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 5 EFYLAMPFATP 15
| : ||: || |
Db 36 EVFLAIPFAKP 46
RESULT 10
EST1_CAEBL
ID EST1_CAEBL STANDARD; PRT; 562 AA.
AC Q04457;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE GUT esterase precursor (EC 3.1.1.1) (NON-specific carboxylesterase).
GN GES-1.
OS Caenorhabditis elegans.
```



```
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 17-54.
RX MEDLINE=93188021; PubMed=8445654;
RA Kennedy B.P., Aamodt E.J., Allen F.L., Chung M.A., Heschl M.F.P.,
RA McGhee J.D.;
RT "The gut esterase gene (ges-1) from the nematodes Caenorhabditis
RT elegans and Caenorhabditis briggsae.";
RL J. Mol. Biol. 229:890-908(1993).
CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
CC carboxylic anion.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- TISSUE SPECIFICITY: EXPRESSED ONLY IN THE INTESTINE.
CC -1- DEVELOPMENTAL STAGE: APPEARS IN MID-PROLIFERATION PHASE WHEN
CC THE DEVELOPING GUT HAS FOUR TO EIGHT CELLS.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
CC -----
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CC -----
DR EMBL; M96145; AAA28057.1; -.
DR PIR; S27800; S27800.
DR HSSP; P37967; 1QE3.
DR InterPro; IPR002018; Carboxylesterase_B.
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR000379; Est_lip_thioest_actsite.
DR Pfam; PF00135; COesterase; 2.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase; Serine esterase; Signal; Endoplasmic reticulum.
FT SIGNAL 1 16
FT CHAIN 17 562 GUT ESTERASE.
FT ACT_SITE 198 198 BY SIMILARITY.
FT ACT_SITE 452 452 BY SIMILARITY.
FT DISULFID 75 93 BY SIMILARITY.
FT DISULFID 250 258 BY SIMILARITY.
FT SITE 559 562 PREVENT SECRETION FROM ER.
SQ SEQUENCE 562 AA; 63722 MW; 1366AA79ED84D96A CRC64;

Query Match 42.9%; Score 39; DB 1; Length 562;
Best Local Similarity 63.6%; Pred. No. 48;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 EFYLAMPFATP 15
| :||:||||
Db 36 EVFLAIPFAKP 46

RESULT 11
VG14_BPPH2 STANDARD; PRT; 131 AA.
AC P11188;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lysis protein (Late protein GP14).
GN 14.
OS Bacteriophage phi-29.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae.
OX NCBI_TaxID=10756;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87106857; PubMed=3803926;
RA Vicek C., Paces V.;

Query Match 41.8%; Score 38; DB 1; Length 131;
Best Local Similarity 44.4%; Pred. No. 17;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 SRLLEFYLAMPPFATPMEA 18
| :|:|||||
Db 62 SEMILALLAIPFAVPFPA 79

RESULT 12
VG14_BPPZA STANDARD; PRT; 131 AA.
AC P07539;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Lysis protein (Late protein GP14).
GN 14.
OS Bacteriophage PZA.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae.
OX NCBI_TaxID=10757;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87031573; PubMed=3095188;
RA Paces V., Vicek C., Urbanek P.;
RT "Nucleotide sequence of the late region of Bacillus subtilis phage
RT PZA, a close relative of phi 29.";
RL Gene 44:107-114(1986).
CC -----
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CC -----
DR EMBL; M11813; AAA88491.1; -.
DR PIR; I24831; WMBP14.
KW Late protein; Phage lysis protein.
SQ SEQUENCE 131 AA; 14977 MW; 46A23AE25A79C3D4 CRC64;
```

```
RT "Nucleotide sequence of the late region of Bacillus phage phi 29
RT completes the 19,285-bp sequence of phi 29 genome. Comparison with
RT the homologous sequence of phage PZA.";
RL Gene 46:215-225(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87117505; PubMed=3027653;
RA Garvey K.J., Saedi M.S., Ito J.;
RT "Nucleotide sequence of Bacillus phage phi 29 genes 14 and 15:
RT homology of gene 15 with other phage lysozymes.";
RL Nucleic Acids Res. 14:10001-10008(1986).
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CC -----
DR EMBL; M14782; AAA32287.1; -.
DR EMBL; X04962; CAA28631.1; -.
DR PIR; A24721; WMBP29.
KW Late protein; Phage lysis protein.
FT CONFLICT 78 81 PAGL -> LRVY (IN REF. 1).
SQ SEQUENCE 131 AA; 15032 MW; 9739B9F0D566C3D9 CRC64;

Query Match 41.8%; Score 38; DB 1; Length 131;
Best Local Similarity 44.4%; Pred. No. 17;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 SRLLEFYLAMPPFATPMEA 18
| :|:|||||
Db 62 SEMILALLAIPFAVPFPA 79

RESULT 12
VG14_BPPZA STANDARD; PRT; 131 AA.
AC P07539;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Lysis protein (Late protein GP14).
GN 14.
OS Bacteriophage PZA.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae.
OX NCBI_TaxID=10757;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87031573; PubMed=3095188;
RA Paces V., Vicek C., Urbanek P.;
RT "Nucleotide sequence of the late region of Bacillus subtilis phage
RT PZA, a close relative of phi 29.";
RL Gene 44:107-114(1986).
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CC -----
DR EMBL; M11813; AAA88491.1; -.
DR PIR; I24831; WMBP14.
KW Late protein; Phage lysis protein.
SQ SEQUENCE 131 AA; 14977 MW; 46A23AE25A79C3D4 CRC64;
```

Query Match 41.8%; Score 38; DB 1; Length 131;
Best Local Similarity 44.4%; Pred. No. 17;

Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 SRLLEFYLAMPFATPMEA 18
| :: ||:|||| |
Db 62 SEMILALLAVPFAVPPFA 79

RESULT 13
PETD_CHLEU STANDARD; PRT; 160 AA.
AC P11093;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Cytochrome B6-F complex subunit 4 (17 kDa polypeptide).
GN PETD.
OS Chlamydomonas eugametos.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3053;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UTEX 9;
RX MEDLINE=89263804; PubMed=2726496;
RA Turmel M., Boulanger J., Bergeron A.;
RT "Nucleotide sequence of the chloroplast petD gene of Chlamydomonas eugametos.";
RL Nucleic Acids Res. 17:3593-3593(1989).
CC -!- FUNCTION: THIS POLYPEPTIDE OF UNKNOWN FUNCTION IS ONE OF THE COMPONENTS OF THE CYTOCHROME B6-F COMPLEX.
CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B6-F ARE: CYTOCHROME B6, 17 kDa POLYPEPTIDE (PETD), CYTOCHROME F AND THE RIESKE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY. CORRESPONDS TO THE CARBOXYL END OF MITOCHONDRIAL CYTOCHROME B.
CC -----
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CC -----
DR EMBL; X14503; CAA32656.1; -.
DR PIR; S04089; S04089.
DR Mendel; 2559; CHLEU;petD;1.
DR InterPro; IPR000179; Cyt_b_b6.
DR Pfam; PF00032; cytochrome_b_c; 1.
DR PROSITE; PS00193; CYTOCHROME_B_QQ; 1.
KW Electron transport; Chloroplast; Photosynthesis; Transmembrane.
SQ SEQUENCE 160 AA; 17475 MW; 0609D6C3702F299A CRC64;

Query Match 41.8%; Score 38; DB 1; Length 160;
Best Local Similarity 77.8%; Pred. No. 21;
Matches 7; Conservative 1; Mismatches 0; Gaps 0;

QY 9 AMPFATPME 17
| |||||:|
Db 66 ANPFATPLE 74

RESULT 14
PETD_CHLPR STANDARD; PRT; 160 AA.
AC P13348;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Cytochrome B6-F complex subunit 4 (17 kDa polypeptide).
GN PETD.
OS Chlorella protothecoides.

Chloroplast.
Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
Chlorellaceae; Chlorella.
OX NCBI_TaxID=3075;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=211-7A;
RX MEDLINE=92003673; PubMed=2519117;
RA Reimann A., Kueck U.;
RT "Nucleotide sequence of the plastid genes for apocytochrome b6 (petB) and subunit IV of the cytochrome b6-f complex (petD) from the green alga Chlorella protothecoides: lack of introns.";
RL Plant Mol. Biol. 13:255-256(1989).
CC -!- FUNCTION: THIS POLYPEPTIDE OF UNKNOWN FUNCTION IS ONE OF THE COMPONENTS OF THE CYTOCHROME B6-F COMPLEX.
CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B6-F ARE: CYTOCHROME B6, 17 kDa POLYPEPTIDE (PETD), CYTOCHROME F AND THE RIESKE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY. CORRESPONDS TO THE CARBOXYL END OF MITOCHONDRIAL CYTOCHROME B.
CC -----
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CC -----
DR EMBL; X15244; CAA33323.1; -.
DR PIR; S06160; WMKL17.
DR Mendel; 11631; CHLpr;petD;1.
DR InterPro; IPR000179; Cyt_b_b6.
DR Pfam; PF00032; cytochrome_b_c; 1.
DR PROSITE; PS00193; CYTOCHROME_B_QQ; 1.
KW Electron transport; Chloroplast; Photosynthesis; Transmembrane.
SQ SEQUENCE 160 AA; 17432 MW; F865D53D4BE16A5F CRC64;

Query Match 41.8%; Score 38; DB 1; Length 160;
Best Local Similarity 77.8%; Pred. No. 21;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 AMPFATPME 17
| |||||:|
Db 66 ANPFATPLE 74

RESULT 15
PETD_CHLRE STANDARD; PRT; 160 AA.
AC P23230;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Cytochrome B6-F complex subunit 4 (17 kDa polypeptide).
GN PETD.
OS Chlamydomonas reinhardtii.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2137;
RX MEDLINE=91204459; PubMed=2017378;
RA Yu W., Spreitzer R.J.;
RT "Sequences of trnR-ACG and petD that contain a tRNA-like element within the chloroplast genome of Chlamydomonas reinhardtii.";
RL Nucleic Acids Res. 19:957-957(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=137C / CC-125;
RX MEDLINE=91285146; PubMed=2060646;

RA Bueschlen S., Choquet Y., Kuras R., Wollman F.A.;
RT "Nucleotide sequences of the continuous and separated petA, petB and
RL petD chloroplast genes in Chlamydomonas reinhardtii."; FEBS Lett. 284:257-262(1991).
RN [3]
RP SEQUENCE OF 1-8 FROM N.A.
RX MEDLINE=93133815; PubMed=8421681;
RA Sakamoto W., Kindle K.L., Stern D.B.;
RT "In vivo analysis of Chlamydomonas chloroplast petD gene expression
RT using stable transformation of beta-glucuronidase translational
RT fusions."; J. Biol. Chem. 270:29342-29349(1995).
RL J. Biol. Chem. 270:29342-29349(1995).
RN [4]
RP PROC. Natl. Acad. Sci. U.S.A. 90:497-501(1993).
RN [4]
RP CHARACTERIZATION.
RC STRAIN=WT12;
RX MEDLINE=96094329; PubMed=7493968;
RA Pierre Y., Breyton C., Kramer D., Popot J.-L.;
RT "Purification and characterization of the cytochrome b6 f complex
RT from Chlamydomonas reinhardtii."; J. Biol. Chem. 270:29342-29349(1995).
RL J. Biol. Chem. 270:29342-29349(1995).
RN [4]
RP FUNCTION: THIS POLYPEPTIDE OF UNKNOWN FUNCTION IS ONE OF THE
CC COMPONENTS OF THE CYTOCHROME B6-F COMPLEX.
CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B6-F ARE: CYTOCHROME B6,
CC 17 kDa POLYPEPTIDE (PETD), CYTOCHROME F AND THE RIESKE PROTEIN.
CC -!- PTM: THE N-TERMINUS IS BLOCKED.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY. CORRESPONDS TO THE
CC CARBOXYL END OF MITOCHONDRIAL CYTOCHROME B.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X56700; CAA40030.1; -;
DR EMBL; X72919; CAA51424.1; -;
DR EMBL; L05506; AAA84153.1; -;
DR PIR; S16918; S16918.
DR PIR; S26837; S26837.
DR Mendel; 4397; CHLre; petD; 1.
DR InterPro; IPR000179; Cyt_b_b6.
DR Pfam; PF00032; cytochrome_b_c; 1.
DR PROSITE; PS00193; CYTOCHROME_B_QQ; 1.
KW Electron transport; Chloroplast; Photosynthesis; Transmembrane.
FT CONFLICT 67 N -> F (IN REF. 2).
SQ SEQUENCE 160 AA; 17442 MW; 6B1C77BBB8E857A8 CRC64;

Query Match 41.8%; Score 38; DB 1; Length 160;
Best Local Similarity 77.8%; Pred. No. 21;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 AMPFATPME 17
| | | | | | | |
Db 66 ANPFATPLE 74

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:24:09 ; Search time 107.89 Seconds
(without alignments)
28.862 Million cell updates/sec

Title: US-09-165-546A-12
Perfect score: 91
Sequence: 1 SRLEFYLAMPFATPMEA 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archheap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	91	100.0	142	4	Q9NY13	Q9ny13 homo sapien
2	67	73.6	210	4	Q9BU80	Q9bu80 homo sapien
3	64	70.3	180	4	Q9Y479	Q9y479 homo sapien
4	64	70.3	210	4	Q9UJ89	Q9uj89 homo sapien
5	54	59.3	219	11	Q9D9S4	Q9d9s4 mus musculu
6	47	51.6	426	16	Q9HW63	Q9hw63 pseudomonas
7	47	51.6	1249	16	Q9I1H0	Q9i1h0 pseudomonas
8	44	48.4	398	4	Q9UNI0	Q9uni0 homo sapien
9	44	48.4	456	4	Q9P1V2	Q9p1v2 homo sapien
10	44	48.4	510	4	Q9BUL2	Q9bul2 homo sapien
11	44	48.4	521	4	Q9UKU8	Q9uku8 homo sapien
12	44	48.4	521	4	Q9UNF8	Q9unf8 homo sapien
13	44	48.4	521	4	Q96T60	Q96t60 homo sapien
14	44	48.4	700	10	Q9LRV2	Q9lrsv2 arabidopsis
15	42	46.2	264	16	Q9PM93	Q9pm93 campylobact
16	42	46.2	394	5	Q9NJS6	Q9njs6 aplysia kur

17	42	46.2	537	5	Q9VDP5	Q9vdp5 drosophila
18	42	46.2	547	5	Q9GQ01	Q9gq01 nilaparvata
19	42	46.2	757	16	Q98FC7	Q98fc7 rhizobium l
20	41.5	45.6	475	10	Q9SKT8	Q9skt8 arabidopsis
21	41	45.1	183	2	Q53443	Q53443 azotobacter
22	41	45.1	258	11	Q99PD3	Q99pd3 rattus norv
23	41	45.1	266	16	Q930I5	Q930i5 rhizobium m
24	41	45.1	417	16	P74302	P74302 synechocyst
25	41	45.1	422	11	Q9CYC6	Q9cyc6 mus musculu
26	41	45.1	430	16	Q987C3	Q987c3 rhizobium l
27	41	45.1	494	11	Q9JLV6	Q9jlv6 mus musculu
28	40	44.0	132	10	Q9LDP4	Q9ldp4 oryza sativ
29	40	44.0	250	12	Q85210	Q85210 pseudorabie
30	40	44.0	899	5	Q960W0	Q960w0 drosophila
31	40	44.0	919	12	Q911W0	Q911w0 pseudorabie
32	40	44.0	974	2	Q9S0Y6	Q9s0y6 streptomyc
33	40	44.0	1248	5	Q9NGK5	Q9ngk5 drosophila
34	39.5	43.4	1108	5	Q9TYG5	Q9tyg5 drosophila
35	39.5	43.4	1108	5	Q9VHD8	Q9vhd8 drosophila
36	39	42.9	74	5	Q9N7V9	Q9n7v9 leishmania
37	39	42.9	80	12	O41020	O41020 paramecium
38	39	42.9	160	16	P73387	P73387 synechocyst
39	39	42.9	216	16	Q9CND7	Q9cnd7 pasteurella
40	39	42.9	363	13	O42376	O42376 brachydanio
41	39	42.9	384	10	Q9SFB9	Q9sfb9 arabidopsis
42	39	42.9	392	2	Q9F849	Q9f849 streptomyc
43	39	42.9	403	16	Q9HVV5	Q9hvy5 pseudomonas
44	39	42.9	442	10	Q940B4	Q940b4 arabidopsis
45	39	42.9	459	10	Q9SZ25	Q9sz25 arabidopsis

ALIGNMENTS

RESULT 1
Q9NY13
ID Q9NY13 PRELIMINARY; PRT; 142 AA.
AC Q9NY13;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE HYPOTHETICAL 13.9 KDA PROTEIN (FRAGMENT).
GN LAGE-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lethe B.G.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ275978; CAB76945.1; .
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 142 AA; 13895 MW; 27EBE922AC4ACC7B CRC64;

Query Match 100.0%; Score 91; DB 4; Length 142;
Best Local Similarity 100.0%; Pred. NO. 2.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLEFYLAMPFATPMEA 18
|||||
Db 59 SRLEFYLAMPFATPMEA 76

RESULT 2
Q9BU80
ID Q9BU80 PRELIMINARY; PRT; 210 AA.
AC Q9BU80;

DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)


```
DE  CANCER/TESTIS ANTIGEN 2.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=PLACENTA, CHORIOCARCINOMA;
RA  Strausberg R.;
RL  Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BC002833; AAH02833.1; -.
SQ  SEQUENCE 210 AA; 21089 MW; 8FB5BF04FB04E8BE CRC64;

Query Match      73.6%; Score 67; DB 4; Length 210;
Best Local Similarity 66.7%; Pred. No. 0.00064;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 SRLLFFYLAMPFATPMEA 18
Db 85 SRLLQLHITMPFSSPMEA 102

RESULT 3
Q9Y479
ID Q9Y479 PRELIMINARY; PRT; 180 AA.
AC Q9Y479;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE LAGE-IS PROTEIN (CANCER/TESTIS ANTIGEN 2).
GN LAGE1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MELANOMA;
RX MEDLINE=99325550; PubMed=10399963;
RA Aarnoudse C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.;
RT "Interleukin-2-induced, melanoma-specific T cells recognize CAMEL, an
RT unexpected translation product of LAGE-1.";
RL Int. J. Cancer 82:442-448(1999).
SQ SEQUENCE 180 AA; 18236 MW; 9077FAF953543A25 CRC64;

Query Match      70.3%; Score 64; DB 4; Length 180;
Best Local Similarity 61.1%; Pred. No. 0.0018;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 SRLLFFYLAMPFATPMEA 18
Db 85 SRLLQLHITMPFSSPMEA 102

RESULT 4
Q9UJ89
ID Q9UJ89 PRELIMINARY; PRT; 210 AA.
AC Q9UJ89;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
```

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DE  LAGE-1L PROTEIN.
GN  LAGE-1L.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=MELANOMA;
RX  MEDLINE=99325550; PubMed=10399963;
RA  Aarnoudse C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.;
RT  "Interleukin-2-induced, melanoma-specific T cells recognize CAMEL, an
RT  unexpected translation product of LAGE-1.";
RL  Int. J. Cancer 82:442-448(1999).
DR  EMBL; AJ012835; CAA10196.1; -.
SQ  SEQUENCE 210 AA; 21060 MW; 1DD0B1829735B60A CRC64;

Query Match      70.3%; Score 64; DB 4; Length 210;
Best Local Similarity 61.1%; Pred. No. 0.0022;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 SRLLFFYLAMPFATPMEA 18
Db 85 SRLLQLHITMPFSSPMEA 102

RESULT 5
Q9D9S4
ID Q9D9S4 PRELIMINARY; PRT; 219 AA.
AC Q9D9S4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE 1700030B21RIK PROTEIN.
GN 1700030B21RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK006526; BAB24635.1; -.
DR MGD; MGI:1917312; 1700030B21Rik.
SQ SEQUENCE 219 AA; 23670 MW; FB9B7B5A11FA2C37 CRC64;

Query Match      59.3%; Score 54; DB 11; Length 219;
Best Local Similarity 61.1%; Pred. No. 0.13;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
```

QY 1 SRLLEFYLAMPPFATPMEA 18
||||| : ||| : ||
Db 126 SRLLEFSVTVPFRTAVEA 143

RESULT 6
Q9HW63
ID Q9HW63 PRELIMINARY; PRT; 426 AA.
AC Q9HW63;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)
DE HYPOTHETICAL PROTEIN PA4338.
GN PA4338.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltz L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen."
RL Nature 406:959-964 (2000).
DR EMBL; AE004850; AAG07726.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 426 AA; 48323 MW; AB00AA9643AF5257 CRC64;

Query Match 51.6%; Score 47; DB 16; Length 426;
Best Local Similarity 60.0%; Pred. No. 4.3;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 SRLLEFYLAMPPFATP 15
| : ||||| |
Db 178 STLMEFYLAFFVAP 192

RESULT 7
Q9I1H0
ID Q9I1H0 PRELIMINARY; PRT; 1249 AA.
AC Q9I1H0;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE PROBABLE NON-RIBOSOMAL PEPTIDE SYNTHETASE.
GN PA2305.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltz L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen."
RL Nature 406:959-964 (2000).
DR EMBL; AE004656; AAG05693.1; -.
DR HSSP; P14687; 1AMU.

DR InterPro; IPR000873; AMP-bind.
DR InterPro; IPR000977; DNA_ligase.
DR InterPro; IPR001242; DUF4.
DR InterPro; IPR003880; Phosphopant_attach.
DR Pfam; PF00501; AMP-binding; 1.
DR Pfam; PF00668; Condensation; 1.
DR Pfam; PF00550; pp-binding; 1.
DR PRINTS; PR00154; AMPBINDING.
DR PROSITE; PS00075; ACP_DOMAIN; 1.
DR PROSITE; PS00455; AMP_BINDING; 1.
DR PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN_1.
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
KW Complete proteome; Phosphopantetheine.
SQ SEQUENCE 1249 AA; 134446 MW; B189E7FD3CB2C5BA CRC64;

Query Match 51.6%; Score 47; DB 16; Length 1249;
Best Local Similarity 58.8%; Pred. No. 13;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 RLLEFYLAMPPFATPMEA 18
| | ||| ||| | : |
Db 668 RRLVGYLAAPFAPPLQA 684

RESULT 8
Q9UNIO
ID Q9UNIO PRELIMINARY; PRT; 398 AA.
AC Q9UNIO;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE DEM1 PROTEIN.
GN DEM1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang H.W., Piao H.Y., Chen Y.Z., Hayashi Y.;
RT "Cloning a cDNA which is differently expressed in malignancies."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AF120499; AAD47379.1; -.
SQ SEQUENCE 398 AA; 43040 MW; A8F7E3425613BA9F CRC64;

Query Match 48.4%; Score 44; DB 4; Length 398;
Best Local Similarity 56.2%; Pred. No. 14;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 RLLEFYLAMPPFATPME 17
| | : ||||| |
Db 311 RLFAALNLGLPFATPEE 326

RESULT 9
Q9P1V2
ID Q9P1V2 PRELIMINARY; PRT; 456 AA.
AC Q9P1V2;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE POLYNUCLEOTIDE KINASE 3'-PHOSPHATASE, PARTIAL SEQUENCE
DE (FRAGMENT).
GN PNKP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., MCCready P.M., Skowronski E., Viswanathan V.,

RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,
RA Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
RA Andreise T., Trankheim M., Attix C., Amico-Keller G., Coefield J.,
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA Olsen A.S., Carrano A.V.;
RT "Sequence analysis of a 3 Mb region in 19q13.3.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AC018766; AAF44716.1; -.
KW Kinase.
FT NON_TER 1 1
SQ SEQUENCE 456 AA; 50198 MW; FB5A7F62E97FBD31 CRC64;

Query Match 48.4%; Score 44; DB 4; Length 456;
Best Local Similarity 56.2%; Pred. No. 16;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 RLLEFYLAMPFATPME 17
||| :|||||
Db 246 RLFA NLGLPFATPEE 261

RESULT 10
Q9BUL2
ID Q9BUL2 PRELIMINARY; PRT; 510 AA.
AC Q9BUL2;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE SIMILAR TO POLYNUCLEOTIDE KINASE 3'-PHOSPHATASE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-OVARY, ADENOCARCINOMA;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBDJ databases.
DR EMBL; BC002519; AAH02519.1; -.
KW Kinase.
FT NON_TER 1 1
SQ SEQUENCE 510 AA; 56044 MW; A1F9FE316C37B672 CRC64;

Query Match 48.4%; Score 44; DB 4; Length 510;
Best Local Similarity 56.2%; Pred. No. 18;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 RLLEFYLAMPFATPME 17
||| :|||||
Db 300 RLFA NLGLPFATPEE 315

RESULT 11
Q9UKU8
ID Q9UKU8 PRELIMINARY; PRT; 521 AA.
AC Q9UKU8;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE DNA 5'-KINASE/3'-PHOSPHATASE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99377056; PubMed=10446193;

RA Karimi-Busheri F., Daly G., Robins P., Canas B., Pappin D.J.C.,
RA Sgouros J., Miller G.G., Fakhrat H., Davis E.M., Le Beau M.M.,

RA Weinfeld M.;
RT "Molecular Characterization of a human DNA kinase.";
RL J. Biol.Chem. 274:24187-24194(1999).
DR EMBL; AF125807; AAD50639.1; -.
KW Kinase.
SQ SEQUENCE 521 AA; 57102 MW; 22B5C949EF569516 CRC64;

Query Match 48.4%; Score 44; DB 4; Length 521;
Best Local Similarity 56.2%; Pred. No. 18;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 RLLEFYLAMPFATPME 17
||| :|||||
Db 311 RLFA NLGLPFATPEE 326

RESULT 12
Q9UNF8
ID Q9UNF8 PRELIMINARY; PRT; 521 AA.
AC Q9UNF8;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE POLYNUCLEOTIDE KINASE-3'-PHOSPHATASE.
GN PNKP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99377055; PubMed=10446192;
RA Jilani A., Ramotar D., Slack C., Ong C., Yang X.M., Scherer S.W.,
RA Lasko D.D.;
RT "Molecular cloning of the human gene, PNKP, encoding a polynucleotide
RT kinase 3'-phosphatase and evidence for its role in repair of DNA
RT strand breaks caused by oxidative damage.";
RL J. Biol. Chem. 274:24176-24186(1999).
DR EMBL; AF126486; AAD51135.1; -.
KW Kinase.
SQ SEQUENCE 521 AA; 57148 MW; D477C94D41E62516 CRC64;

Query Match 48.4%; Score 44; DB 4; Length 521;
Best Local Similarity 56.2%; Pred. No. 18;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 RLLEFYLAMPFATPME 17
||| :|||||
Db 311 RLFA NLGLPFATPEE 326

RESULT 13
Q96T60
ID Q96T60 PRELIMINARY; PRT; 521 AA.
AC Q96T60;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE POLYNUCLEOTIDE KINASE-3'-PHOSPHATASE.
GN PNKP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99377055; PubMed=10446192;

RA Jilani A., Ramotar D., Slack C., Ong C., Yang X.M., Scherer S.W.,
RA Lasko D.D.;
RT "Molecular cloning of the human gene, PNKP, encoding a polynucleotide
RT kinase 3'-phosphatase and evidence for its role in repair of DNA

RT strand breaks caused by oxidative damage.";

RL J. Biol. Chem. 274:24176-24186(1999).

RN [2]

RP SEQUENCE FROM N.A.

RA Scorillas A., Katsaros N.;

RT "Genomic organization, physical mapping and expression analysis of the

RT human polynucleotide kinase-3'-phosphatase (PNKP) gene.";

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF354258; AAK57340.1; -.

KW Kinase.

SQ SEQUENCE 521 AA; 57076 MW; 22B5C94D41E62516 CRC64;

Query Match 48.4%; Score 44; DB 4; Length 521;

Best Local Similarity 56.2%; Pred. No. 18;

Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 RLLEFYLAMPFATPME 17

Db 311 RLFAALNLGLPFATPEE 326

RESULT 14

Q9LRV2 PRELIMINARY; PRT; 700 AA.

AC Q9LRV2;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE SELENIUM-BINDING PROTEIN-LIKE.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=COLUMBIA;

RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=COLUMBIA;

RX MEDLINE=20277480; PubMed=10819329;

RA Nakamura Y.;

RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence

RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC

RT clones.";

RL DNA Res. 7:131-135(2000).

DR EMBL; AB028611; BAB01836.1; -.

DR InterPro; IPR002885; PPR.

DR Pfam; PF01535; PPR; 8.

SQ SEQUENCE 700 AA; 79194 MW; 1525A5DE7F242682 CRC64;

Query Match 48.4%; Score 44; DB 10; Length 700;

Best Local Similarity 56.2%; Pred. No. 24;

Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 RLLEFYLAMPFATPME 17

Db 651 QLEFLLMPFDPMPQ 666

RESULT 15

Q9PM93 PRELIMINARY; PRT; 264 AA.

ID Q9PM93

AC Q9PM93;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE PUTATIVE PEPTIDE ABC-TRANSPORT SYSTEM PERMEASE PROTEIN.

GN CJ1582C.

OS Campylobacter jejuni.

OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;

OC Campylobacter.

OX NCBI_TaxID=197;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NCTC 11168;

RX MEDLINE=20150912; PubMed=10688204;

RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,

RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,

RA Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,

RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,

RA Whitehead S., Barrell B.G.;

RT "The genome sequence of the food-borne pathogen Campylobacter jejuni

RT reveals hypervariable sequences.";

RL Nature 403:665-668(2000).

DR EMBL; AL139079; CAB73570.1; -.

DR InterPro; IPR000515; BPD_transp.

DR Pfam; PF00528; BPD_transp; 1.

KW Complete proteome.

SQ SEQUENCE 264 AA; 30382 MW; 2B50263DBF2340E8 CRC64;

Query Match 46.2%; Score 42; DB 16; Length 264;

Best Local Similarity 70.0%; Pred. No. 20;

Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLLEFYLAMP 11

Db 101 RILEFFLALP 110

Search completed: July 3, 2002, 11:24:10

Job time: 917 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 11:08:50 ; Search time 136.43 Seconds
(without alignments)
14.655 Million cell updates/sec

Title: US-09-165-546A-12
Perfect score: 91
Sequence: 1 SRLLEFYLAMPFATPMEA 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :	A_Geneseq_032802:*	
	1:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT:*
	2:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT:*
	3:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT:*
	4:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT:*
	5:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT:*
	6:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT:*
	7:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT:*
	8:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT:*
	9:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT:*
	10:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT:*
	11:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT:*
	12:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT:*
	13:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT:*
	14:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT:*
	15:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT:*
	16:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT:*
	17:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT:*
	18:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT:*
	19:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:*
	20:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT:*
	21:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:*
	22:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	91	100.0	18	21	AAV52439 Human tumour antig
2	91	100.0	18	22	AAU01543 HLA-DR53 recognisi
3	91	100.0	18	22	AAAB69943 Human NY-ESO-1 HLA
4	91	100.0	180	19	AAAB69665 Human NY-ESO-1 pro
5	91	100.0	180	19	AAAB62584 Cancer associated
6	91	100.0	180	20	AAAY05965 Human cancer antig
7	91	100.0	180	21	AAAB03154 Human oesophageal
8	91	100.0	180	21	AAAY70862 Human tumour antig
9	91	100.0	180	21	AAAY52430 Human tumour antig
10	91	100.0	180	22	AAAG67164 Amino acid sequenc
11	91	100.0	180	22	AAE07714 Human NY ESO-1 pro

12	91	100.0	180	22	AAU01535 Human NY-ESO-1 tum
13	91	100.0	180	22	AAAB69946 Human NY-ESO-1 pro
14	91	100.0	397	22	AAE13122 NY-ESO-IC-HER-2 me
15	82	90.1	20	22	AAE07741 Human ESO p82-101
16	70	76.9	14	22	AAU01549 Human NY-ESO-1 tum
17	64	70.3	180	19	AAAB69664 Human LAGE-1 clone
18	64	70.3	180	21	AAAY70860 Human LAGE-1 splic
19	64	70.3	210	19	AAAB69663 Human LAGE-1 clone
20	64	70.3	210	21	AAAY70861 Human LAGE-1 unspl
21	63	69.2	20	22	AAE07747 Human ESO p91-110
22	54	59.3	10	20	AAAY06013 Human cancer antig
23	52	57.1	10	20	AAAY06004 Human cancer antig
24	52	57.1	10	20	AAAY06007 Human cancer antig
25	52	57.1	10	22	AAAG67193 Cancer testis tumo
26	52	57.1	10	22	AAAB69925 Human NY-ESO-1 HLA
27	51	56.0	10	20	AAAY06010 Human cancer antig
28	48	52.7	9	22	AAAG67185 Cancer testis tumo
29	48	52.7	9	22	AAAB69917 Human NY-ESO-1 HLA
30	44	48.4	9	20	AAAY06021 Human cancer antig
31	44	48.4	9	21	AAAY78465 NY-ESO-1 derived H
32	44	48.4	9	22	AAU01545 Human NY-ESO-1 tum
33	44	48.4	232	21	AAAB43453 Human cancer assoc
34	44	48.4	328	21	AAAB41724 Human ORFX ORF1488
35	43	47.3	80	21	AAAG01586 Human secreted pro
36	42	46.2	272	21	AAAB25486 Eucalyptus grandis
37	42	46.2	416	21	AAAB25562 Eucalyptus grandis
38	42	46.2	537	22	ABBB61204 Drosophila melanog
39	41	45.1	89	21	AAAG01533 Human secreted pro
40	41	45.1	151	21	AAAB41637 Human ORFX ORF1401
41	41	45.1	321	22	AAE04774 Human vesicle traf
42	41	45.1	950	22	ABG21538 Novel human diagno
43	40.5	44.5	68	22	ABG07484 Novel human diagno
44	40	44.0	142	22	AAAM24261 Human EST encoded
45	40	44.0	392	22	AAE04176 Human gene 2 encod

ALIGNMENTS

RESULT 1	
AAV52439	AAV52439 standard; Protein; 18 AA.
ID	AAV52439 standard; Protein; 18 AA.
XX	
AC	AAV52439;
XX	
DT	15-FEB-2000 (first entry)
DE	Human tumour antigen NY-ESO-1 peptide #12.
XX	
KW	Cancer; tumour; antigen; MHC; major histocompatibility complex; Class II;
KW	T-cell; helper; stimulation; proliferation; treatment;
KW	diagnosis; prevention; melanoma; breast cancer; ovarian cancer;
KW	prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer;
KW	lymphoma.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
PN	WO9953938-A1.
XX	
PD	28-OCT-1999.
XX	
PF	24-MAR-1999; 99WO-US06875.
XX	
PR	17-APR-1998; 98US-0062422.
PR	02-OCT-1998; 98US-0165546.
XX	
PA	(LUDW-) LUDWIG INST CANCER RES.
XX	
PI	Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
PI	Gure A, Ritter G;
XX	
DR	WPI; 2000-038483/03.

XX Novel peptides which bind to MHC class I and MHC class II molecules,
PT useful for therapeutic and diagnostic purposes -
XX
XX
PS Claim 4; Page 22; 49pp; English.
XX
CC Peptides #8-#13 (AAY52435-Y52440) are peptides derived from the human
CC tumour antigen, NY-ESO-1 (AAY52430) which can bind to MHC(major
CC histocompatibility Class II HLA-DR53 molecules, thereby stimulating
CC proliferation of helper T-cells. cDNA encoding NY-ESO-1 was initially
CC isolated from an oesophagus squamous cell cancer cDNA library. Tissue
CC localisation studies revealed it to be expressed at high levels
CC in normal ovary and testis but not in normal colon, kidney, liver,
CC brain, oesophagus and skin. It was expressed in certain tumours and
CC tumour cell lines with some degree of frequency - these included
CC melanoma specimens and cell lines, and breast and bladder cancer
CC specimens, with expression in other tumour types being sporadic.
CC These NY-ESO-1-derived peptides may be used in methods and
CC compositions used for the treatment, diagnosis and prevention of
CC cancers (such as melanoma, breast cancer, prostate cancer, lung
CC cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer,
CC or lymphoma) and to stimulate the proliferation of T cells.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 91; DB 21; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLEFYLAMPFATPMEA 18
Db 1 srlliefylampfatpmea 18

RESULT 2
AAU01543
ID AAU01543 standard; Peptide; 18 AA.
XX
AC AAU01543;
XX
DT 18-JUL-2001 (first entry)
XX
DE HLA-DR53 recognising NY-ESO-1 peptide #5.
XX
KW NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
KW human leukocyte antigen-determining region; disease progression;
KW disease regression; disease onset; body tissue; body fluid; enzyme label;
KW radioactive label; monoclonal antibody.
XX
OS Homo sapiens.
XX
PN WO200123560-A2.
XX
PD 05-APR-2001.
XX
PF 26-SEP-2000; 2000WO-US26411.
XX
PR 29-SEP-1999; 99US-0408036.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Tureci O, Sahin U, Pfreundschuh M;
XX
DR WPI; 2001-266156/27.
XX
PT Polypeptides binding to major histocompatibility complex class II human
PT leukocyte antigen-determining region molecule having amino acid
PT sequence found in tumour rejection antigen precursor used for
PT stimulating proliferation of helper T cells -
XX
PS Example 13; Page 19; 62pp; English.

XX The sequence represents a human NY-ESO-1 tumour rejection antigen
CC precursor fragment which recognises and binds to HLA-DR53. NY-ESO-1 and
CC SSX-2 polypeptides, or fragments of, bind to major histocompatibility
CC complex (MHC) Class II molecules such as human leukocyte
CC antigen-determining region (HLA-DR) molecules and stimulate proliferation
CC of helper T cells. The peptides can be administered to an HLA-DR positive
CC subject in order to stimulate the helper T cells. An MHC Class II
CC HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell or
CC present in free form is useful for this stimulation. The nucleic acid is
CC useful for screening for a cancerous condition, which involves contacting
CC a subject sample to a cell line transfected with the immunoreactive cell
CC (helper T cell), where interaction is indicative of cancer. In addition,
CC a sample from a patient (for example, a body fluid or tissue) can be
CC monitored for the amount of the complex present in the bloodstream. This
CC is useful for determining regression, progression or onset of a cancerous
CC condition. The method involves contacting the sample with a radioactive
CC labelled or enzyme labelled monoclonal antibody which specifically binds
CC with the complex.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 91; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLEFYLAMPFATPMEA 18
Db 1 srlliefylampfatpmea 18

RESULT 3
AAB69943
ID AAB69943 standard; Peptide; 18 AA.
XX
AC AAB69943;
XX
DT 27-APR-2001 (first entry)
XX
DE Human NY-ESO-1 HLA-DR53 binding motif #5.
XX
KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW non-small cell lung carcinoma; tumour status determination.
XX
OS Homo sapiens.
XX
PN WO200107917-A1.
XX
PD 01-FEB-2001.
XX
PF 14-JUL-2000; 2000WO-US19220.
XX
PR 23-JUL-1999; 99US-0359503.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.
XX
PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
XX
DR WPI; 2001-182822/18.
XX
PT Method useful for determining the status (e.g. progression, regression
PT or stability of the disease) of a cancerous condition, involves
PT determining the levels of NY-ESO-1 specific antibodies in a sample
PT taken from a patient -
XX
PS Example 16; Page 28; 50pp; English.
XX
CC The present sequence is given in a specification relating to a method
CC for determining the status of a cancerous condition in a patient

CC with a tumour that expresses NY-ESO-1. The method comprises assaying a
CC sample taken from the patient for antibodies that specifically bind to
CC the NY-ESO-1 and comparing the value obtained to a prior value obtained
CC from assay of a prior sample taken from the patient. Any difference
CC between the values is indicative of a change in status of the cancerous
CC condition. The method is useful for determining whether a cancerous
CC condition is progressing, regressing or remaining stable, in particular
CC in patients receiving treatment for a melanoma, adenocarcinoma,
CC non-small cell lung carcinoma or bladder carcinoma.

XX Sequence 18 AA;

SQ

Query Match 100.0%; Score 91; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLLEFYLAMPFATPMEA 18
Db 1 srllefyfampfpmea 18
|||||

RESULT 4
AAW69665
ID AAW69665 standard; Protein; 180 AA.
XX
AC AAW69665;
XX
DT 27-OCT-1998 (first entry)
XX
DE Human NY-ESO-1 protein sequence, formerly known as LL-1.2 clone.
XX
KW Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour.
XX
OS Homo sapiens.
XX
PN WO9832855-A1.
XX
PD 30-JUL-1998.
XX
PF 27-JAN-1998; 98WO-US01445.
XX
PR 27-JAN-1997; 97US-0791495.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Boon-Falleur T, De Smet C, Godelaine D, Lethe B;
PI Lucas S;
XX
DR WPI; 1998-427951/36.
DR N-PSDB; AAV50348.
XX
PT New isolated LAGE-1 tumour associated nucleic acids - used to
PT develop products for the diagnosis and treatment of LAGE-1
PT associated disorders, particularly tumours
XX
PS Example 2; Page 57-58; 73pp; English.
XX
CC The present sequence represents human NY-ESO-1, formerly known as LL-1.2
CC clone, which is used in an example from the present invention which
CC describes LAGE-1 tumour associated protein (TAP). The present invention
CC also describes: (1) a method for treating a subject with a disorder
CC characterised by expression of a LAGE-1 nucleic acid molecule or an
CC expression product, comprising administering to the subject autologous
CC cytolytic T cells to ameliorate the disorder, where the cytolytic T
CC cells are specific for complexes of an HLA molecule and a LAGE-1 TAP or
CC an immunogenic fragment; (2) a method for treating a subject with a
CC disorder characterised by expression of a LAGE-1 nucleic acid molecule
CC or an expression product, comprising administering a LAGE-1 TAP or an
CC immunogenic fragment to ameliorate the disorder; and (3) a method for
CC selectively enriching a population of T cells with cytolytic T cells
CC specific for a LAGE-1 TAP comprising contacting an isolated population
CC of T cells with an agent presenting a complex of a LAGE TAP or an

CC immunogenic fragment and a HLA presenting molecule to selectively
CC enrich the isolated population of T cells with the cytolytic T cells.
CC The methods and products from the present invention can be used for the
CC diagnosis and treatment of LAGE-1 associated disorders, particularly
CC tumours.

XX Sequence 180 AA;

SQ

Query Match 100.0%; Score 91; DB 19; Length 180;
Best Local Similarity 100.0%; Pred. No. 6.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLLEFYLAMPFATPMEA 18
Db 85 srllefyfampfpmea 102
|||||

RESULT 5
AAW62584
ID AAW62584 standard; Protein; 180 AA.
XX
AC AAW62584;
XX
DT 17-SEP-1998 (first entry)
XX
DE Cancer associated antigen NY-ESO-1.
XX
KW Cancer associated antigen; NY-ESO-1; regression; progression; onset;
KW cancer; treatment; diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 7 /note= "potential myristoylation site"
FT Misc-difference 9 /note= "potential myristoylation site"
FT Misc-difference 11 /note= "potential phosphorylation site"
FT Misc-difference 98 /note= "potential phosphorylation site"
FT Misc-difference 134 /note= "potential phosphorylation site"
FT Misc-difference 138 /note= "potential phosphorylation site"
FT /note= "potential phosphorylation site"
XX WO9814464-A1.
PN
XX
PD 09-APR-1998.
XX
PF 15-SEP-1997; 97WO-US16335.
XX
PR 03-OCT-1996; 96US-0725182.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Chen Y, Drijfhout JW, Gure A, Jager E, Knuth A;
PI Old LJ, Scanlan M;
XX
DR WPI; 1998-286417/25.
DR N-PSDB; AAV38566.
XX
PT New isolated cancer associated antigen - is used to develop products
PT for the diagnosis and treatment of cancers and for monitoring cancer
PT therapy
XX
PS Claim 8; Fig 3; 49pp; English.
XX
CC The present sequence represents a cancer associated antigen. The clone
CC from which the DNA sequence is obtained is designated NY-ESO-1. The
CC specification described a method for determining regression, progression
CC of onset of a cancerous condition, comprising monitoring a sample from a

XX Example 5; Fig 3; 9pp; English.

PS This sequence represents a human oesophageal cancer-associated antigen,

XX NY-ESO-1. The cDNA encoding this sequence was isolated from a

CC cDNA library prepared from a specimen of well-to-moderately

CC differentiated squamous cell cancer of the oesophagus. Expression

CC analysis demonstrated that NY-ESO-1 was expressed in oesophageal

CC carcinoma, certain melanoma cell lines and in normal ovary and testis

CC tissue, but not in normal colon, kidney, liver or brain tissue. Analysis

CC of the amino acid sequence of the protein indicates that the protein has

CC a transmembrane domain, several N-myristoylation sites and

CC O-phosphorylation sites and that it contains antigenic sequences in the

CC N-terminal half of the protein. The antigen is useful as an immunogen

CC when combined with an adjuvant, in both precursor and post-

CC translationally modified forms, and may be used to generate anti-NY-ESO-1

CC antibodies. It can also be used as a diagnostic marker for oesophageal

CC cancer, and can be utilised as a marker for the targetted delivery of

CC therapeutic agents to oesophageal cancer cells. It can also be used to

CC generate diagnostic or therapeutic agents.

XX

SQ Sequence 180 AA;

Query Match 100.0%; Score 91; DB 21; Length 180;

Best Local Similarity 100.0%; Pred. No. 6.3e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLLEFYLAMPFATPMEA 18

Db 85 srllefyfampfatpmea 102

RESULT 8

AAY70862

ID AAY70862 standard; Protein; 180 AA.

XX AAY70862;

XX

DT 31-JUL-2000 (first entry)

XX

DE Human tumour antigen, NY-ESO-1 protein.

XX

KW NY-ESO-1; CAMEL; CTL-recognised Antigen on MELanoma; human; cancer; CTL;

KW cytotoxic T lymphocyte; tumour-associated antigen; LAGE-1; anticancer;

KW melanoma; immunotherapy; immune response.

XX

OS Homo sapiens.

XX

PN WO200023584-A1.

PD 27-APR-2000.

XX

PF 15-OCT-1999; 99WO-EP07832.

XX

PR 16-OCT-1998; 98EP-0119583.

XX

PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.

PA (UYHO-) UNIV HOSPITAL LEIDEN.

XX

PI Schrier PI, Aarnoudse CA, Heider K, Klade C;

XX

DR WPI; 2000-339685/29.

DR N-PSDB; AAD00152.

XX

PT Tumor-associated antigen useful for cancer immunotherapy is encoded by

PT the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA -

XX

PS Example 3; Page 62-63; 73pp; English.

XX

CC The present sequence is the human NY-ESO-1 protein, a tumour antigen,

CC identified by screening an esophagus carcinoma cDNA library. This protein

CC is derived from open reading frame (ORF)-1 that contain epitopes of

CC tumour specific T-cells. NY-ESO-1 is expressed in different tumour types,

CC but not in healthy tissues except in testis. It also shows homology with

CC the CAMEL (Cytotoxic T lymphocytes (CTL)-recognised Antigen on MELanoma)

CC protein, a tumour-associated antigen. The tumour-associated antigen

CC displayed on melanoma cells is recognised by cytotoxic T lymphocytes.

CC This sequence has anticancer activity. CAMEL tumour antigen and

CC immunogenic peptides derived from it are useful for cancer immunotherapy.

CC They have the potential to induce an immune response, by eliciting a

CC CTL response. The DNA molecule is used for the construction of

CC recombinant or fusion proteins.

XX

SQ Sequence 180 AA;

Query Match 100.0%; Score 91; DB 21; Length 180;

Best Local Similarity 100.0%; Pred. No. 6.3e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLLEFYLAMPFATPMEA 18

Db 85 srllefyfampfatpmea 102

RESULT 9

AAY52430

ID AAY52430 standard; Protein; 180 AA.

XX AAY52430;

XX

DT 15-FEB-2000 (first entry)

XX

DE Human tumour antigen NY-ESO-1.

XX

KW Cancer; tumour; antigen; MHC; major histocompatibility complex;

KW T-cell; cytotoxic; helper; stimulation; proliferation; treatment;

KW diagnosis; prevention; melanoma; breast cancer; ovarian cancer;

KW prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer;

KW lymphoma.

XX

OS Homo sapiens.

XX

FH Key

FT Peptide 44..53 Location/Qualifiers

FT /note= "Peptide presented by MHC Class I HLA-B7"

FT Peptide 60..68

FT /note= "Peptide presented by MHC Class I HLA-B7"

FT Peptide 60..69

FT /note= "Peptide presented by MHC Class I HLA-B7"

FT Peptide 63..72

FT /note= "Peptide presented by MHC Class I HLA-B7"

FT Peptide 79..87

FT /note= "Peptide presented by MHC Class I HLA-B7, HLA-B8 and HLA-B35"

FT Peptide 79..88

FT /note= "Peptide presented by MHC Class I HLA-B7"

FT Peptide 82..90

FT /note= "Peptide presented by MHC Class I HLA-A1"

FT Peptide 82..91

FT /note= "Peptide presented by MHC Class I HLA-A1"

FT Peptide 83..91

FT /note= "Peptide presented by MHC Class I HLA-B44"

FT Peptide 84..92

FT /note= "Peptide presented by MHC Class I HLA-B7, HLA-B8 and HLA-B35"

FT Peptide 87..96

FT /note= "Peptide presented by MHC Class I HLA-A1"

FT Peptide 88..96

FT /note= "Peptide presented by MHC Class I HLA-B44"

FT Peptide 96..104

FT /note= "Peptide presented by MHC Class I HLA-B7"

FT Peptide 100..108

FT /note= "Peptide presented by MHC Class I HLA-B44"

FT Peptide 102..110

FT Peptide /note= "Peptide presented by MHC Class I HLA-B44"
FT 107..116
FT Peptide /note= "Peptide presented by MHC Class I HLA-A24"
FT 110..118
FT Peptide /note= "Peptide presented by MHC Class I HLA-B52"
FT 113..121
FT Peptide /note= "Peptide presented by MHC Class I HLA-B7"
FT 113..122
FT /note= "Peptide presented by MHC Class I HLA-B7 and
FT HLA-B52"
FT 115..124
FT Peptide /note= "Peptide presented by MHC Class I HLA-A3"
FT 118..126
FT Peptide /note= "Peptide presented by MHC Class I HLA-B35"
FT 124..133
FT Peptide /note= "Peptide presented by MHC Class I HLA-B52"
FT 125..133
FT Peptide /note= "Peptide presented by MHC Class I HLA-A24"
FT 138..147
FT Peptide /note= "Peptide presented by MHC Class I HLA-B8"
FT 139..147
FT Peptide /note= "Peptide presented by MHC Class I HLA-B7"
FT 145..153
FT Peptide /note= "Peptide presented by MHC Class I HLA-A24 and
FT HLA-B52"
FT 153..162
FT Peptide /note= "Peptide presented by MHC Class I HLA-B52"
FT 154..162
FT Peptide /note= "Peptide presented by MHC Class I HLA-B52"
FT 154..163
FT Peptide /note= "Peptide presented by MHC Class I HLA-B52"
FT 156..167
FT Peptide /note= "Peptide (AAV52434) presented by MHC Class I
FT HLA-A2" Peptide 158..166
FT /note= "Peptide presented by MHC Class I HLA-A3"
FT 159..167
FT Peptide /note= "Peptide presented by MHC Class I HLA-A3"
FT 162..170
FT Peptide /note= "Peptide presented by MHC Class I HLA-B52"
FT
XX WO9953938-A1.
PN
XX 28-OCT-1999.
PD
XX 24-MAR-1999; 99WO-US06875.
PF
XX 17-APR-1998; 98US-0062422.
PR 02-OCT-1998; 98US-0165546.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
PI Gure A, Ritter G;
XX
DR WPI; 2000-038483/03.
DR N-PSDB; AA238380.
XX
PT Novel peptides which bind to MHC class I and MHC class II molecules,
PT useful for therapeutic and diagnostic purposes -
XX
XX Claim 30; Fig 3; 49pp; English.
PS
XX This sequence represents a human tumour antigen, NY-ESO-1, the cDNA
CC encoding which was isolated from an oesophagus squamous cell cancer
CC library. Tissue localisation studies revealed it to be expressed at
CC high levels in normal ovary and testis but not in normal colon, kidney,
CC liver, brain, oesophagus and skin. It was expressed in certain tumours
CC and tumour cell lines with some degree of frequency - these included
CC melanoma specimens and cell lines, and breast and bladder cancer
CC specimens, with expression in other tumour types being sporadic.
CC Peptides derived from NY-ESO-1 are bound by both MHC (major
CC histocompatibility complex) Class I and Class II molecules for
CC presentation to T-cells. Peptides AAV52431-Y52434 bind to Class I HLA-A2

CC molecules, thereby stimulating proliferation of cytotoxic T-cells, while
CC peptides AAY52435-Y52440 bind to Class II HLA-DR53 molecules, stimulating
CC helper T-cell proliferation. The peptides derived from NY-ESO-1 may be
CC used in methods and compositions used for the treatment, diagnosis and
CC prevention of cancers (such as melanoma, breast cancer, prostate cancer,
CC lung cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer,
CC or lymphoma) and to stimulate the proliferation of T cells.
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 91; DB 21; Length 180;
Best Local Similarity 100.0%; Pred. No. 6.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLLFFYLAMPFPATPMEA 18
|||||
Db 85 srllfylvampfatpmea 102

RESULT 10
AAG67164
ID AAG67164 standard; Protein; 180 AA.
XX
AC AAG67164;
XX
DT 13-NOV-2001 (first entry)
XX
DE Amino acid sequence of cancer testis tumour antigen NY-ESO-1.
XX
KW Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;
KW HLA; HLA binding peptide; major histocompatibility complex; MHC;
KW tumour; cancer; testis tumour.
XX
OS Homo sapiens.
XX
PN WO200162917-A1.
XX
PD 30-AUG-2001.
XX
PF 22-JAN-2001; 2001WO-US02126.
XX
PR 22-FEB-2000; 2000US-0510635.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Lethe B, Boon-Falleur T;
XX
DR WPI; 2001-550091/61.
DR N-PSDB; AAH75118.
XX
PT Genomic sequences of tumour associated antigen EY-ESO-1 (LAGE-2) useful
PT for diagnosing testicular tumours -
XX
PS Example 5; Fig 3; 50pp; English.
XX
CC The present sequence represents cancer testis tumour antigen NY-ESO-1
CC (also called LAGE-2). NY-ESO-1 is a molecule that is processed to at
CC least one human leukocyte antigen (HLA) binding peptide, which binds
CC to Class I and Class II major histocompatibility complex (MHC).
CC NY-ESO-1 is expressed in tumour mRNA and in testis, but not normal
CC colon, kidney, liver or brain tissue. The presence or level of expression
CC of NY-ESO-1 may be assayed for the diagnosis of cancer, especially
CC testis tumours.
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 91; DB 22; Length 180;
Best Local Similarity 100.0%; Pred. No. 6.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLLFFYLAMPFPATPMEA 18

CC onset of a cancerous condition. The method involves contacting the sample
CC with a radioactive labelled or enzyme labelled monoclonal antibody which
CC specifically binds with the complex.

XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 91; DB 22; Length 180;
Best Local Similarity 100.0%; Pred. No. 6.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLLEFYLAMPFATPMEA 18
Db 85 srllefyfampfatpmea 102
|||||

RESULT 13
AAB69946
ID AAB69946 standard; Protein; 180 AA.
XX
AC AAB69946;
XX
DT 27-APR-2001 (first entry)
XX
DE Human NY-ESO-1 protein.
XX
KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW non-small cell lung carcinoma; tumour status determination.
XX
OS Homo sapiens.
XX
PN WO200107917-A1.
XX
PD 01-FEB-2001.
XX
PF 14-JUL-2000; 2000WO-US19220.
XX
PR 23-JUL-1999; 99US-0359503.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.
XX
PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
XX
DR WPI; 2001-182822/18.
DR N-PSDB; AAF58634.
XX
PT Method useful for determining the status (e.g. progression, regression
PT or stability of the disease) of a cancerous condition, involves
PT determining the levels of NY-ESO-1 specific antibodies in a sample
PT taken from a patient -
XX
PS Example 5; Fig 3; 50pp; English.
XX
CC The present sequence is human NY-ESO-1 protein. It is provided in a
CC specification relating to a method for determining the status of a
CC cancerous condition in a patient with a tumour that expresses NY-ESO-1.
CC The method comprises assaying a sample taken from the patient for
CC antibodies that specifically bind to the NY-ESO-1 and comparing the
CC value obtained to a prior value obtained from assay of a prior sample
CC taken from the patient. Any difference between the values is indicative
CC of a change in status of the cancerous condition. The method is useful
CC for determining whether a cancerous condition is progressing, regressing
CC or remaining stable, in particular in patients receiving treatment for a
CC melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder
CC carcinoma.
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 91; DB 22; Length 180;

Best Local Similarity 100.0%; Pred. No. 6.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLLEFYLAMPFATPMEA 18
Db 85 srllefyfampfatpmea 102
|||||

RESULT 14
AAE13122
ID AAE13122 standard; Protein; 397 AA.
XX
AC AAE13122;
XX
DT 28-JAN-2002 (first entry)
XX
DE NY-ESO-IC-HER-2 membrane distal intracellular domain fusion protein.
XX
KW Immunostimulatory fusion protein; IFP; antigen component; therapy;
KW immunostimulatory component; T-cell mediated immune response; DC;
KW dendritic cell; colon cancer; breast carcinoma; ovarian cancer;
KW human; HER-2 membrane distal intracellular domain; NY-ESO-IC;
KW autoimmunogenic cancer/testis antigen.
XX
OS Homo sapiens.
XX
PN WO200174855-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US10515.
XX
PR 30-MAR-2000; 2000US-193504P.
XX
PA (DEND-) DENDREON CORP.
XX
PI Laus R, Vidovic D, Graddis T;
XX
DR WPI; 2001-662965/76.
DR N-PSDB; AAD21573.
XX
PT An immunostimulatory fusion protein comprising the intracellular domain
PT of HER-2 and an antigen elicits an immune response to the antigen and
PT is useful for the treatment of associated cancer associated -
XX
PS Disclosure; Page 54-55; 59pp; English.
XX
CC The invention relates to immunostimulatory fusion proteins (IFP) and
CC nucleic acid molecules encoding such proteins. The IFPs comprise a
CC polypeptide antigen component and an immunostimulatory component derived
CC from the intracellular domain of HER-2 protein which is effective to
CC elicit a protective dendritic cell (DC)-induced T-cell mediated cellular
CC immune response to the antigen. IFP or superactivated dendritic cells
CC are used to treat cancer e.g. breast carcinoma, ovarian and colon cancer
CC associated with a particularly antigen. The present sequence is a
CC fusion protein which comprises human autoimmunogenic
CC cancer/testis antigen, NY-ESO-IC and mature human HER-2 membrane distal
CC intracellular domain.
XX
SQ Sequence 397 AA;

Query Match 100.0%; Score 91; DB 22; Length 397;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLLEFYLAMPFATPMEA 18
Db 85 srllefyfampfatpmea 102
|||||

RESULT 15
AAE07741

ID AAE07741 standard; peptide; 20 AA.
XX AC AAE07741;
XX DT 06-NOV-2001 (first entry)
XX DE Human ESO p82-101 peptide, to identify MHC class II-restricted epitopes.
XX KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.
XX OS Homo sapiens.
XX PN WO200155393-A2.
XX PD 02-AUG-2001.
XX PF 26-JAN-2001; 2001WO-US02765.
XX PR 28-JAN-2000; 2000US-0179004.
XX PR 29-SEP-2000; 2000US-0237107.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Wang R, Rosenberg SA, Zeng G;
XX DR WPI; 2001-496851/54.
XX PT New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -
XX PS Example 3; Fig 3; 134pp; English.
XX CC The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or haptens and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is human
CC ESO p82-101 peptide used in the identification of putative MHC class II
CC -restricted epitopes from HLA-DR4-transgenic mice.
XX SQ Sequence 20 AA;

Query Match 90.1%; Score 82; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SRLLEPYLAMPFATPM 16
Db |||||||||||||||
5 srllepylampfatpm 20

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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:21:01 ; Search time 599.92 Seconds
(without alignments)
10.561 Million cell updates/sec

Title: US-09-165-546A-12

Perfect score: 91

Sequence: 1 SRLLEFYLAMPFATPMEA 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents_AA_Main:*

- 1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
- 2: /cgn2_6/ptodata/2/paa/US06_COMB.pep:*
- 3: /cgn2_6/ptodata/2/paa/US07_COMB.pep:*
- 4: /cgn2_6/ptodata/2/paa/US080_COMB.pep:*
- 5: /cgn2_6/ptodata/2/paa/US081_COMB.pep:*
- 6: /cgn2_6/ptodata/2/paa/US082_COMB.pep:*
- 7: /cgn2_6/ptodata/2/paa/US083_COMB.pep:*
- 8: /cgn2_6/ptodata/2/paa/US084_COMB.pep:*
- 9: /cgn2_6/ptodata/2/paa/US085_COMB.pep:*
- 10: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*
- 11: /cgn2_6/ptodata/2/paa/US087_COMB.pep:*
- 12: /cgn2_6/ptodata/2/paa/US088_COMB.pep:*
- 13: /cgn2_6/ptodata/2/paa/US089_COMB.pep:*
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- 15: /cgn2_6/ptodata/2/paa/US091_COMB.pep:*
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- 19: /cgn2_6/ptodata/2/paa/US095_COMB.pep:*
- 20: /cgn2_6/ptodata/2/paa/US096_COMB.pep:*
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- 22: /cgn2_6/ptodata/2/paa/US098_COMB.pep:*
- 23: /cgn2_6/ptodata/2/paa/US099_COMB.pep:*
- 24: /cgn2_6/ptodata/2/paa/US100_COMB.pep:*
- 25: /cgn2_6/ptodata/2/paa/US101_COMB.pep:*
- 26: /cgn2_6/ptodata/2/paa/US60_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	91	100.0	18	15	US-09-165-546A-12
2	91	100.0	18	18	US-09-408-036B-11
3	91	100.0	61	19	US-09-529-206-55
4	91	100.0	61	19	US-09-529-206A-55
5	91	100.0	61	19	US-09-529-206B-55
6	91	100.0	122	26	US-60-336-968-17
7	91	100.0	180	11	US-08-791-495-9

8	91	100.0	180	17	US-09-341-829A-9	Sequence 9, Appli
9	91	100.0	180	17	US-09-392-714-25	Sequence 25, Appl
10	91	100.0	180	19	US-09-529-206-4	Sequence 4, Appli
11	91	100.0	180	19	US-09-529-206A-3	Sequence 3, Appli
12	91	100.0	180	19	US-09-529-206B-3	Sequence 3, Appli
13	91	100.0	180	19	US-09-561-571-3	Sequence 3, Appli
14	91	100.0	180	21	US-09-751-798-8	Sequence 8, Appli
15	91	100.0	180	24	US-10-005-905-3	Sequence 3, Appli
16	91	100.0	180	24	US-10-023-182-8	Sequence 8, Appli
17	91	100.0	180	24	US-10-026-066-3	Sequence 3, Appli
18	91	100.0	180	26	US-60-336-968-11	Sequence 11, Appl
19	91	100.0	397	22	US-09-821-883-27	Sequence 27, Appl
20	70	76.9	14	18	US-09-408-036B-31	Sequence 31, Appl
21	64	70.3	180	11	US-08-791-495-7	Sequence 7, Appli
22	64	70.3	180	17	US-09-341-829A-7	Sequence 7, Appli
23	64	70.3	210	11	US-08-791-495-5	Sequence 5, Appli
24	64	70.3	210	17	US-09-341-829A-5	Sequence 5, Appli
25	54	59.3	10	19	US-09-529-206-101	Sequence 101, App
26	54	59.3	10	19	US-09-529-206A-101	Sequence 101, App
27	54	59.3	10	19	US-09-529-206B-101	Sequence 101, App
28	52	57.1	10	19	US-09-529-206-93	Sequence 93, Appl
29	52	57.1	10	19	US-09-529-206-96	Sequence 96, Appl
30	52	57.1	10	19	US-09-529-206A-93	Sequence 93, Appl
31	52	57.1	10	19	US-09-529-206A-96	Sequence 96, Appl
32	52	57.1	10	19	US-09-529-206B-93	Sequence 93, Appl
33	52	57.1	10	19	US-09-529-206B-96	Sequence 96, Appl
34	51	56.0	10	19	US-09-529-206-98	Sequence 98, Appl
35	51	56.0	10	19	US-09-529-206A-98	Sequence 98, Appl
36	51	56.0	10	19	US-09-529-206B-98	Sequence 98, Appl
37	47	51.6	9	2	US-06-670-456A-2	Sequence 2, Appli
38	47	51.6	447	16	US-09-252-991A-24312	Sequence 24312, A
39	47	51.6	934	16	US-09-252-991A-25635	Sequence 25635, A
40	46	50.5	95	21	US-09-758-438-741	Sequence 741, App
41	45	49.5	86	22	US-09-834-366-16443	Sequence 16443, A
42	45	49.5	86	26	US-60-197-873-16443	Sequence 16443, A
43	45	49.5	130	21	US-09-757-026-247	Sequence 247, App
44	45	49.5	156	26	US-60-324-109-32013	Sequence 32013, A
45	44	48.4	9	17	US-09-344-040B-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-09-165-546A-12
; Sequence 12, Application US/09165546A
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao,
; Canlan, Matt; Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO
; AMINO ACID SEQUENCES OF NY-ESO-1, WHICH BIND TO
; MHC CLASS I AND MHC CLASS II MOLECULES, AND
; USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,546A
; FILING DATE: 02-Oct-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998

; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-165-546A-12

Query Match 100.0%; Score 91; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLLFFYLAMPFPATPMEA 18
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Db 1 SRLLFFYLAMPFPATPMEA 18

RESULT 2
US-09-408-036B-11
; Sequence 11, Application US/09408036B
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Isolated Peptides Which Bind to MHC Class II Molecules and Uses T
; FILE REFERENCE: LUD 5624
; CURRENT APPLICATION NUMBER: US/09/408,036B
; CURRENT FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/165,546
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 11
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-408-036B-11

Query Match 100.0%; Score 91; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLLFFYLAMPFPATPMEA 18
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Db 1 SRLLFFYLAMPFPATPMEA 18

RESULT 3
US-09-529-206-55
; Sequence 55, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08

; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-55

Query Match 100.0%; Score 91; DB 19; Length 61;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLLFFYLAMPFPATPMEA 18
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Db 9 SRLLFFYLAMPFPATPMEA 26

RESULT 4
US-09-529-206A-55
; Sequence 55, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206A-55

Query Match 100.0%; Score 91; DB 19; Length 61;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLLFFYLAMPFPATPMEA 18
| | | | | | | | | | | | | | | |
Db 9 SRLLFFYLAMPFPATPMEA 26

RESULT 5
US-09-529-206B-55
; Sequence 55, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-55

Query Match 100.0%; Score 91; DB 19; Length 61;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLEFYLAMPFATPMEA 18
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Db 9 SRLEFYLAMPFATPMEA 26

RESULT 6
US-60-336-968-17
; Sequence 17, Application US/60336968
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: CTLIMM.022PR
; CURRENT APPLICATION NUMBER: US/60/336,968
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-336-968-17

Query Match 100.0%; Score 91; DB 26; Length 122;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLEFYLAMPFATPMEA 18
| | | | | | | | | | | | | | | | | | | | | |
Db 28 SRLEFYLAMPFATPMEA 45

RESULT 7
US-08-791-495-9
; Sequence 9, Application US/08791495
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-9

Query Match 100.0%; Score 91; DB 11; Length 180;
Best Local Similarity 100.0%; Pred. No. 4.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLEFYLAMPFATPMEA 18
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Db 85 SRLEFYLAMPFATPMEA 102

RESULT 8
US-09-341-829A-9
; Sequence 9, Application US/09341829A
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-341-829A-9

Query Match 100.0%; Score 91; DB 17; Length 180;
Best Local Similarity 100.0%; Pred. No. 4.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLEFYLAMPFATPMEA 18
| | | | | | | | | | | | | | | | | | | | | |
Db 85 SRLEFYLAMPFATPMEA 102

RESULT 9
US-09-392-714-25
; Sequence 25, Application US/09392714A
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Gure, Ali O.
; APPLICANT: Williamson, Barbara
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Cancer Associated Antigens and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: L0461/7062
; CURRENT APPLICATION NUMBER: US/09/392,714A
; CURRENT FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: PCT/US98/14679
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25

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; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-392-714-25

Query Match      100.0%; Score 91; DB 17; Length 180;
Best Local Similarity 100.0%; Pred. No. 4.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLEFYLAMPFATPMEA 18
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Db 85 SRLEFYLAMPFATPMEA 102

RESULT 10
US-09-529-206-4
; Sequence 4, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-4

Query Match      100.0%; Score 91; DB 19; Length 180;
Best Local Similarity 100.0%; Pred. No. 4.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLEFYLAMPFATPMEA 18
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Db 85 SRLEFYLAMPFATPMEA 102

RESULT 11
US-09-529-206A-3
; Sequence 3, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206A-3

Query Match      100.0%; Score 91; DB 19; Length 180;
Best Local Similarity 100.0%; Pred. No. 4.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLEFYLAMPFATPMEA 18
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Db 85 SRLEFYLAMPFATPMEA 102

RESULT 12
US-09-529-206B-3
; Sequence 3, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-3

Query Match      100.0%; Score 91; DB 19; Length 180;
Best Local Similarity 100.0%; Pred. No. 4.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLEFYLAMPFATPMEA 18
   |||||
Db 85 SRLEFYLAMPFATPMEA 102

RESULT 13
US-09-561-571-3
; Sequence 3, Application US/09561571
; GENERAL INFORMATION:
; APPLICANT: CTL Immunotherapies Corp.
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; TITLE OF INVENTION: EPITOPE CLUSTERS
; FILE REFERENCE: CTLIMM.010A
; CURRENT APPLICATION NUMBER: US/09/561,571
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-561-571-3

Query Match      100.0%; Score 91; DB 19; Length 180;
Best Local Similarity 100.0%; Pred. No. 4.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLEFYLAMPFATPMEA 18
   |||||
Db 85 SRLEFYLAMPFATPMEA 102

RESULT 14
US-09-751-798-8
; Sequence 8, Application US/09751798
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
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QY 1 SRLEFYLAMPFATPMEA 18
   |||||
Db 85 SRLEFYLAMPFATPMEA 102

RESULT 12
US-09-529-206B-3
; Sequence 3, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-3

Query Match      100.0%; Score 91; DB 19; Length 180;
Best Local Similarity 100.0%; Pred. No. 4.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLEFYLAMPFATPMEA 18
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Db 85 SRLEFYLAMPFATPMEA 102

RESULT 13
US-09-561-571-3
; Sequence 3, Application US/09561571
; GENERAL INFORMATION:
; APPLICANT: CTL Immunotherapies Corp.
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; TITLE OF INVENTION: EPITOPE CLUSTERS
; FILE REFERENCE: CTLIMM.010A
; CURRENT APPLICATION NUMBER: US/09/561,571
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-561-571-3

Query Match      100.0%; Score 91; DB 19; Length 180;
Best Local Similarity 100.0%; Pred. No. 4.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLEFYLAMPFATPMEA 18
   |||||
Db 85 SRLEFYLAMPFATPMEA 102

RESULT 14
US-09-751-798-8
; Sequence 8, Application US/09751798
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
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GenCore version 4.5
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OM protein ~ protein search, using sw model

Run on: July 3, 2002, 11:22:13 ; Search time 64.42 Seconds
(without alignments)
28.270 Million cell updates/sec

Title: US-09-165-546A-12
Perfect score: 91
Sequence: 1 SRLEFYLAMPPFATPMEA 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 308740 seqs, 101176262 residues

Total number of hits satisfying chosen parameters: 308740

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	91	100.0	180	1	PCT-US02-13994-30	Sequence 30, Appl
2	91	100.0	180	5	US-09-807-512-8	Sequence 8, Appl
3	91	100.0	180	6	US-10-117-937-74	Sequence 74, Appl
4	67	73.6	180	6	US-10-117-937-75	Sequence 75, Appl
5	67	73.6	210	6	US-10-117-937-76	Sequence 76, Appl
6	67	73.6	210	6	US-10-157-031-88	Sequence 88, Appl
7	64	70.3	180	5	US-09-807-512-4	Sequence 4, Appl
8	64	70.3	180	6	US-10-146-473-69	Sequence 69, Appl
9	64	70.3	210	5	US-09-807-512-6	Sequence 6, Appl
10	52	57.1	10	6	US-10-117-937-175	Sequence 175, App
11	52	57.1	10	6	US-10-117-937-176	Sequence 176, App
12	48	52.7	9	6	US-10-117-937-174	Sequence 174, App
13	48	52.7	9	6	US-10-117-937-177	Sequence 177, App
14	47	51.6	9	5	US-09-670-456A-2	Sequence 2, Appl
15	46	50.5	696	5	US-09-540-209B-7200	Sequence 7200, Ap
16	45	49.5	130	6	US-10-152-780-247	Sequence 247, App
17	44	48.4	9	5	US-09-344-040C-19	Sequence 19, Appl
18	44	48.4	9	6	US-10-117-937-173	Sequence 173, App
19	42	46.2	272	5	US-09-704-302A-805	Sequence 805, App
20	42	46.2	416	5	US-09-704-302A-937	Sequence 937, App
21	41	45.1	351	1	PCT-US02-09944-599	Sequence 599, App
22	41	45.1	508	7	US-60-360-039-8565	Sequence 8565, Ap
23	40	44.0	318	6	US-10-154-460-46	Sequence 46, Appl
24	40	44.0	394	7	US-60-360-039-9932	Sequence 9932, Ap
25	40	44.0	571	6	US-10-119-480-210	Sequence 210, App
26	40	44.0	571	6	US-10-121-049-542	Sequence 542, App

27	40	44.0	571	6	US-10-121-050-542	Sequence 542, App
28	40	44.0	571	6	US-10-121-053-542	Sequence 542, App
29	40	44.0	571	6	US-10-121-043-542	Sequence 542, App
30	40	44.0	571	6	US-10-121-044-542	Sequence 542, App
31	40	44.0	571	6	US-10-121-047-542	Sequence 542, App
32	40	44.0	571	6	US-10-121-054-542	Sequence 542, App
33	40	44.0	571	6	US-10-121-056-542	Sequence 542, App
34	40	44.0	571	6	US-10-121-057-542	Sequence 542, App
35	40	44.0	571	6	US-10-121-058-542	Sequence 542, App
36	40	44.0	571	6	US-10-121-060-542	Sequence 542, App
37	40	44.0	571	6	US-10-121-063-542	Sequence 542, App
38	40	44.0	571	6	US-10-123-108-542	Sequence 542, App
39	40	44.0	571	6	US-10-123-154-542	Sequence 542, App
40	40	44.0	571	6	US-10-123-156-542	Sequence 542, App
41	40	44.0	571	6	US-10-123-157-542	Sequence 542, App
42	40	44.0	571	6	US-10-123-212-542	Sequence 542, App
43	40	44.0	571	6	US-10-123-213-542	Sequence 542, App
44	40	44.0	571	6	US-10-123-109-542	Sequence 542, App
45	40	44.0	571	6	US-10-121-041-542	Sequence 542, App

ALIGNMENTS

RESULT 1
PCT-US02-13994-30
; Sequence 30, Application PC/TUS0213994
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research
; APPLICANT: Cornell Research Foundation, Inc.
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd
; APPLICANT: Scanlan, Matthew
; APPLICANT: Stockert, Elisabeth
; TITLE OF INVENTION: COLON CANCER ANTIGEN PANEL
; FILE REFERENCE: L00461/70105WO(JRV)
; CURRENT APPLICATION NUMBER: PCT/US02/13994
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US 09/849,602
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-13994-30

Query Match 100.0%; Score 91; DB 1; Length 180;
Best Local Similarity 100.0%; Pred. No. 8.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SRLEFYLAMPPFATPMEA 18
Db 85 SRLEFYLAMPPFATPMEA 102
|||||

RESULT 2
US-09-807-512-8
; Sequence 8, Application US/09807512
; GENERAL INFORMATION:
; APPLICANT: Schrier, Peter I.
; APPLICANT: Aarnoudse, Corlien
; APPLICANT: Heider, Karl-Heinz
; APPLICANT: Klade, Christoph
; TITLE OF INVENTION: Camel, An Alternative Translation Product of the Tumor Antigen-Lage 1
; FILE REFERENCE: 0652.220000
; CURRENT APPLICATION NUMBER: US/09/807,512
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: PCT/EP99/07832
; PRIOR FILING DATE: 1999-10-15

; PRIOR APPLICATION NUMBER: EP 98119583.7
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-807-512-8

Query Match 100.0%; Score 91; DB 5; Length 180;
Best Local Similarity 100.0%; Pred. No. 8.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLEFYLAMPPFATPMEA 18
|||||::|::|
Db 85 SRLEFYLAMPPFATPMEA 102

RESULT 3
US-10-117-937-74
; Sequence 74, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-74

Query Match 100.0%; Score 91; DB 6; Length 180;
Best Local Similarity 100.0%; Pred. No. 8.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLEFYLAMPPFATPMEA 18
|||||::|::|
Db 85 SRLEFYLAMPPFATPMEA 102

RESULT 4
US-10-117-937-75
; Sequence 75, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017

; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-75

Query Match 73.6%; Score 67; DB 6; Length 180;
Best Local Similarity 66.7%; Pred. No. 0.00082;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 SRLEFYLAMPPFATPMEA 18
|||||::|::|
Db 85 SRLEHITMPFSSPMEA 102

RESULT 5
US-10-117-937-76
; Sequence 76, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-76

Query Match 73.6%; Score 67; DB 6; Length 210;
Best Local Similarity 66.7%; Pred. No. 0.00096;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 SRLEFYLAMPPFATPMEA 18
|||||::|::|
Db 85 SRLEHITMPFSSPMEA 102

RESULT 6
US-10-157-031-88
; Sequence 88, Application US/10157031
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobashev, A. V.
; APPLICANT: Krukovskaya, L. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequence
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157,031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 88
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-031-88

Query Match      73.6%; Score 67; DB 6; Length 210;
Best Local Similarity 66.7%; Pred. No. 0.00096;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 SRLEFYLAMPPFATPMEA 18
    |||| : : |||:||||
Db 85 SRLLHLHITMPFSSPMEA 102

RESULT 7
US-09-807-512-4
; Sequence 4, Application US/09807512
; GENERAL INFORMATION:
; APPLICANT: Schrier, Peter I.
; APPLICANT: Aarnoudse, Corlien
; APPLICANT: Heider, Karl-Heinz
; APPLICANT: Klage, Christoph
; TITLE OF INVENTION: Camel, An Alternative Translation Product of the Tumor
; TITLE OF INVENTION: Antigen-Lage 1
; FILE REFERENCE: 0652.2200000
; CURRENT APPLICATION NUMBER: US/09/807,512
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: PCT/EP99/07832
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: EP 98119583.7
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-807-512-4

Query Match      70.3%; Score 64; DB 5; Length 180;
Best Local Similarity 61.1%; Pred. No. 0.0026;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 SRLEFYLAMPPFATPMEA 18
    |||| : : |||:||||
Db 85 SRLLQLHITMPFSSPMEA 102

RESULT 8
US-10-146-473-69
; Sequence 69, Application US/10146473
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Gout, Ivan
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Gure, Ali
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd
; TITLE OF INVENTION: Breast Cancer Antigens
; FILE REFERENCE: L00461/70130(JRV)
; CURRENT APPLICATION NUMBER: US/10/146,473
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/291,150
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 69
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-473-69

Query Match      70.3%; Score 64; DB 6; Length 210;
Best Local Similarity 61.1%; Pred. No. 0.0026;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 SRLEFYLAMPPFATPMEA 18
    |||| : : |||:||||
Db 85 SRLLQLHITMPFSSPMEA 102

RESULT 9
US-09-807-512-6
; Sequence 6, Application US/09807512
; GENERAL INFORMATION:
; APPLICANT: Schrier, Peter I.
; APPLICANT: Aarnoudse, Corlien
; APPLICANT: Heider, Karl-Heinz
; APPLICANT: Klade, Christoph
; TITLE OF INVENTION: Camel, An Alternative Translation Product of the Tumor
; TITLE OF INVENTION: Antigen-Lage 1
; FILE REFERENCE: 0652.2200000
; CURRENT APPLICATION NUMBER: US/09/807,512
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: PCT/EP99/07832
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: EP 98119583.7
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-807-512-6

Query Match      70.3%; Score 64; DB 5; Length 210;
Best Local Similarity 61.1%; Pred. No. 0.003;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 SRLEFYLAMPPFATPMEA 18
    |||| : : |||:||||
Db 85 SRLLQLHITMPFSSPMEA 102

RESULT 10
US-10-117-937-175
; Sequence 175, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPTOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-175
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US-10-146-473-69

Query Match      70.3%; Score 64; DB 6; Length 180;
Best Local Similarity 61.1%; Pred. No. 0.0026;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 SRLEFYLAMPPFATPMEA 18
    |||| : : |||:||||
Db 85 SRLLQLHITMPFSSPMEA 102

RESULT 9
US-09-807-512-6
; Sequence 6, Application US/09807512
; GENERAL INFORMATION:
; APPLICANT: Schrier, Peter I.
; APPLICANT: Aarnoudse, Corlien
; APPLICANT: Heider, Karl-Heinz
; APPLICANT: Klade, Christoph
; TITLE OF INVENTION: Camel, An Alternative Translation Product of the Tumor
; TITLE OF INVENTION: Antigen-Lage 1
; FILE REFERENCE: 0652.2200000
; CURRENT APPLICATION NUMBER: US/09/807,512
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: PCT/EP99/07832
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: EP 98119583.7
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-807-512-6

Query Match      70.3%; Score 64; DB 5; Length 210;
Best Local Similarity 61.1%; Pred. No. 0.003;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 SRLEFYLAMPPFATPMEA 18
    |||| : : |||:||||
Db 85 SRLLQLHITMPFSSPMEA 102

RESULT 10
US-10-117-937-175
; Sequence 175, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPTOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-175
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Query Match 57.1%; Score 52; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLEFYLAMPF 12
| | | | | | | | | |
Db 1 LLEFYLAMPF 10

RESULT 11
US-10-117-937-176
; Sequence 176, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 176
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-176

Query Match 57.1%; Score 52; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AMPFATPMEA 18
| | | | | | | | | |
Db 1 AMPFATPMEA 10

RESULT 12
US-10-117-937-174
; Sequence 174, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 174
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-117-937-174

Query Match 52.7%; Score 48; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LEFYLAMPF 12
| | | | | | | | | |
Db 1 LEFYLAMPF 9

RESULT 13
US-10-117-937-177
; Sequence 177, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 177
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-177

Query Match 52.7%; Score 48; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 MPFATPMEA 18
| | | | | | | | | |
Db 1 MPFATPMEA 9

RESULT 14
US-09-670-456A-2
; Sequence 2, Application US/09670456A
; GENERAL INFORMATION:
; LUD-5668-PCT
; APPLICANT: Gnjatia, Sacha
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA-C MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: LUD 5668
; CURRENT APPLICATION NUMBER: US/09/670,456A
; CURRENT FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-670-456A-2

Query Match 51.6%; Score 47; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LAMPFATPM 16
| | | | | | | |
Db 1 LAMPFATPM 9

RESULT 15
US-09-540-209B-7200
; Sequence 7200, Application US/09540209B
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FRA
; FILE REFERENCE: 2709.1001-001
; CURRENT APPLICATION NUMBER: US/09/540,209B
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 7200
; LENGTH: 696
; TYPE: PRT
; ORGANISM: B.fragilis
US-09-540-209B-7200

Query Match 50.5%; Score 46; DB 5; Length 696;
Best Local Similarity 52.9%; Pred. No. 10;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 SRLLEFYLAMFPATPME 17
| | | | | | | |
Db 521 SRALDFYLVQDFASSIE 537

Search completed: July 3, 2002, 11:22:13
Job time: 945 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:09:47 ; Search time 49.27 Seconds
(without alignments)
8.923 Million cell updates/sec

Title: US-09-165-546A-12
Perfect score: 91
Sequence: 1 SRLLFFYLAMPFATPMEA 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	91	100.0	18	4	US-09-359-503-12
2	91	100.0	180	2	US-08-791-495-9
3	91	100.0	180	4	US-08-937-263B-8
4	64	70.3	180	2	US-08-791-495-7
5	64	70.3	210	2	US-08-791-495-5
6	38	41.8	574	4	US-09-383-586-36
7	38	41.8	597	1	US-08-462-884A-1
8	38	41.8	597	1	US-08-461-881B-1
9	38	41.8	597	2	US-09-123-960-1
10	38	41.8	605	1	US-08-462-884A-3
11	38	41.8	605	1	US-08-461-881B-3
12	38	41.8	605	2	US-09-123-960-3
13	38	41.8	723	6	5200183-4
14	37.5	41.2	665	3	US-08-844-059-2
15	37.5	41.2	665	4	US-09-431-202-2
16	37	40.7	365	1	US-08-674-612-2
17	37	40.7	365	2	US-08-920-296-2
18	37	40.7	365	2	US-08-746-788-2
19	37	40.7	365	3	US-09-189-602-2
20	37	40.7	365	4	US-09-025-580-26
21	37	40.7	365	4	US-09-025-580-27
22	37	40.7	365	4	US-09-124-163-2
23	37	40.7	367	4	US-09-025-580-24
24	37	40.7	393	1	US-08-029-404-2
25	37	40.7	393	3	US-08-459-953A-2
26	37	40.7	404	3	US-08-459-953A-7
27	36	39.6	475	4	US-08-274-121B-4

28	36	39.6	476	2	US-08-569-150A-3	Sequence 3, Appli
29	35	38.5	317	1	US-08-463-090B-9	Sequence 9, Appli
30	35	38.5	317	2	US-08-874-347-18	Sequence 18, Appl
31	35	38.5	317	3	US-09-093-522-18	Sequence 18, Appl
32	35	38.5	511	4	US-09-201-641-2	Sequence 2, Appli
33	35	38.5	571	6	5200183-17	Patent No. 5200183
34	35	38.5	668	1	US-08-445-050-9	Sequence 9, Appli
35	35	38.5	668	2	US-08-204-691-9	Sequence 9, Appli
36	35	38.5	722	1	US-08-347-718B-1	Sequence 1, Appli
37	35	38.5	722	1	US-08-445-050-3	Sequence 3, Appli
38	35	38.5	722	1	US-08-445-050-7	Sequence 7, Appli
39	35	38.5	722	2	US-08-482-262-1	Sequence 1, Appli
40	35	38.5	722	2	US-08-204-691-3	Sequence 3, Appli
41	35	38.5	722	2	US-08-204-691-7	Sequence 7, Appli
42	35	38.5	722	6	5200183-3	Patent No. 5200183
43	35	38.5	742	1	US-08-347-718B-2	Sequence 2, Appli
44	35	38.5	742	2	US-08-482-262-2	Sequence 2, Appli
45	35	38.5	742	6	5200183-2	Patent No. 5200183

ALIGNMENTS

RESULT 1
US-09-359-503-12
; Sequence 12, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid


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; TOPOLOGY: linear
US-09-359-503-12

Query Match 100.0%; Score 91; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLEFYLAMPPFATPMEA 18
   |||
Db 1 SRLEFYLAMPPFATPMEA 18

RESULT 2
US-08-791-495-9
; Sequence 9, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-9

Query Match 100.0%; Score 91; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLEFYLAMPPFATPMEA 18
   |||
Db 85 SRLEFYLAMPPFATPMEA 102

RESULT 3
US-08-937-263B-8
; Sequence 8, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
; APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;

; APPLICANT: Alexander, Knuth; Drijfhout, Jan W.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
; TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
; TITLE OF INVENTION: ITSELF, AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,263B
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sinn, Eric, Patent Agent
; REGISTRATION NUMBER: 40,177
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
US-08-937-263B-8

Query Match 100.0%; Score 91; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLEFYLAMPPFATPMEA 18
   |||
Db 85 SRLEFYLAMPPFATPMEA 102

RESULT 4
US-08-791-495-7
; Sequence 7, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-9

Query Match 100.0%; Score 91; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLEFYLAMPPFATPMEA 18
   |||
Db 85 SRLEFYLAMPPFATPMEA 102

RESULT 3
US-08-937-263B-8
; Sequence 8, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
; APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
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; FILING DATE: 435
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-7

Query Match 70.3%; Score 64; DB 2; Length 180;
Best Local Similarity 61.1%; Pred. No. 0.0007;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 SRLLFYLAMFPFATPMEA 18
| | | | : : | | | |
Db 85 SRLLQLHITMPFSSPMEA 102

RESULT 5
US-08-791-495-5
; Sequence 5, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-5

Query Match 70.3%; Score 64; DB 2; Length 210;
Best Local Similarity 61.1%; Pred. No. 0.00083;

Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 1 SRLLFYLAMFPFATPMEA 18
| | | | : : | | | |
Db 85 SRLLQLHITMPFSSPMEA 102
RESULT 6
US-09-383-586-36
; Sequence 36, Application US/09383586
; Patent No. 6242419
; GENERAL INFORMATION:
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Abernethy, Nevin
; APPLICANT: Onrust, Rene
; APPLICANT: Kumble, Anand
; APPLICANT: Murison, Greg
; TITLE OF INVENTION: Compounds isolated from stromal cells
; TITLE OF INVENTION: and methods for their use
; FILE REFERENCE: 11000.1037c1
; CURRENT APPLICATION NUMBER: US/09/383,586
; CURRENT FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Mouse
US-09-383-586-36

Query Match 41.8%; Score 38; DB 4; Length 574;
Best Local Similarity 50.0%; Pred. No. 82;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 3-LLEFYLAMFPFATPMEA 18
| : | : | | | |
Db 413 LMDFTVTCKGATPMEA 428

RESULT 7
US-08-462-884A-1
; Sequence 1, Application US/08462884A
; Patent No. 5624836
; GENERAL INFORMATION:
; APPLICANT: Lange III, Louis G
; APPLICANT: Spilburg, Curtis A
; TITLE OF INVENTION: Mammalian Pancreatic Cholesterol
; TITLE OF INVENTION: Esterase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti
; STREET: 10 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,884A
; FILING DATE: Unknown
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Blair Hughes
; REGISTRATION NUMBER: 32,901
; REFERENCE/DOCKET NUMBER: 89,852-J
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/715-1000

APPLICANT: Spilburg, Curtis A
TITLE OF INVENTION: Mammalian Pancreatic Cholesterol
TITLE OF INVENTION: Esterase
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti
STREET: 10 South Wacker Drive
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,884A
FILING DATE: Unknown
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: A. Blair Hughes
REGISTRATION NUMBER: 32,901
REFERENCE/DOCKET NUMBER: 89,852-J
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/715-1000
TELEFAX: 312/715-1234
TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-884A-3

Query Match 41.8%; Score 38; DB 1; Length 605;
Best Local Similarity 46.2%; Pred. No. 87;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 LEFYLAMPPFATPM 16
I:: I:::
Db 465 LQYVFGKPFATPL 477

RESULT 11
US-08-461-881B-3
Sequence 3, Application US/08461881B
Patent No. 5792832
GENERAL INFORMATION:
APPLICANT: Lange III, Louis G
APPLICANT: Spilburg, Curtis A
TITLE OF INVENTION: Mammalian Pancreatic Cholesterol Esterase
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" hard disc
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,881B
FILING DATE: June 5, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: A. Blair Hughes

REGISTRATION NUMBER: 32,901
REFERENCE/DOCKET NUMBER: 89,852-J
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/913-0001
TELEFAX: 312/913-0002
TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-881B-3

Query Match 41.8%; Score 38; DB 1; Length 605;
Best Local Similarity 46.2%; Pred. No. 87;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 LEFYLAMPPFATPM 16
I:: I:::
Db 465 LQYVFGKPFATPL 477

RESULT 12
US-09-123-960-3
Sequence 3, Application US/09123960
Patent No. 5981299
GENERAL INFORMATION:
APPLICANT: Lange III, Louis G
APPLICANT: Spilburg, Curtis A
TITLE OF INVENTION: Mammalian Pancreatic
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" hard disc
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/123,960
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,881
FILING DATE: June 5, 1995
ATTORNEY/AGENT INFORMATION:
NAME: A. Blair Hughes
REGISTRATION NUMBER: 32,901
REFERENCE/DOCKET NUMBER: 89,852-K
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/913-0001
TELEFAX: 312/913-0002
TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-123-960-3

Query Match 41.8%; Score 38; DB 2; Length 605;
Best Local Similarity 46.2%; Pred. No. 87;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 LEFYLAMPFATPM 16
|::| | | | | |
Db 465 LQYVFGKPFATPL 477

RESULT 13
5200183-4
; Patent No. 5200183
; APPLICANT: TANG, JORDAN J.N.; WANG, CHI-SUN
; TITLE OF INVENTION: RECOMBINANT BILE SALT ACTIVATED LIPASES
; NUMBER OF SEQUENCES: 22
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/537,426
; FILING DATE: 12-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 504,635
; FILING DATE: 04-APR-1990
; APPLICATION NUMBER: 122,410
; FILING DATE: 19-NOV-1987
; SEQ ID NO: 4:
; LENGTH: 723
5200183-4

Query Match 41.8%; Score 38; DB 6; Length 723;
Best Local Similarity 46.2%; Pred. No. 1.1e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 LEFYLAMPFATPM 16
|::| | | | | |
Db 440 LQYVFGKPFATPL 452

RESULT 14
US-08-844-059-2
; Sequence 2, Application US/08844059
; Patent No. 6001601
; GENERAL INFORMATION:
; APPLICANT: Lawlor, Elizabeth
; TITLE OF INVENTION: No. 6001601el Compounds
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19046
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/844,059
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9607999.1
; FILING DATE: 16-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P31456
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 665 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-844-059-2

Query Match 41.2%; Score 37.5; DB 3; Length 665;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 9; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 2 RLLEFYLAMF-FATP 15
| | | | | | | | | |
Db 180 RLVEFFKAHPEFITP 194

RESULT 15
US-09-431-202-2
; Sequence 2, Application US/09431202
; Patent No. 6294175
; GENERAL INFORMATION:
; APPLICANT: Lawlor, Elizabeth
; TITLE OF INVENTION: No. 6294175el Compounds
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19046
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/431,202
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/844,059
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P31456
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 665 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-431-202-2

Query Match 41.2%; Score 37.5; DB 4; Length 665;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 9; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 2 RLLEFYLAMF-FATP 15
| | | | | | | | | |
Db 180 RLVEFFKAHPEFITP 194

Search completed: July 3, 2002, 11:09:48
Job time: 270 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:10:57 ; Search time 61.47 Seconds
(without alignments)
28.137 Million cell updates/sec

Title: US-09-165-546A-13
Perfect score: 88
Sequence: 1 TVSGNILTIRLTAADHRQ 18
Scoring table:
 BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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Database :      PIR_71:*
1:  pir1:*
2:  pir2:*
3:  pir3:*
4:  pir4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	45	51.1	262	2	T50660	alpha-expansin 2 (probable oxidoreductase)
2	45	51.1	289	2	C87158	strI protein - Str
3	45	51.1	348	1	S17779	N-methyl-D-aspartate receptor 1 (probable)
4	42	47.7	181	2	JN0342	PTS system IICB component
5	41.5	47.2	297	2	AB0342	phosphotransferase system IICB component
6	41.5	47.2	627	2	F95200	iodine-binding protein
7	41.5	47.2	627	2	E98067	hypothetical protein
8	41	46.6	629	2	AB3581	hypothetical protein
9	40	45.5	149	2	D90071	hypothetical protein
10	40	45.5	149	2	AC2483	hypothetical protein
11	40	45.5	234	2	JT0874	purine-nucleoside phosphorylase
12	40	45.5	261	2	T07630	expansin 1 - tomato
13	40	45.5	305	2	D75306	purine nucleoside phosphorylase
14	40	45.5	444	2	B84292	hypothetical protein
15	40	45.5	449	2	T14376	self-incompatibility protein
16	40	45.5	545	2	D90159	hypothetical protein
17	39.5	44.9	3083	2	AH2493	hypothetical protein
18	39	44.3	102	2	AI2815	30S ribosomal protein
19	39	44.3	102	2	AF3346	30S ribosomal protein
20	39	44.3	125	2	A71697	hypothetical protein
21	39	44.3	195	2	H86768	GTP-binding protein
22	39	44.3	233	2	D69614	purine nucleoside phosphorylase
23	39	44.3	245	2	T13099	major tail protein
24	39	44.3	344	2	H82656	twitching motility protein
25	39	44.3	407	2	T48280	hypothetical protein
26	39	44.3	425	2	B43717	raffinose permease
27	39	44.3	542	2	A98021	hypothetical protein
28	39	44.3	546	2	G64803	phosphoglucosyltransferase
29	39	44.3	546	2	G90718	phosphoglucosyltransferase

30	39	44.3	546	2	G85568	phosphoglucutase
31	39	44.3	546	2	AG0586	phosphoglucutase
32	39	44.3	684	2	T25603	hypothetical prote
33	39	44.3	747	2	E91049	probable cytochrom
34	39	44.3	747	2	F65026	hypothetical prote
35	39	44.3	747	2	A85894	probable cytochrom
36	39	44.3	790	2	I50178	cadherin-6B - chic
37	39	44.3	841	2	T14398	S-receptor kinase
38	39	44.3	1112	2	T02848	hsp70-related prot
39	38	43.2	72	2	C64776	hemolysin expressi
40	38	43.2	72	2	A99693	hemolysin expressi
41	38	43.2	72	2	E85543	haemolysin express
42	38	43.2	72	2	AD0561	haemolysin express
43	38	43.2	242	2	H82061	hypothetical prote
44	38	43.2	301	2	A70787	hypothetical prote
45	38	43.2	328	2	C87451	hypothetical prote

ALIGNMENTS

```

RESULT      1
T50660
alpha-expansin 2 [imported] - Triphysaria versicolor
C:Species: Triphysaria versicolor
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 28-Jul-2000
C:Accession: T50660
R:Wrobel, R.L.; Yoder, J.I.
submitted to the EMBL Data Library, April 2000
A:Description: Differential RNA-expression of alpha-expansin gene family members during
A:Reference number: Z25162
A:Accession: T50660
A>Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-262 <WRO>
A:Cross-references: EMBL:AF230277; PIDN:AAF32410.1
C:Superfamily: expansin

```

Query Match	51.1%	Score 45;	DB 2;	Length 262;
Best Local Similarity	57.1%;	Pred. No. 3.3;		
Matches 8;	Conservative	3;	Mismatches 3;	Indels 0;
Gaps 0;				

QY 4 GNILTIRLTAADHR 17
| | : | : | : | : |
Db 224 GOALSFRVTSADHR 237

RESULT 2
C87158
probable oxidoreductase ML1992 [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: C87158
R:Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.;
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.;
A>Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; PMID:21128732; PMID:11234002
A:Accession: C87158
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-289 <STO>
A:Cross-references: GB:AL450380; NID:g13093634; PIDN:CAC30947.1; GSPDB:GN00147
C:Genetics:
A:Gene: ML1992

Query Match 51.1%; Score 45; DB 2; Length 289;
Best Local Similarity 60.0%; Pred. NO. 3.7;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 TVSGNILTIRLTAAD 15
||||:| ||| |
Db 266 TVSGTLITYRLTLDD 280

RESULT 3
S17779
strI protein - Streptomyces griseus
C:Species: Streptomyces griseus
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S17779
R:Mansouri, K.; Piepersberg, W.
Mol. Gen. Genet. 228, 459-469, 1991
A:Title: Genetics of streptomycin production in Streptomyces griseus: nucleotide sequence
A:Reference number: S17775; MUID:91375432
A:Accession: S17779
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-348 <MAN>
A:Cross-references: GB:Y00459; GB:S55493; NID:g1621271; PID:g49268
C:Genetics:
A:Gene: strI
C:Superfamily: Streptomyces griseus strI protein

Query Match 51.1%; Score 45; DB 1; Length 348;
Best Local Similarity 57.1%; Pred. No. 4.4;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 GNILTIRLTAADHR 17
|:|:| || |||
Db 142 GRVLLVRCTAFDHR 155

RESULT 4
JN0342
N-methyl-D-aspartate receptor 1, truncated splice form - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 15-Sep-2000
C:Accession: JN0342
R:Sugihara, H.; Moriyoshi, K.; Ishii, T.; Masu, M.; Nakanishi, S.
Biochem. Biophys. Res. Commun. 185, 826-832, 1992
A:Title: Structures and properties of seven isoforms of the NMDA receptor generated by a
A:Reference number: JN0336; MUID:92328785
A:Accession: JN0342
A:Molecule type: mRNA
A:Residues: 1-181 <SUG>
A:Cross-references: GB:S39221; NID:g250884; PIDN:AAB22435.1; PID:g250885
A:Experimental source: forebrain
C:Comment: This protein plays a key role in memory acquisition, learning and neurological
C:Comment: This protein is an isoform of N-methyl-D-aspartate receptor 1A generated via
C:Keywords: alternative splicing; phosphoprotein; transmembrane protein

Query Match 47.7%; Score 42; DB 2; Length 181;
Best Local Similarity 50.0%; Pred. No. 7.7;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 5 NILTIRLTAADHRQ 18
||||:| |||:
Db 161 NILSLQCTAPDHQE 174

RESULT 5
AB0342
probable LysR-family transcription regulatory protein ptxR [imported] - Yersinia pestis
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C:Accession: AB0342
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,

Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AB0342
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-297 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC93041.1; PID:g15980779; GSPDB:GN00175
C:Genetics:
A:Gene: ptxR
C:Superfamily: hypothetical protein b1328

Query Match 47.2%; Score 41.5; DB 2; Length 297;
Best Local Similarity 62.5%; Pred. No. 16;
Matches 10; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

QY 1 TVSGNILTIRLTAADH 16
||||| |||:|:|
Db 91 TVSGN---IRLSAGEH 103

RESULT 6
F95200
PTS system IIABC components [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C:Accession: F95200
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; H
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzappl
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: F95200
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-627 <KUR>
A:Cross-references: GB:AE005672; PIDN:AAK75799.1; PID:g14973217; GSPDB:GN00164; TIGR:
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP1722
C:Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotransfera

Query Match 47.2%; Score 41.5; DB 2; Length 627;
Best Local Similarity 50.0%; Pred. No. 34;
Matches 10; Conservative 3; Mismatches 2; Indels 5; Gaps 1;

QY 2 VSG-----NILTIRLTAADH 16
||| |:|:| ||||
Db 304 VSGVHHIFNLLEVQLLAADH 323

RESULT 7
E98067
phosphotransferase system enzyme II (EC 2.7.1.69) scrA [imported] - Streptococcus pne
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C:Accession: E98067
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: E98067
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-627 <KUR>
A:Cross-references: GB:AE007317; PIDN:AAL00370.1; PID:g15459232; GSPDB:GN00174

C;Genetics:
A;Gene: scrA
C;Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotransferase
C;Keywords: phosphotransferase

Query Match 47.2%; Score 41.5; DB 2; Length 627;
Best Local Similarity 50.0%; Pred. No. 34;
Matches 10; Conservative 3; Mismatches 2; Indels 5; Gaps 1;

QY 2 VSG-----NILTIRLTAADH 16
||| | : | ||||
Db 304 VSGVHHIFNLLEVQLAADH 323

RESULT 8
AB3581
iolD protein [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AB3581
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, .; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A;Reference number: AD3252; PMID:11756688
A;Accession: AB3581
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-629 <KUR>
A;Cross-references: GB:AE008918; PIDN:AAL53813.1; PID:g17984746; GSPDB:GN00191
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEII0571
A;Map position: II

Query Match 46.6%; Score 41; DB 2; Length 629;
Best Local Similarity 72.7%; Pred. No. 42;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 GNILTIRLTAA 14
||:|:|||||
Db 21 GNMKTVRLTAA 31

RESULT 9
D90071
hypothetical protein SA2429 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: D90071
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogud ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A;Reference number: A89758; PMID:21311952; PMID:11418146
A;Accession: D90071
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-149 <KUR>
A;Cross-references: GB:BA000018; PID:g13702594; PIDN:BAB43734.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA2429

Query Match 45.5%; Score 40; DB 2; Length 149;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 TVSGNILTIRLTAAD 15

Db 123 TVSGNDTTLILTASN 137

RESULT 10
AC2483
hypothetical protein alr7043 [imported] - Anabaena sp. (strain PCC 7120) plasmid pCC7
C;Species: Anabaena sp.
A;Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
C;Accession: AC2483
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpō, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AC2483
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-149 <KUR>
A;Cross-references: GB:BA000020; PIDN:BA078127.1; PID:g17135581; GSPDB:GN00180
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr7043
A;Genome: plasmid

Query Match 45.5%; Score 40; DB 2; Length 149;
Best Local Similarity 46.7%; Pred. No. 14;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 GNILTIRLTAADHRQ 18
| : | || | | : :
Db 128 GQVQTLRLTFAGHQE 142

RESULT 11
JT0874
purine-nucleoside phosphorylase (EC 2.4.2.1) II - Bacillus stearothermophilus
C;Species: Bacillus stearothermophilus
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 20-Jun-2000
C;Accession: JC5563; JT0874
R;Hamamoto, T.; Noguchi, T.; Midorikawa, Y.
Biosci. Biotechnol. Biochem. 61, 276-280, 1997
A;Title: Cloning of purine nucleoside phosphorylase II gene from Bacillus stearotherm
A;Reference number: JC5563; MUID:97212026
A;Accession: JC5563
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-234 <HAM>
A;Cross-references: DDBJ:D87960; NID:g1638806; PIDN:BAA13510.1; PID:g1638807
A;Experimental source: strain TH6-2
C;Superfamily: purine-nucleoside phosphorylase pnp
C;Keywords: glycosyltransferase; pentosyltransferase

Query Match 45.5%; Score 40; DB 2; Length 234;
Best Local Similarity 55.6%; Pred. No. 23;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 TVSGNILTIRLTAADHRQ 18
||| : ||| | : | :
Db 200 TVSDHILTGETTAERQ 217

RESULT 12
T07630
expansin 1 - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 26-May-2000
C;Accession: T07630
R;Rose, J.K.C.; Lee, H.H.; Bennett, A.B.
Proc. Natl. Acad. Sci. U.S.A. 94, 5955-5960, 1997

A;Title: Expression of a divergent expansin gene is fruit-specific and ripening-regulated
A;Reference number: Z16063; MUID:97303239
A;Accession: T07630
A;Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A;Residues: 1-261 <ROS>
A;Cross-references: EMBL:U82123; NID:g2062420; PIDN:AAC63088.1; PID:g2062421
A;Experimental source: cultivar Castlemart; fruit
C;Genetics:
A;Gene: EXPL
A;Note: specifically expressed in ripening fruit, regulated by ethylene
C;Superfamily: expansin

Query Match 45.5%; Score 40; DB 2; Length 261;
Best Local Similarity 43.8%; Pred. No. 25;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 VSGNILTIRLTAAADHR 17
Db 221 LTGQSLSFRVKASDHR 236

RESULT 13
D75306
purine nucleoside phosphorylase - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 19-May-2000
C;Accession: D75306
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896
A;Accession: D75306
A;Status: preliminary
A:Molecule type: DNA
A;Residues: 1-305 <WHI>
A;Cross-references: GB:AE002050; GB:AE000513; NID:g6459965; PIDN:AAF11716.1; PID:g645996
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR2166
A;Map position: 1
C;Superfamily: purine-nucleoside phosphorylase pnp

Query Match 45.5%; Score 40; DB 2; Length 305;
Best Local Similarity 38.9%; Pred. No. 30;
Matches 7; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 TVSGNILTIRLTAAADHRQ 18
Db 267 TISDLVTHEVTSAERQ 284

RESULT 14
B84292
hypothetical protein Vngl375c [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: B84292
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky,
Leithausner, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483
A;Accession: B84292
A;Status: preliminary
A:Molecule type: DNA
A;Residues: 1-444 <STO>

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 11:24:45 ; Search time 29.65 Seconds
(without alignments)
23.506 Million cell updates/sec

Title: US-09-165-546A-13
Perfect score: 88
Sequence: 1 TVSGNLTIRLTAAADHRQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	88	100.0	180	1 CTAG_HUMAN	P78358 homo sapien
2	45	51.1	348	1 STRI_STRGR	P09400 streptomyce
3	44	50.0	454	1 TMS3_HUMAN	P57727 homo sapien
4	40	45.5	234	1 DEOD_BACST	P77835 bacillus st
5	40	45.5	315	1 OAA4_HUMAN	Q9h209 homo sapien
6	39	44.3	102	1 RS10_RHILO	Q98n58 rhizobium l
7	39	44.3	125	1 Y394_RICPR	Q9zdd7 rickettsia
8	39	44.3	195	1 ENGB_LACLA	Q9cge5 lactococcus
9	39	44.3	233	1 ENGB_LACLC	Q9l6g1 lactococcus
10	39	44.3	425	1 DEOD_BACSU	O34925 bacillus su
11	39	44.3	546	1 RAFB_ECOLI	P16552 escherichia
12	39	44.3	597	1 PGMU_ECOLI	P36938 escherichia
13	39	44.3	747	1 WD42_DICDI	P54686 dictyosteli
14	39	44.3	790	1 YFGF_ECOLI	P77172 escherichia
15	39	44.3	72	1 CAD6_CHICK	Q90762 gallus gall
16	38	43.2	301	1 YM16_MYCTU	P23870 escherichia
17	38	43.2	322	1 LIPA_RHIET	O05941 rhizobium e
18	38	43.2	341	1 PUR7_VIGAC	Q07463 vigna aconi
19	38	43.2	423	1 YJ54_YEAST	P47130 saccharomyc
20	38	43.2	478	1 GYRB_CYTTHU	Q91ck1 cytophaga h
21	38	43.2	504	1 5H2B_MOUSE	Q02152 mus musculu
22	38	43.2	132	1 FABH_ONCMY	O13008 oncorhynchu
23	37	42.0	181	1 AG19_COCIM	Q00398 coccidioidi
24	37	42.0	234	1 DEOD_LACLC	O32810 lactococcus
25	37	42.0	271	1 VIUB_VIBVU	Q56743 vibrio vuln
26	37	42.0	281	1 REPL_BPPI	P19654 bacterioph
27	37	42.0	312	1 LPXK_HELPY	O25095 helicobacte
28	37	42.0	312	1 O1D2_HUMAN	P34982 homo sapien
29	37	42.0	320	1 Y054_MYCPN	P75049 mycoplasma
30	37	42.0	321	1 O5V1_HUMAN	Q9ugf6 homo sapien
31	37	42.0	613	1 HS75_CANAL	P87222 candida alb
32	37	42.0	613	1 ML1X_HUMAN	Q13585 homo sapien
33	37	42.0			

34	37	42.0	866	1 LOX1_LENCU	P38414 lens culina
35	36.5	41.5	332	1 G3P_STRAU	Q59800 streptomyce
36	36	40.9	97	1 CYTI_VIGUN	Q06445 vigna ungui
37	36	40.9	238	1 DEOD_HAEIN	P44417 haemophilus
38	36	40.9	240	1 VA46_VARV	P33876 variola vir
39	36	40.9	250	1 LFA3_HUMAN	P19256 homo sapien
40	36	40.9	306	1 OPRR_PSEAE	Q01610 pseudomonas
41	36	40.9	309	1 O1A2_HUMAN	Q9y585 homo sapien
42	36	40.9	309	1 O7AA_HUMAN	O76100 homo sapien
43	36	40.9	309	1 O7AH_HUMAN	O14581 homo sapien
44	36	40.9	312	1 LPXK_HELPJ	Q9zmb1 helicobacte
45	36	40.9	312	1 OAC1_HUMAN	Q96kk4 homo sapien

ALIGNMENTS

RESULT 1					
CTAG_HUMAN					
ID	CTAG_HUMAN	STANDARD;	PRT;	180 AA.	
AC	P78358;				
DT	15-DEC-1998 (Rel. 37, Created)				
DT	15-DEC-1998 (Rel. 37, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Autoimmunogenic cancer/testis antigen NY-ESO-1.				
GN	CTAG.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=97203161; PubMed=9050879;				
RA	Chen Y.-T., Scanlan M.J., Sahin U., Tuereci O., Gure A.O., Tsang S.,				
RA	Williamson B., Stockert E., Pfreundschuh M., Old L.J.;				
RT	"A testicular antigen aberrantly expressed in human cancers detected				
RT	by autologous antibody screening."				
RL	Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Melanoma;				
RX	MEDLINE=98289662; PubMed=9626360;				
RA	Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,				
RA	de Plaen E., Boon T.;				
RT	"LAGE-1 a new gene with tumor specificity."				
RL	Int. J. Cancer 76:903-908(1998).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=98430682; PubMed=9759882;				
RA	Wang R.-F., Johnston S.L., Zeng G., Topalian S.L.,				
RA	Schwartzentruber D.J., Rosenberg S.A.;				
RT	"A breast and melanoma-shared tumor antigen: T cell responses to				
RT	antigenic peptides translated from different open reading frames.";				
RL	J. Immunol. 161:3596-3606(1998).				
CC	-!- TISSUE SPECIFICITY: EXPRESSED IN TESTIS AND OVARY AND IN A WIDE				
CC	VARIETY OF CANCERS. DETECTED IN UTERINE MYOMETRIUM.				
CC	-!- SIMILARITY: STRONG, TO LAGE-1.				
CC	-----				
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CC	use by non-profit institutions as long as its content is in no way				
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CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; U87459; AAB49693.1; -.				
DR	EMBL; AJ003149; CAA05908.1; -.				
DR	EMBL; AF038567; AAD05202.1; -.				
DR	MIM; 300156; -.				
KW	Transmembrane; Antigen.				
FT	DOMAIN 5 82				
FT	TRANSMEM 156 172				
FT	GLY-RICH.				
FT	POTENTIAL.				

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DR EMBL; AF321237; AAG45205.1; --
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 26 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 27 50 1 (POTENTIAL).
FT DOMAIN 51 58 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 59 80 2 (POTENTIAL).
FT DOMAIN 81 101 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 102 121 3 (POTENTIAL).
FT DOMAIN 122 140 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 141 159 4 (POTENTIAL).
FT DOMAIN 160 196 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 197 220 5 (POTENTIAL).
FT DOMAIN 221 237 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 238 260 6 (POTENTIAL).
FT DOMAIN 261 273 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 274 293 7 (POTENTIAL).
FT DOMAIN 294 315 CYTOPLASMIC (POTENTIAL).
FT DISULFID 98 190 BY SIMILARITY.
FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 315 AA; 35100 MW; 68DF6780CA800A4A CRC64;

Query Match 45.5%; Score 40; DB 1; Length 315;
Best Local Similarity 53.3%; Pred. No. 12;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLTAAD 15
I: ||:| | :|||
Db 39 TLMGNVLILVTIAD 53

RESULT 6
RS10_RHILO
ID RS10_RHILO STANDARD; PRT; 102 AA.
AC Q98N58;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S10.
GN RPSJ OR MLR0289.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
CC -!- FUNCTION: Involved in the binding of tRNA to the ribosomes (By
CC similarity).
CC -!- SIMILARITY: BELONGS TO THE S10P FAMILY OF RIBOSOMAL PROTEINS.

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CC -----

DR EMBL; AP002994; BAB47905.1; --
DR InterPro; IPR001848; Ribosomal_S10.
DR Pfam; PF00338; Ribosomal_S10; 1.
DR PRINTS; PR00971; RIBOSOMALS10.
DR PROSITE; PD001272; Ribosomal_S10; 1.
DR PROSITE; PS00361; RIBOSOMAL_S10; 1.
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 102 AA; 11555 MW; E8E87F7889273179 CRC64;

Query Match 44.3%; Score 39; DB 1; Length 102;
Best Local Similarity 50.0%; Pred. No. 5;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 VSGNLTIRLTAADHR 17
:| | : ||| | |||
Db 1 MNGQNIIRLKAFDHR 16

RESULT 7
Y394_RICPR
ID Y394_RICPR STANDARD; PRT; 125 AA.
AC Q9ZDD7;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein RP394.
GN RP394.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=782;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MADRID E;
RX MEDLINE=99039499; PubMed=9823893;
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sacheritz-Ponten T., Almark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria.";
RL Nature 396:133-140(1998).
CC -----

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DR EMBL; AJ235271; CAA14851.1; --
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 10 26 POTENTIAL.
SQ SEQUENCE 125 AA; 14438 MW; 9DC8EC812E6DFAF0 CRC64;

Query Match 44.3%; Score 39; DB 1; Length 125;
Best Local Similarity 46.2%; Pred. No. 6.3;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 5 NILTIRLTAADHR 17
||| :||| ||:
Db 37 NILEVKITIKDHK.49

```
RESULT 8
ENGB_LACLA
ID   ENGB_LACLA          STANDARD;          PRT;      195 AA.
AC   Q9CGE5;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Probable GTP-binding protein engB.
GN   ENGB OR LL1152.
OS   Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC   Lactococcus.
OX   NCBI_TaxID=1360;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IL1403;
RX   MEDLINE=21235186; PubMed=11337471;
RA   Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
RA   Weissenbach J., Ehrlich S.D., Sorokin A.;
RT   "The complete genome sequence of the lactic acid bacterium Lactococcus
RT   lactis ssp. lactis IL1403.";
RL   Genome Res. 11:731-753(2001).
CC   -!- FUNCTION: NECESSARY FOR NORMAL CELL DIVISION AND FOR THE
CC   MAINTENANCE OF NORMAL SEPTATION (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE ENGB FAMILY.
CC   -----
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CC   -----
DR   EMBL; AE006347; AAK05250.1; -.
DR   InterPro; IPR001806; Ras_trnsfrmng.
DR   PRINTS; PR00449; RASTRNSFRMNG.
KW   Cell division; Septation; GTP-binding;
FT   NP_BIND          32      39      GTP (POTENTIAL).
FT   NP_BIND          77      81      GTP (POTENTIAL).
FT   NP_BIND          144     147      GTP (POTENTIAL).
SQ   SEQUENCE 195 AA; 22551 MW; F2750DB86AF93FBF CRC64;

Query Match          44.3%; Score 39; DB 1; Length 195;
Best Local Similarity 44.4%; Pred. No. 10;
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY   1 TVSGNLTIRLTAAADHRQ 18
    I:: I | | | : | | : |
Db    2 TINTNNLTITISAASKKQ 19

RESULT 9
ENGB_LACLC
ID   ENGB_LACLC          STANDARD;          PRT;      195 AA.
AC   Q9L6G1;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Probable GTP-binding protein engB.
GN   ENGB.
OS   Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC   Lactococcus.
OX   NCBI_TaxID=1359;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MG1363;
RA   Skinner M.M., Trempey J.E.;
RT   "Sequence analysis and comparison of the clpX region from Lactococcus

lactis.";
RT   Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC   -!- FUNCTION: NECESSARY FOR NORMAL CELL DIVISION AND FOR THE
CC   MAINTENANCE OF NORMAL SEPTATION (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE ENGB FAMILY.
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CC   -----
DR   EMBL; AF236863; AAF63739.1; -.
DR   InterPro; IPR001806; Ras_trnsfrmng.
DR   PRINTS; PR00449; RASTRNSFRMNG.
KW   Cell division; Septation; GTP-binding.
FT   NP_BIND          32      39      GTP (POTENTIAL).
FT   NP_BIND          77      81      GTP (POTENTIAL).
FT   NP_BIND          144     147      GTP (POTENTIAL).
SQ   SEQUENCE 195 AA; 22460 MW; F2751A8499F9250F CRC64;

Query Match          44.3%; Score 39; DB 1; Length 195;
Best Local Similarity 44.4%; Pred. No. 10;
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY   1 TVSGNLTIRLTAAADHRQ 18
    I:: I | | | : | | : |
Db    2 TINTNNLTITISAASKKQ 19

RESULT 10
DEOD_BACSU
ID   DEOD_BACSU          STANDARD;          PRT;      233 AA.
AC   O34925;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Purine nucleoside phosphorylase II (EC 2.4.2.1) (PNP II) (PU-NPASE
DE   II).
GN   DEOD OR PUNB.
OS   Bacillus subtilis.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group;
OC   Bacillus/Staphylococcus group; Bacillus.
OX   NCBI_TaxID=1423;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wambutt R., Wedler H., Lapidus A., Sorokin A., Ehrlich D.;
RT   "Sequence analysis of the Bacillus subtilis chromosome region between
RT   the odhAB and sspC loci cloned in a yeast artificial chromosome.";
RL   Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=168;
RA   Ghim S.-Y., Jeong Y.-M., Choi S.-K., Park S.-H.;
RT   "Sequence analysis of the 30 kb region (182') of the Bacillus subtilis
RT   chromosome containing the cge cluster.";
RL   Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC   -!- FUNCTION: CLEAVAGE OF ADENOSINE AND ITS DERIVATIVES.
CC   -!- CATALYTIC ACTIVITY: Purine nucleoside + phosphate = purine +
CC   alpha-D-ribose 1-phosphate.
CC   -!- SIMILARITY: BELONGS TO THE PNP/UDP FAMILY 1 OF PHOSPHORYLASES.
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DR EMBL; AF015775; AAB72065.1; -.
DR EMBL; AF006665; AAB81164.1; -.
DR EMBL; Z99114; CAB13854.1; -.
DR HSSP; P09743; 1A69.
DR Subtilist; BG12581; deoD.
DR InterPro; IPR000845; PNP_UDP.
DR Pfam; PF01048; PNP_UDP_1; 1.
DR PROSITE; PS01232; PNP_UDP_1; 1.
KW Transferase; Glycosyltransferase; Complete proteome.
SQ SEQUENCE 233 AA; 25378 MW; 645FD21146E8F613 CRC64;

Query Match 44.3%; Score 39; DB 1; Length 233;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 TVSGNILTIRLTAADHRQ 18
||| :|| | | :||
Db 200 TVSDHVLGTGETTAERQ 217

RESULT 11
RAFB_ECOLI STANDARD; PRT; 425 AA.
AC P16552;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Raffinose permease.
GN RAFB.
OS Escherichia coli.
OG Plasmid pRSD2.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12; PubMed=2556373;
RX MEDLINE=90078124; PubMed=2556373;
RA Aslanidis C., Schmid K., Schmitt R.;
RT "Nucleotide sequences and operon structure of plasmid-borne genes
mediating uptake and utilization of raffinose in Escherichia coli.";
RL J. Bacteriol. 171:6753-6763(1989).
CC -!- FUNCTION: RESPONSIBLE FOR TRANSPORT OF RAFFINOSE INTO THE
CELL, WITH THE CONCOMITANT IMPORT OF A PROTON (SYMPORT SYSTEM).
CC -!- SUBUNIT: MONOMER.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
CC -!- SIMILARITY: BELONGS TO THE LACY/RAFB FAMILY OF PERMEASES.
CC -----
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CC -----
DR EMBL; M27273; AAA24498.1; -.
DR PIR; B43717; B43717.
DR InterPro; IPR000576; Lacy_symp.
DR Pfam; PF01306; Lacy_symp; 1.
DR PRINTS; PR00174; LACYSMPORT.
DR PROSITE; PS00896; LACY_1; 1.
DR PROSITE; PS00897; LACY_2; 1.
KW Transport; Sugar transport; Symport; Inner membrane; Transmembrane;
KW Plasmid.
FT DOMAIN 1 11 CYTOPLASMIC.
FT TRANSMEM 12 32 1 (POTENTIAL).
FT DOMAIN 33 48 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 49 69 2 (POTENTIAL).
FT DOMAIN 70 78 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 79 99 3 (POTENTIAL).
FT DOMAIN 100 105 PERIPLASMIC (POTENTIAL).
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FT TRANSMEM 106 126 4 (POTENTIAL).
FT DOMAIN 127 147 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 148 166 5 (POTENTIAL).
FT DOMAIN 167 169 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 170 190 6 (POTENTIAL).
FT DOMAIN 192 229 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 230 250 7 (POTENTIAL).
FT DOMAIN 251 265 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 266 286 8 (POTENTIAL).
FT DOMAIN 287 294 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 295 313 9 (POTENTIAL).
FT DOMAIN 314 316 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 317 337 10 (POTENTIAL).
FT DOMAIN 338 351 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 352 372 11 (POTENTIAL).
FT DOMAIN 373 383 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 384 404 12 (POTENTIAL).
FT DOMAIN 405 425 CYTOPLASMIC.
SQ SEQUENCE 425 AA; 46693 MW; CAEA12A78B8B1A1C CRC64;

Query Match 44.3%; Score 39; DB 1; Length 425;
Best Local Similarity 53.8%; Pred. No. 24;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSGNILTIRLTAA 14
|:| |::||:| :
Db 297 VAGGIMTIRITGS 309

RESULT 12
PGMU_ECOLI STANDARD; PRT; 546 AA.
AC P36938;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Phosphoglucumutase (EC 5.4.2.2) (Glucose phosphomutase) (PGM).
GN PGM OR B0688.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=94364967; PubMed=8083177;
RA Lu M., Kleckner N.;
RT "Molecular cloning and characterization of the pgm gene encoding
phosphoglucumutase of Escherichia coli.";
RL J. Bacteriol. 176:5847-5851(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map.";
RT
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RL DNA Res. 3:137-155(1996).
RN [4]
RP SEQUENCE OF 1-20 FROM N.A.
RC STRAIN=K12;
RX MEDLINE=94236686; PubMed=8011018;
RA Lu M., Campbell J.L., Boye E., Kleckner N.;
RT "SeqA: a negative modulator of replication initiation in E. coli.";
RL Cell 77:413-426(1994).
RN [5]
RP CHARACTERIZATION.
RA Joshi J.G., Handler P.;
RT "Phosphoglucutase. II. Purification and properties of
RT phosphoglucutase from Escherichia coli.";
RL J. Biol. Chem. 239:2741-2751(1964).
CC -!- FUNCTION: THIS ENZYME PARTICIPATES IN BOTH THE BREAKDOWN AND
CC SYNTHESIS OF GLUCOSE.
CC -!- CATALYTIC ACTIVITY: Alpha-D-glucose 1-phosphate = alpha-D-glucose
CC 6-phosphate.
CC -!- SIMILARITY: BELONGS TO THE PHOSPHOHEXOSE MUTASES FAMILY.
CC -----
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CC -----
DR EMBL; U08369; AAA57067.1; -.
DR EMBL; AE000172; AAC73782.1; -.
DR EMBL; D90707; BAA35337.1; -.
DR EMBL; D90708; BAA35345.1; -.
DR EMBL; U07651; -; NOT_ANNOTATED_CDS.
DR EcoGene; EG12144; pgm.
DR InterPro; IPR001485; PGM_PMM.
DR Pfam; PF00408; PGM_PMM; 1.
DR Pfam; PF02878; PGM_PMM_I; 1.
DR Pfam; PF02879; PGM_PMM_II; 1.
DR Pfam; PF02880; PGM_PMM_III; 1.
DR PROSITE; PS00710; PGM_PMM; 1.
KW Isomerase; Phosphorylation; Complete proteome.
FT ACT_SITE 146 146 FORMS THE PHOSPHOSERINE INTERMEDIATE
FT (BY SIMILARITY).
SQ SEQUENCE 546 AA; 58361 MW; 666B6B9C2F2ECD59 CRC64;

Query Match 44.3%; Score 39; DB 1; Length 546;
Best Local Similarity 57.1%; Pred. No. 32;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLTAA 14
|:|:|:|:|:|:|
Db 472 TLAGDPITARLTAA 485

RESULT 13
WD42_DICDI
ID WD42_DICDI STANDARD; PRT; 597 AA.
AC P54686;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE WD40-repeat protein 2.
GN WDPA.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX3;
RA Mueller-Taubenberger A., Gerisch G.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 11 WD REPEATS (TRP-ASP DOMAINS).
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CC -!- SIMILARITY: BELONGS TO THE AIP1 FAMILY OF WD-REPEAT PROTEINS.
CC -----
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CC -----
DR EMBL; U36936; AAB05588.1; -.
DR DictyDb; DD00098; wdpa.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 10.
DR PRINTS; PR00320; GPROTEINBRPT.
DR SMART; SM00320; WD40; 10.
DR PROSITE; PS00678; WD_REPEATS_1; 2.
DR PROSITE; PS50082; WD_REPEATS_2; 7.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
FT REPEAT 56 95 WD 1.
FT REPEAT 100 143 WD 2.
FT REPEAT 144 186 WD 3.
FT REPEAT 189 228 WD 4.
FT REPEAT 234 273 WD 5.
FT REPEAT 320 359 WD 6.
FT REPEAT 363 397 WD 7.
FT REPEAT 438 475 WD 8.
FT REPEAT 480 517 WD 9.
FT REPEAT 521 561 WD 10.
FT REPEAT 566 596 WD 11.
SQ SEQUENCE 597 AA; 64025 MW; 5A19249F363636B3 CRC64;

Query Match 44.3%; Score 39; DB 1; Length 597;
Best Local Similarity 52.9%; Pred. No. 36;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLTAAADR 17
|:|:|:|:|:|:|
Db 466 TLSGNLTASHTLDNR 482

RESULT 14
YFGF_ECOLI
ID YFGF_ECOLI STANDARD; PRT; 747 AA.
AC P77172;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein yfgF.
GN YFGF OR B2503.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97349980; PubMed=9205837;
RA Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,
RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
```

RA Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S.,
RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
RA Yamagata S., Horiuchi T.;
RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
RT K12 genome corresponding to 50.0-68.8 min on the linkage map and
RT analysis of its sequence features.";
RL DNA Res. 4:91-113(1997).
CC -!- SIMILARITY: CONTAINS 1 DUF2 DOMAIN.
CC -----
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CC -----
DR EMBL; AE000336; AAC75556.1; -.
DR EMBL; D90880; BAA16393.1; -.
DR Ecogene; EG14202; yfgF.
DR InterPro; IPR001633; DUF2.
DR InterPro; IPR000160; DUF9.
DR Pfam; PF00563; EAL; 1.
DR SMART; SM00267; DUF1; 1.
DR SMART; SM00052; DUF2; 1.
KW Hypothetical protein; Complete proteome.
FT DOMAIN 492 736 DUF2.
SQ SEQUENCE 747 AA; 85607 MW; 7D5E8B0E646C8EDF CRC64;

Query Match 44.3%; Score 39; DB 1; Length 747;
Best Local Similarity 41.2%; Pred. No. 45;
Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 VSGNLTIRLTAAADHRQ 18
:|||||:|:|:|:
Db 400 LSGNDLALRLNTESHQE 416

RESULT 15
CAD6_CHICK STANDARD; PRT; 790 AA.
AC Q90762;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cadherin-6 precursor (Cadherin-6B) (c-cad6B).
GN CDH6.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A., AND DEVELOPMENTAL STAGE.
RC STRAIN=WHITE LEGHORN; TISSUE=Brain;
RX MEDLINE=95309115; PubMed=7540531;
RA Nakagawa S., Takeichi M.;
RT "Neural crest cell-cell adhesion controlled by sequential and
RT subpopulation-specific expression of novel cadherins.";
RL Development 121:1321-1332(1995).
CC -!- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.
CC THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC
CC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE
CC SORTING OF HETEROGENEOUS CELL TYPES.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- DEVELOPMENTAL STAGE: FIRST EXPRESSED IN SPLANCHNIC MESODERM OF
CC STAGE 4 EMBRYOS. AT STAGE 6, STRONGLY EXPRESSED ALONG THE NEURAL
CC FOLD IN A REGION CORRESPONDING TO THE FUTURE NEURAL CREST.
CC EXPRESSION IN THE NEURAL FOLD CONTINUES DURING CLOSURE OF THE
CC NEURAL TUBE BUT DIMINISHES AFTER NEURAL CREST CELLS HAVE LEFT THE
CC NEURAL TUBE.
CC -!- SIMILARITY: CONTAINS 5 CADHERIN DOMAINS.

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CC -----
DR EMBL; D42149; BAA07720.1; -.
DR HSSP; P15116; INCJ.
DR InterPro; IPR002126; Cadherin.
DR InterPro; IPR000233; Cadherin_C_term.
DR Pfam; PF00028; cadherin; 5.
DR Pfam; PF01049; Cadherin_C_term; 1.
DR PRINTS; PR00205; CADHERIN.
DR SMART; SM00112; CA; 5.
DR PROSITE; PS00232; CADHERIN_1; 3.
DR PROSITE; PS00268; CADHERIN_2; 5.
KW Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
KW Signal.
FT SIGNAL 1 30 POTENTIAL.
FT PROPEP 31 53 POTENTIAL.
FT CHAIN 54 790 CADHERIN-6.
FT DOMAIN 54 615 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 616 636 POTENTIAL.
FT DOMAIN 637 790 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 54 159 CADHERIN 1.
FT DOMAIN 160 268 CADHERIN 2.
FT DOMAIN 269 383 CADHERIN 3.
FT DOMAIN 384 486 CADHERIN 4.
FT DOMAIN 487 608 CADHERIN 5.
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 255 255 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 437 437 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 455 455 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 536 536 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 790 AA; 88659 MW; 0FD3756749DB5CC5 CRC64;

Query Match 44.3%; Score 39; DB 1; Length 790;
Best Local Similarity 53.3%; Pred. No. 48;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 SGNLTIRLTAAADHR 17
:|||||:
Db 580 STETVTIRVCACDHR 594

Search completed: July 3, 2002, 11:24:46
Job time: 893 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:24:10 ; Search time 107.89 Seconds
(without alignments)
28.862 Million cell updates/sec

Title: US-09-165-546A-13
Perfect score: 88
Sequence: 1 TVSGNILTIRLTAAADHRQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_invertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archheap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	79	89.8	180	4 Q9Y479	Q9y479 homo sapien
2	46	52.3	327	11 O70269	O70269 rattus norv
3	46	52.3	327	11 O70270	O70270 rattus norv
4	45	51.1	262	10 Q9M5I6	Q9m5i6 triphysaria
5	45	51.1	289	16 Q9CBG4	Q9cbg4 mycobacteri
6	44	50.0	309	11 Q62007	Q62007 mus musculu
7	43	48.9	263	10 Q9ZP32	Q9zp32 lycopersico
8	43	48.9	327	11 O70271	O70271 rattus norv
9	43	48.9	597	11 O55011	O55011 rattus norv
10	43	48.9	640	11 O55012	O55012 rattus norv
11	43	48.9	652	4 Q13492	Q13492 homo sapien
12	43	48.9	655	11 Q921L0	Q921l0 mus musculu
13	42	47.7	272	2 Q9F6X8	Q9f6x8 chloroflexu
14	42	47.7	344	2 Q9F667	Q9f667 pseudomonas
15	42	47.7	344	2 Q9RLD6	Q9rlD6 pseudomonas
16	42	47.7	792	13 Q9DFS1	Q9dfs1 xenopus lae

17	42	47.7	792	13 Q9DFS0	Q9dfs0 xenopus lae
18	41.5	47.2	627	16 Q97PB8	Q97pb8 streptococc
19	41	46.6	133	1 O93762	O93762 uncultured
20	41	46.6	142	4 Q9NY13	Q9ny13 homo sapien
21	41	46.6	207	3 O94107	O94107 pneumocysti
22	41	46.6	315	11 Q9JKA6	Q9jka6 mus musculu
23	40.5	46.0	140	10 Q9LHF4	Q9lhf4 arabiidopsis
24	40	45.5	149	16 Q99R01	Q99r01 staphylococ
25	40	45.5	188	10 Q9FGM1	Q9fgm1 arabiidopsis
26	40	45.5	207	3 O94108	O94108 pneumocysti
27	40	45.5	261	10 O04359	O04359 lycopersico
28	40	45.5	284	10 Q946H6	Q946h6 oryza sativ
29	40	45.5	305	16 Q9RSF8	Q9rsf8 deinococcus
30	40	45.5	349	2 Q9AHF0	Q9ahf0 agrobacteri
31	40	45.5	406	16 Q98FT9	Q98ft9 rhizobium 1
32	40	45.5	438	10 Q9AYP8	Q9ayp8 brassica ca
33	40	45.5	444	17 Q9HQ15	Q9hq15 halobacteri
34	40	45.5	449	10 O80343	O80343 brassica ca
35	40	45.5	545	17 Q980U2	Q980u2 sulfolobus
36	40	45.5	586	4 Q9NV17	Q9nv17 homo sapien
37	40	45.5	586	4 Q96A50	Q96a50 homo sapien
38	40	45.5	591	11 Q925I1	Q925i1 mus musculu
39	40	45.5	1124	17 Q9HKQ3	Q9hkq3 thermoplasm
40	39	44.3	102	16 Q92QH1	Q92qh1 rhizobium m
41	39	44.3	115	12 Q99GR6	Q99gr6 culex nigri
42	39	44.3	121	2 Q56293	Q56293 thiobacillu
43	39	44.3	245	9 O64327	O64327 bacterioph
44	39	44.3	314	11 Q9EPG5	Q9epg5 mus musculu
45	39	44.3	344	16 Q9PCX1	Q9pcx1 xylella fas

ALIGNMENTS

RESULT 1
Q9Y479
ID Q9Y479 PRELIMINARY; PRT; 180 AA.
AC Q9Y479;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE LAGE-1S PROTEIN (CANCER/TESTIS ANTIGEN 2).
GN LAGE1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MELANOMA;
RX MEDLINE=99325550; PubMed=10399963;
RA Aarnoudse C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.;
RT "Interleukin-2-induced, melanoma-specific T cells recognize CAMEL, an
RT unexpected translation product of LAGE-1.";
RL Int. J. Cancer 82:442-448(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Aradhya S., Bardaro T., Galgoczy P., Yamagata T., Esposito T.,
RA Patlan H., Ciccodicola A., Kenwrick S., Platzner M., D'Urso M.,
RA Nelson D.L.;
RT "Multiple pathogenic and benign genomic rearrangements occur at a 35-
RT kb duplication involving the NEMO and the LAGE2 genes.";
RL Hum. Mol. Genet. 0:0-0(2001).
DR EMBL; AJ012834; CAA10194.1; -.
DR EMBL; AF277315; AAL27015.1; -.
SQ SEQUENCE 180 AA; 18236 MW; 9077FAF953543A25 CRC64;

Query Match 89.8%; Score 79; DB 4; Length 180;
Best Local Similarity 88.9%; Pred. No. 3.5e-06;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVSGNILTIRLTAAADHRQ 18

RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011(2001).
DR EMBL; AL583924; CAC30947.1; -.
DR Leproma; ML1992; -.
DR InterPro; IPR003819; TauD_Tfda.
DR Pfam; PF02668; TauD; 1.
KW Complete proteome.
SQ SEQUENCE 289 AA; 32372 MW; F5E521B73FB86959 CRC64;

Query Match 51.1%; Score 45; DB 16; Length 289;
Best Local Similarity 60.0%; Pred. No. 7.3;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLTAAD 15
|:|:|:|:|:|:|
Db 266 TVSGTLITYRLTLDD 280

RESULT 6
Q62007 PRELIMINARY; PRT; 309 AA.
AC Q62007;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ODORANT RECEPTOR.
GN OLFRL16 OR OR23.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=96192035; PubMed=8619840;
RA Asai H., Kasai H., Matsuda Y., Yamazaki N., Nagawa F., Sakano H.,
RA Tsuboi A.;
RT "Genomic structure and transcription of a murine odorant receptor
RT gene: differential initiation of transcription in the olfactory and
RT testicular cells.";
RL Biochem. Biophys. Res. Commun. 221:240-247(1996).
DR EMBL; X92969; CAA63545.1; -.
DR MGD; MGI:106648; Olfrl16.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR000985; Lectin_lega.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.
DR PROSITE; PS00308; LECTIN_LEGUME_ALPHA; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 309 AA; 34255 MW; BEE5CF666D0F7D68 CRC64;

Query Match 50.0%; Score 44; DB 11; Length 309;
Best Local Similarity 43.8%; Pred. No. 12;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLTAADH 16
|:|:|:|:|:|:|
Db 38 TLAGNIIIVTITHIDH 53

RESULT 7
Q92P32 PRELIMINARY; PRT; 263 AA.
AC Q92P32;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE EXPANSIN PRECURSOR.
GN EXP4.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. 91347; TISSUE=FRUIT;
RX MEDLINE=9917803; PubMed=10080718;
RA Brummell D.A., Harpster M.H., Dunsmuir P.;
RT "Differential expression of expansin gene family members during growth
RT and ripening of tomato fruit.";
RL Plant Mol. Biol. 39:161-169(1999).
DR EMBL; AF059488; AAD13632.1; -.
DR InterPro; IPR000882; Pollen_allergen.
DR Pfam; PF01357; Pollen_allergen; 1.
DR PRINTS; PR01225; EXPANSINFAMILY.
DR ProDom; PD002179; Pollen_allergen; 1.
KW Signal.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 263 EXPANSIN.
SQ SEQUENCE 263 AA; 28701 MW; 8CD4552A2FA73761 CRC64;

Query Match 48.9%; Score 43; DB 10; Length 263;
Best Local Similarity 57.1%; Pred. No. 15;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 GNILTIRLTAADHR 17
|:|:|:|:|:|:|
Db 225 GQALSIRVKASDHR 238

RESULT 8
O70271 PRELIMINARY; PRT; 327 AA.
AC O70271;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE OLFACTORY RECEPTOR-LIKE PROTEIN.
GN SCR G-16.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=98211958; PubMed=9545261;
RA Walensky L.D., Ruat M., Bakin R.E., Blackshaw S., Ronnett G.V.,
RA Snyder S.H.;
RT "Two novel odorant receptor families expressed in spermatids undergo
RT 5'-splicing.";
RL J. Biol. Chem. 273:9378-9387(1998).
DR EMBL; AF034903; AAC17227.1; -.
DR InterPro; IPR002106; AA_tRNA_ligase_II.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00339; AA_tRNA_LIGASE_II_2; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 327 AA; 37229 MW; A300D8ABF0E61A82 CRC64;

Query Match 48.9%; Score 43; DB 11; Length 327;
Best Local Similarity 47.1%; Pred. No. 19;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLTAADHR 17

Db	44	SLMGNMLIITYTCVDHR	60	:: :	
RESULT	9				
O55011	ID	O55011	PRELIMINARY;	PRT;	597 AA.
AC	O55011;				
DT	01-JUN-1998	(TReMBLrel. 06, Created)			
DT	01-JUN-1998	(TReMBLrel. 06, Last sequence update)			
DT	01-DEC-2001	(TReMBLrel. 19, Last annotation update)			
DE	CLATHRIN ASSEMBLY PROTEIN SHORT FORM.				
GN	CALM.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;				
RX	MEDLINE=20094069; PubMed=10630373;				
RA	Kim H.-L., Lee S.-C.;				
RT	"Molecular cloning of clathrin assembly protein gene (rCALM) and its				
RT	differential expression to AP180 in rat brain.";				
RL	Exp. Mol. Med. 31:191-196(1999).				
DR	EMBL; AF041373; AAB97078.1; -.				
DR	InterPro; IPR001026; ENTH.				
DR	Pfam; PF01417; ENTH; 1.				
DR	SMART; SM00273; ENTH; 1.				
SQ	SEQUENCE 597 AA; 64656 MW; 42CA9A1426B9E6A4 CRC64;				
Query Match	48.9%;	Score 43;	DB 11;	Length 597;	
Best Local Similarity	60.0%;	Pred. No. 37;			
Matches	9;	Conservative 2;	Mismatches 4;	Indels 0;	Gaps 0;
QY	2	VSGNILTIRLTAADH	16	::	
Db	1	MSGQSLTDTRITAAQH	15		
RESULT	10				
O55012	ID	O55012	PRELIMINARY;	PRT;	640 AA.
AC	O55012;				
DT	01-JUN-1998	(TReMBLrel. 06, Created)			
DT	01-JUN-1998	(TReMBLrel. 06, Last sequence update)			
DT	01-DEC-2001	(TReMBLrel. 19, Last annotation update)			
DE	CLATHRIN ASSEMBLY PROTEIN LONG FORM.				
GN	CALM.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;				
RX	MEDLINE=20094069; PubMed=10630373;				
RA	Kim H.-L., Lee S.-C.;				
RT	"Molecular cloning of clathrin assembly protein gene (rCALM) and its				
RT	differential expression to AP180 in rat brain.";				
RL	Exp. Mol. Med. 31:191-196(1999).				
DR	EMBL; AF041374; AAB97079.1; -.				
DR	InterPro; IPR001026; ENTH.				
DR	Pfam; PF01417; ENTH; 1.				
DR	SMART; SM00273; ENTH; 1.				
SQ	SEQUENCE 640 AA; 69286 MW; 7395A92C285FA10A CRC64;				
Query Match	48.9%;	Score 43;	DB 11;	Length 640;	
Best Local Similarity	60.0%;	Pred. No. 40;			
Matches	9;	Conservative 2;	Mismatches 4;	Indels 0;	Gaps 0;

QY	2	VSGNILTIRLTAADH	16	::	
Db	1	MSGQSLTDTRITAAQH	15		
RESULT	11				
Q13492	ID	Q13492	PRELIMINARY;	PRT;	652 AA.
AC	Q13492; O60700;				
DT	01-NOV-1996	(TReMBLrel. 01, Created)			
DT	01-NOV-1996	(TReMBLrel. 01, Last sequence update)			
DT	01-JUN-2001	(TReMBLrel. 17, Last annotation update)			
DE	CLATHRIN ASSEMBLY LYMPHOID MYELOID LEUKEMIA PROTEIN (CALM).				
GN	CALM.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A., CHROMOSOMAL TRANSLOCATION, AND TISSUE SPECIFICITY.				
RX	MEDLINE=96209813; PubMed=8643484;				
RA	Dreyling M.H., Martinez-Climent J.A., Zheng M., Mao J., Rowley J.D.,				
RA	Bohlander S.K.;				
RT	"The t(10;11)(p13;q14) in the U937 cell line results in the fusion of				
RT	the AF10 gene and CALM, encoding a new member of the AP-3 clathrin				
RT	assembly protein family.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 93:4804-4809(1996).				
RN	[2]				
RP	SEQUENCE OF 575-652 FROM N.A., AND ALTERNATIVE SPLICING.				
RC	TISSUE=BONE MARROW;				
RX	MEDLINE=98407707; PubMed=9737689;				
RA	Silliman C.C., McCavran L., Wei Q., Miller L.A., Li S., Hunger S.P.;				
RT	"Alternative splicing in wild-type AF10 and CALM cDNAs and in AF10-				
RT	CALM and CALM-AF10 fusion cDNAs produced by the t(10;11)(p13-14;q14-				
RT	q21) suggests a potential role for truncated AF10 polypeptides.";				
RL	Leukemia 12:1404-1410(1998).				
CC	-!- ALTERNATIVE PRODUCTS: TWO FORMS; TYPE I (SHOWN HERE) AND TYPE II;				
CC	ARE PRODUCED BY ALTERNATIVE SPLICING.				
CC	-!- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED.				
CC	-!- DISEASE: INVOLVED IN A T(10;11)(P13;Q14) CHROMOSOMAL TRANSLOCATION				
CC	IN DIFFUSE HISTIOCYTIC LYMPHOMAS CAUSING FUSION TO THE AF10 GENE				
CC	PRODUCT.				
DR	EMBL; U45976; AAB07762.1; -.				
DR	EMBL; AF060939; AAC16711.1; -.				
DR	EMBL; AF060940; AAC16712.1; -.				
DR	MIM; 603025; -.				
DR	InterPro; IPR001026; ENTH.				
DR	Pfam; PF01417; ENTH; 1.				
DR	SMART; SM00273; ENTH; 1.				
KW	Alternative splicing; Chromosomal translocation.				
FT	SITE 648 649				
FT	VARSP LIC 594 594				
FT	VARSP LIC 596 613				
SQ	SEQUENCE 652 AA; 70695 MW; 43BEC31EE237F003 CRC64;				
Query Match	48.9%;	Score 43;	DB 4;	Length 652;	
Best Local Similarity	60.0%;	Pred. No. 40;			
Matches	9;	Conservative 2;	Mismatches 4;	Indels 0;	Gaps 0;
QY	2	VSGNILTIRLTAADH	16	::	
Db	1	MSGQSLTDTRITAAQH	15		
RESULT	12				
Q921L0	ID	Q921L0	PRELIMINARY;	PRT;	655 AA.
AC	Q921L0;				
DT	01-DEC-2001	(TReMBLrel. 19, Created)			
DT	01-DEC-2001	(TReMBLrel. 19, Last sequence update)			
DT	01-DEC-2001	(TReMBLrel. 19, Last annotation update)			

DE SIMILAR TO PHOSPHATIDYLINOSITOL BINDING CLATHRIN ASSEMBLY
DE PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011470; AAH11470.1; -.
SQ SEQUENCE 655 AA; 70981 MW; F729CEF5D3D82781 CRC64;

Query Match 48.9%; Score 43; DB 11; Length 655;
Best Local Similarity 60.0%; Pred. No. 41;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 VSGNILTIRLTAADH 16
: || || || || ||
Db 1 MSGQSLTDRIATAQH 15

RESULT 13
Q9F6X8
ID Q9F6X8 PRELIMINARY; PRT; 272 AA.
AC Q9F6X8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ACN (FRAGMENT).
GN ACN.
OS Chloroflexus aurantiacus.
OC Bacteria; Green non-sulfur bacteria; Chloroflexaceae group;
OC Chloroflexaceae; Chloroflexus.
OX NCBI_TaxID=1108;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20433268; PubMed=10976061;
RA Xiong J., Fischer W.M., Inoue K., Nakahara M., Bauer C.E.;
RT "Molecular evidence for the early evolution of photosynthesis.";
RL Science 289:1724-1730(2000).
DR EMBL; AF288459; AAG15207.1; -.
DR InterPro; IPR00573; Aconitase_C.
DR Pfam; PF00694; Aconitase_C; 1.
FT NON_TER 1
SQ SEQUENCE 272 AA; 29511 MW; CB8E7C295B199BF7 CRC64;

Query Match 47.7%; Score 42; DB 2; Length 272;
Best Local Similarity 61.5%; Pred. No. 24;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 SGNILTIRLTAAD 15
: | |||: | ||
Db 219 NGRILTVRATAGD 231

RESULT 14
Q9F667
ID Q9F667 PRELIMINARY; PRT; 344 AA.
AC Q9F667;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PILIN BIOGENESIS PROTEIN PILT.
GN PILT.
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=294;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=WCS365; TISSUE=TYPE 4 PILI;
RA Camacho Carvajal M.M., de Priester W., Lugtenberg B.J.J.,
RA Bloemberg G.V.;
RT "Involvement of type 4 pili of Pseudomonas fluorescens in tomato root
colonization.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF297458; AAG18590.1; -.
DR InterPro; IPR003593; AAA.
DR InterPro; IPR001687; ATP_GTP_A.
DR InterPro; IPR001482; GSPII_E.
DR Pfam; PF00437; GSPII_E; 1.
DR SMART; SM00382; AAA; 1.
KW ATP-binding.
SQ SEQUENCE 344 AA; 38163 MW; 42BCDC8FD9761966 CRC64;

Query Match 47.7%; Score 42; DB 2; Length 344;
Best Local Similarity 47.1%; Pred. No. 30;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 VSGNILTIRLTAADHRQ 18
| |:: | | | ||:
Db 30 VGDVRRINLPALDHKQ 46

RESULT 15
Q9RLD6
ID Q9RLD6 PRELIMINARY; PRT; 344 AA.
AC Q9RLD6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE TWITCHING MOTILITY PROTEIN.
GN PILT.
OS Pseudomonas stutzeri (Pseudomonas perfectomarina).
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=316;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JM300;
RX MEDLINE=21359310; PubMed=11466271;
RA Graupner S., Weger N., Sohni M., Wackernagel W.;
RT "Requirement of bovel competence genes pilt and pilU of Pseudomonas
stutzeri for natural transformation and suppression of pilt deficiency
by a Hexahistidine tag on the type IV pilus protein PilAI.";
RL J. Bacteriol. 183:4694-4701(2001).
DR EMBL; AJ249385; CAB56295.1; -.
DR InterPro; IPR001687; ATP_GTP_A.
DR InterPro; IPR001482; GSPII_E.
DR Pfam; PF00437; GSPII_E; 1.
DR PROSITE; PS00662; T2SP_E; 1.
SQ SEQUENCE 344 AA; 37946 MW; 052C3F33B7DA3A1A CRC64;

Query Match 47.7%; Score 42; DB 2; Length 344;
Best Local Similarity 47.1%; Pred. No. 30;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 VSGNILTIRLTAADHRQ 18
| |:: | | | ||:
Db 30 VGDVRRINLPAMDHKQ 46

Search completed: July 3, 2002, 11:24:11
Job time: 918 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:08:50 ; Search time 136.43 Seconds
(without alignments)
14.655 Million cell updates/sec

Title: US-09-165-546A-13

Perfect score: 88

Sequence: 1 TVSGNILTIRLTAADHRQ 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A_Geneseq_032802.*
- 1: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT.*
 - 2: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT.*
 - 3: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT.*
 - 4: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT.*
 - 5: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT.*
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 - 9: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT.*
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 - 16: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT.*
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 - 19: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT.*
 - 20: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT.*
 - 21: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT.*
 - 22: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	100.0	18	21	AA52440 Human tumour antig
2	88	100.0	18	22	AAU01544 HLA-DR53 recognisi
3	88	100.0	18	22	AAB69944 Human NY-ESO-1 HLA
4	88	100.0	20	22	AAE07742 Human ESO p126-145
5	88	100.0	180	19	AAW69665 Human NY-ESO-1 pro
6	88	100.0	180	19	AAW62584 Cancer associated
7	88	100.0	180	20	AA505965 Human cancer antig
8	88	100.0	180	21	AAB03154 Human oesophageal
9	88	100.0	180	21	AA570862 Human tumour antig
10	88	100.0	180	21	AA52430 Human tumour antig
11	88	100.0	180	22	AAG67164 Amino acid sequenc

12	88	100.0	180	22	AAE07714 Human NY ESO-1 pro
13	88	100.0	180	22	AAU01535 Human NY-ESO-1 tum
14	88	100.0	180	22	AAB69946 Human NY-ESO-1 pro
15	88	100.0	397	22	AAE13122 NY-ESO-1C-HER-2 me
16	79	89.8	180	19	AAW69664 Human LAGE-1 clone
17	79	89.8	180	21	AA570860 Human LAGE-1 splic
18	69	78.4	20	22	AAE07743 Human ESO p131-150
19	56	63.6	18	22	AAE07769 Human NY ESO-1 HLA
20	56	63.6	18	22	AAU01540 HLA-DR53 recognisi
21	56	63.6	18	22	AAB69940 Human NY-ESO-1 HLA
22	51	58.0	14	22	AAE07728 Human NY ESO-1 MHC
23	51	58.0	14	22	AAE07788 Human NY ESO-1 pep
24	51	58.0	15	22	AAE07727 Human NY ESO-1 MHC
25	51	58.0	15	22	AAE07787 Human NY ESO-1 MHC
26	51	58.0	17	21	AA52436 Human tumour antig
27	51	58.0	25	22	AAE07718 Human NY ESO-1 MHC
28	51	58.0	27	22	AAE07717 Human NY ESO-1 MHC
29	50	56.8	10	20	AA506055 Human cancer antig
30	50	56.8	10	20	AA505989 Human cancer antig
31	49	55.7	10	20	AA506017 Human cancer antig
32	47	53.4	10	20	AA505988 Human cancer antig
33	47	53.4	10	20	AA505980 Human cancer antig
34	47	53.4	15	22	AAE07726 Human NY ESO-1 MHC
35	47	53.4	15	22	AAE07786 Human NY ESO-1 pep
36	47	53.4	316	22	AAG71447 Human olfactory re
37	46	52.3	327	18	AAW21666 Rat spermatid chem
38	46	52.3	327	22	AAB30874 Amino acid sequenc
39	46	52.3	327	22	AAB30877 Amino acid sequenc
40	46	52.3	327	22	AAB30878 Amino acid sequenc
41	45	51.1	9	20	AA506054 Human cancer antig
42	45	51.1	9	20	AA506038 Human cancer antig
43	45	51.1	9	20	AA506045 Human cancer antig
44	45	51.1	10	20	AA506000 Human cancer antig
45	44	50.0	225	22	AAU18692 Renal and cardiova

ALIGNMENTS

RESULT 1

AA52440

ID AA52440 standard; Protein; 18 AA.

XX AA52440;

XX 15-FEB-2000 (first entry)

XX Human tumour antigen NY-ESO-1 peptide #13.

DE Cancer; tumour; antigen; MHC; major histocompatibility complex; Class II;
XX T-cell; helper; stimulation; proliferation; treatment;
KW diagnosis; prevention; melanoma; breast cancer; ovarian cancer;
KW prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer;
KW lymphoma.

XX Synthetic.

OS Homo sapiens.

XX WO9953938-A1.

XX 28-OCT-1999.

XX 24-MAR-1999; 99WO-US06875.

XX 17-APR-1998; 98US-0062422.

PR 02-OCT-1998; 98US-0165546.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;

PI Gure A, Ritter G;

XX WPI; 2000-038483/03.

XX Novel peptides which bind to MHC class I and MHC class II molecules,
PT useful for therapeutic and diagnostic purposes -
XX Claim 4; Page 22; 49pp; English.
XX Peptides #8-#13 (AAV52435-Y52440) are peptides derived from the human
CC tumour antigen, NY-ESO-1 (AAV52430) which can bind to MHC(major
CC histocompatibility Class II HLA-DR53 molecules, thereby stimulating
CC proliferation of helper T-cells. cDNA encoding NY-ESO-1 was initially
CC isolated from an oesophagus squamous cell cancer cDNA library. Tissue.
CC localisation studies revealed it to be expressed at high levels
CC in normal ovary and testis but not in normal colon, kidney, liver,
CC brain, oesophagus and skin. It was expressed in certain tumours and
CC tumour cell lines with some degree of frequency - these included
CC melanoma specimens and cell lines, and breast and bladder cancer
CC specimens, with expression in other tumour types being sporadic.
CC These NY-ESO-1-derived peptides may be used in methods and
CC compositions used for the treatment, diagnosis and prevention of
CC cancers (such as melanoma, breast cancer, prostate cancer, lung
CC cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer,
CC or lymphoma) and to stimulate the proliferation of T cells.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 88; DB 21; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.9e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNILTIRLTAADHRQ 18
Db 1 tvsgniltirltaadhrq 18
|||||

RESULT 2
AAU01544
ID AAU01544 standard; Peptide; 18 AA.
XX
AC AAU01544;
XX
DT 18-JUL-2001 (first entry)
XX
DE HLA-DR53 recognising NY-ESO-1 peptide #6.
XX
KW NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
KW human leukocyte antigen-determining region; disease progression;
KW disease regression; disease onset; body tissue; body fluid; enzyme label;
KW radioactive label; monoclonal antibody.
XX
OS Homo sapiens.
XX
PN WO200123560-A2.
XX
PD 05-APR-2001.
XX
XX 26-SEP-2000; 2000WO-US26411.
PF
XX 29-SEP-1999; 99US-0408036.
PR
XX (LUDW-) LUDWIG INST CANCER RES.
PA
XX Tureci O, Sahin U, Pfreundschuh M;
PI
XX WPI; 2001-266156/27.
DR
XX Polypeptides binding to major histocompatibility complex class II human
PT leukocyte antigen-determining region molecule having amino acid
PT sequence found in tumour rejection antigen precursor used for
PT stimulating proliferation of helper T cells -
XX
PS Example 13; Page 19; 62pp; English.

XX The sequence represents a human NY-ESO-1 tumour rejection antigen
CC precursor fragment which recognises and binds to HLA-DR53. NY-ESO-1 and
CC SSX-2 polypeptides, or fragments of, bind to major histocompatibility
CC complex (MHC) Class II molecules such as human leukocyte
CC antigen-determining region (HLA-DR) molecules and stimulate proliferation
CC of helper T cells. The peptides can be administered to an HLA-DR positive
CC subject in order to stimulate the helper T cells. An MHC Class II
CC HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell or
CC present in free form is useful for this stimulation. The nucleic acid is
CC useful for screening for a cancerous condition, which involves contacting
CC a subject sample to a cell line transfected with the immunoreactive cell
CC (helper T cell), where interaction is indicative of cancer. In addition,
CC a sample from a patient (for example, a body fluid or tissue) can be
CC monitored for the amount of the complex present in the bloodstream. This
CC is useful for determining regression, progression or onset of a cancerous
CC condition. The method involves contacting the sample with a radioactive
CC labelled or enzyme labelled monoclonal antibody which specifically binds
CC with the complex.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 88; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.9e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNILTIRLTAADHRQ 18
Db 1 tvsgniltirltaadhrq 18
|||||

RESULT 3
AAB69944
ID AAB69944 standard; Peptide; 18 AA.
XX
AC AAB69944;
XX
DT 27-APR-2001 (first entry)
XX
DE Human NY-ESO-1 HLA-DR53 binding motif #6.
XX
KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW non-small cell lung carcinoma; tumour status determination.
XX
OS Homo sapiens.
XX
PN WO200107917-A1.
XX
PD 01-FEB-2001.
XX
PF 14-JUL-2000; 2000WO-US19220.
XX
PR 23-JUL-1999; 99US-0359503.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.
XX
PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
XX WPI; 2001-182822/18.
DR
XX Method useful for determining the status (e.g. progression, regression
PT or stability of the disease) of a cancerous condition, involves
PT determining the levels of NY-ESO-1 specific antibodies in a sample
PT taken from a patient -
XX
PS Example 16; Page 28; 50pp; English.
XX
CC The present sequence is given in a specification relating to a method
CC for determining the status of a cancerous condition in a patient

CC with a tumour that expresses NY-ESO-1. The method comprises assaying a
CC sample taken from the patient for antibodies that specifically bind to
CC the NY-ESO-1 and comparing the value obtained to a prior value obtained
CC from assay of a prior sample taken from the patient. Any difference
CC between the values is indicative of a change in status of the cancerous
CC condition. The method is useful for determining whether a cancerous
CC condition is progressing, regressing or remaining stable, in particular
CC in patients receiving treatment for a melanoma, adenocarcinoma,
CC non-small cell lung carcinoma or bladder carcinoma.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 88; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.9e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLTAAADHRQ 18
| | | | | | | | | | | | | | | |
Db 1 tvsgniltirltaadhrq 18

RESULT 4
AAE07742
ID AAE07742 standard; peptide; 20 AA.
XX
AC AAE07742;

DT 06-NOV-2001 (first entry)
XX Human ESO pl26-145 peptide, to identify MHC class II-restricted epitopes.
DE
KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.
XX
OS Homo sapiens.
XX
PN WO200155393-A2.
XX
PD 02-AUG-2001.

XX 26-JAN-2001; 2001WO-US02765.
PF 28-JAN-2000; 2000US-0179004.
PR 29-SEP-2000; 2000US-0237107.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Wang R, Rosenberg SA, Zeng G;
XX WPI; 2001-496851/54.
DR
XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -
XX
PS Example 3; Fig 3; 134pp; English.

XX The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also

CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or hapten and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is human
CC ESO pl26-145 peptide used in the identification of putative MHC class II
CC -restricted epitopes from HLA-DR4-transgenic mice.
XX
SQ Sequence 20 AA;

Query Match 100.0%; Score 88; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLTAAADHRQ 18
| | | | | | | | | | | | | | | |
Db 2 tvsgniltirltaadhrq 19

RESULT 5
AAW69665
ID AAW69665 standard; Protein; 180 AA.
XX
AC AAW69665;

DT 27-OCT-1998 (first entry)
XX Human NY-ESO-1 protein sequence, formerly known as LL-1.2 clone.
DE Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour.
KW Homo sapiens.
XX
OS WO9832855-A1.
XX
PD 30-JUL-1998.

XX 27-JAN-1998; 98WO-US01445.
PF 27-JAN-1997; 97US-0791495.
XX (LUDW-) LUDWIG INST CANCER RES.
XX
PI Boon-Falleur T, De Smet C, Godelaine D, Lethe B;
PI Lucas S;
XX
DR WPI; 1998-427951/36.
DR N-PSDB; AAV50348.

XX New isolated LAGE-1 tumour associated nucleic acids - used to
PT develop products for the diagnosis and treatment of LAGE-1
PT associated disorders, particularly tumours
XX
PS Example 2; Page 57-58; 73pp; English.

XX The present sequence represents human NY-ESO-1, formerly known as LL-1.2
CC clone, which is used in an example from the present invention which
CC describes LAGE-1 tumour associated protein (TAP). The present invention
CC also describes: (1) a method for treating a subject with a disorder
CC characterised by expression of a LAGE-1 nucleic acid molecule or an
CC expression product, comprising administering to the subject autologous
CC cytolytic T cells to ameliorate the disorder, where the cytolytic T
CC cells are specific for complexes of an HLA molecule and a LAGE-1 TAP or
CC an immunogenic fragment; (2) a method for treating a subject with a
CC disorder characterised by expression of a LAGE-1 nucleic acid molecule
CC or an expression product, comprising administering a LAGE-1 TAP or an
CC immunogenic fragment to ameliorate the disorder; and (3) a method for
CC selectively enriching a population of T cells with cytolytic T cells
CC specific for a LAGE-1 TAP comprising contacting an isolated population
CC of T cells with an agent presenting a complex of a LAGE TAP or an
CC immunogenic fragment and a HLA presenting molecule to selectively
CC enrich the isolated population of T cells with the cytolytic T cells.
CC The methods and products from the present invention can be used for the

CC diagnosis and treatment of LAGE-1 associated disorders, particularly
CC tumours.
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 88; DB 19; Length 180;
Best Local Similarity 100.0%; Pred. No. 9.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLTAAADHRQ 18
|||||
Db 127 tvsgniltirltaadhrq 144

RESULT 6
AAW62584
ID AAW62584 standard; Protein; 180 AA.
XX
AC AAW62584;
XX
DT 17-SEP-1998 (first entry)
XX
DE Cancer associated antigen NY-ESO-1.
XX
KW Cancer associated antigen; NY-ESO-1; regression; progression; onset;
KW cancer; treatment; diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 7 /note= "potential myristoylation site"
FT Misc-difference 9 /note= "potential myristoylation site"
FT Misc-difference 11 /note= "potential myristoylation site"
FT Misc-difference 98 /note= "potential phosphorylation site"
FT Misc-difference 134 /note= "potential phosphorylation site"
FT Misc-difference 138 /note= "potential phosphorylation site"
FT /note= "potential phosphorylation site"
XX
PN WO9814464-A1.
XX
PD 09-APR-1998.
XX
PF 15-SEP-1997; 97WO-US16335.
XX
PR 03-OCT-1996; 96US-0725182.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Chen Y, Drijfhout JW, Gure A, Jager E, Knuth A;
PI Old LJ, Scanlan M;
XX
DR WPI; 1998-286417/25.
DR N-PSDB; AAV38566.
XX
PT New isolated cancer associated antigen - is used to develop products
PT for the diagnosis and treatment of cancers and for monitoring cancer
PT therapy
XX
PS Claim 8; Fig 3; 49pp; English.
XX
CC The present sequence represents a cancer associated antigen. The clone
CC from which the DNA sequence is obtained is designated NY-ESO-1. The
CC specification described a method for determining regression, progression
CC of onset of a cancerous condition, comprising monitoring a sample from a
CC patient with the cancerous condition for a parameter selected from
CC NY-ESO-1 protein, a peptide derived from NY-ESO-1 protein and cytolytic
CC T cells specific for the peptide and an MHC molecule with which it

CC non-covalently complexes. Methods for the treatment of a cancerous
CC condition are also described. The NY-ESO-1 protein and peptides derived
CC from it can be used for diagnosis and treatment of cancers and to monitor
CC the efficacy of a therapeutic regime.
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 88; DB 19; Length 180;
Best Local Similarity 100.0%; Pred. No. 9.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLTAAADHRQ 18
|||||
Db 127 tvsgniltirltaadhrq 144

RESULT 7
AAAY05965
ID AAAY05965 standard; Protein; 180 AA.
XX
AC AAAY05965;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 ORF1 protein.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer antigen; human; leukaemia;
KW non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; ORF1.
XX
OS Homo sapiens.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US19609.
XX
PR 08-OCT-1997; 97US-0061428.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rosenberg SA, Wang RF;
XX
DR WPI; 1999-277270/23.
DR N-PSDB; AAX58599.
XX
PT Cancer antigen NY ESO1/CAG-3
XX
PS Claim 4; Fig 3A; 88pp; English.
XX
CC The present sequence represents the ORF1 protein encoded by
CC open reading frame 1 of the human ESO-1/CAG-3 (or CAG-3) gene.
CC CAG-3 is a new and potent tumour antigen capable of eliciting an
CC antigen specific immune response by T cells. Cancer peptides
CC comprising ORF1, ORF2 (see AAY05966), portions of these peptides and
CC their variants (see AAY05965-87), are useful as cancer vaccines that
CC protect the recipient from development of cancer. The invention
CC provides: vectors and host cells (also useful as vaccines); a
CC method of diagnosis of cancer or precancer; a transgenic animal;
CC antisense oligonucleotides that inhibit expression of the cancer
CC peptide or tumour antigen; antibodies reacting with the CAG-3
CC cancer peptide, useful in diagnostic and detection assays; and
CC methods for preventing or inhibiting cancer by administering a
CC cancer peptide, with or without an HLA molecule. The cancer
CC peptides form part of, or are derived from, cancers such as primary
CC or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer,
CC liver cancer, leukaemia, uterine cancer, cervical cancer, bladder

CC cancer, kidney cancer and adenocarcinomas such as breast, prostate,
CC ovarian, pancreatic and thyroid cancers. Melanoma is treated by
CC inducing cancer-specific T cells in vitro for subsequent return to
CC a patient.
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 88; DB 20; Length 180;
Best Local Similarity 100.0%; Pred. No. 9.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNILTIRLTAADHRQ 18
Db 127 tvsgniltirltaadhrq 144

RESULT 8
AAB03154
ID AAB03154 standard; Protein; 180 AA.
XX
AC AAB03154;
XX
DT 23-OCT-2000 (first entry)
XX
DE Human oesophageal cancer-associated antigen NY-ESO-1.
XX
KW Oesophageal cancer associated antigen; NY-ESO-1; human;
KW immunogen; oesophageal carcinoma; melanoma; ovary; testis;
KW transmembrane domain; antibody; diagnostic marker; drug delivery target.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 7
FT Modified-site /note= "Potential N-myristoylation site"
FT Modified-site 9
FT Modified-site /note= "Potential N-myristoylation site"
FT Modified-site 11
FT Modified-site /note= "Potential O-phosphorylation site"
FT Modified-site 98
FT Modified-site /note= "Potential O-phosphorylation site"
FT Modified-site 134
FT Modified-site /note= "Potential O-phosphorylation site"
FT Modified-site 138
FT Modified-site /note= "Potential O-phosphorylation site"
FT Domain 152..172
FT /note= "Potential transmembrane domain"
XX
PN US6069233-A.
XX
PD 30-MAY-2000.
XX
PF 26-JAN-1998; 98US-0013150.
XX
PR 03-OCT-1996; 96US-0725381.
XX
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Scanlan M, Gure AO, Chen Y, Tureci O, Sahin U, Pfreundschuh M;
PI Old LJ;
XX
DR WPI; 2000-410880/35.
DR N-PSDB; AAA61483.
XX
PT New isolated esophageal cancer-associated antigen useful as markers for
PT producing antibodies and as targets for identifying abnormal
PT conditions, e.g. infections and cancer -
XX
PS Example 5; Fig 3; 9pp; English.
XX

CC This sequence represents a human oesophageal cancer-associated antigen,
CC NY-ESO-1. The cDNA encoding this sequence was isolated from a
CC cDNA library prepared from a specimen of well-to-moderately
CC differentiated squamous cell cancer of the oesophagus. Expression
CC analysis demonstrated that NY-ESO-1 was expressed in oesophageal
CC carcinoma, certain melanoma cell lines and in normal ovary and testis
CC tissue, but not in normal colon, kidney, liver or brain tissue. Analysis
CC of the amino acid sequence of the protein indicates that the protein has
CC a transmembrane domain, several N-myristoylation sites and
CC O-phosphorylation sites and that it contains antigenic sequences in the
CC N-terminal half of the protein. The antigen is useful as an immunogen
CC when combined with an adjuvant, in both precursor and post-
CC translationally modified forms, and may be used to generate anti-NY-ESO-1
CC antibodies. It can also be used as a diagnostic marker for oesophageal
CC cancer, and can be utilised as a marker for the targetted delivery of
CC therapeutic agents to oesophageal cancer cells. It can also be used to
CC generate diagnostic or therapeutic agents.
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 88; DB 21; Length 180;
Best Local Similarity 100.0%; Pred. No. 9.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNILTIRLTAADHRQ 18
Db 127 tvsgniltirltaadhrq 144

RESULT 9
AAY70862
ID AAY70862 standard; Protein; 180 AA.
XX
AC AAY70862;
XX
DT 31-JUL-2000 (first entry)
XX
DE Human tumour antigen, NY-ESO-1 protein.
XX
KW NY-ESO-1; CAMEL; CTL-recognised Antigen on MELanoma; human; cancer; CTL;
KW cytotoxic T lymphocyte; tumour-associated antigen; LAGE-1; anticancer;
KW melanoma; immunotherapy; immune response.
XX
OS Homo sapiens.
XX
PN WO200023584-A1.
XX
PD 27-APR-2000.
XX
PF 15-OCT-1999; 99WO-EP07832.
XX
PR 16-OCT-1998; 98EP-0119583.
XX
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
PA (UYHO-) UNIV HOSPITAL LEIDEN.
XX
PI Schrier PI, Aarnoudse CA, Helder K, Klade C;
XX
DR WPI; 2000-339685/29.
DR N-PSDB; AAD00152.
XX
PT Tumor-associated antigen useful for cancer immunotherapy is encoded by
PT the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA -
XX
PS Example 3; Page 62-63; 73pp; English.
XX
CC The present sequence is the human NY-ESO-1 protein, a tumour antigen,
CC identified by screening an esophagus carcinoma cDNA library. This protein
CC is derived from open reading frame (ORF)-1 that contain epitopes of
CC tumour specific T-cells. NY-ESO-1 is expressed in different tumour types,
CC but not in healthy tissues except in testis. It also shows homology with
CC the CAMEL (Cytotoxic T lymphocytes (CTL)-recognised Antigen on MELanoma)
CC

CC protein, a tumour-associated antigen. The tumour-associated antigen
CC displayed on melanoma cells is recognised by cytotoxic T lymphocytes.
CC This sequence has anticancer activity. CAMEL tumour antigen and
CC immunogenic peptides derived from it are useful for cancer immunotherapy.
CC They have the potential to induce an immune response, by eliciting a
CC CTL response. The DNA molecule is used for the construction of
CC recombinant or fusion proteins.
XX

.SQ Sequence 180 AA;

Query Match 100.0%; Score 88; DB 21; Length 180;
Best Local Similarity 100.0%; Pred. No. 9.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNILTIRLTAAADHRQ 18
|||||
Db 127 tvsgniltirлтаадhrq 144

RESULT 10
AAV52430
ID AAV52430 standard; Protein; 180 AA.

XX AAV52430;

XX 15-FEB-2000 (first entry)

DE Human tumour antigen NY-ESO-1.

XX Cancer; tumour; antigen; MHC; major histocompatibility complex;
KW T-cell; cytotoxic; helper; stimulation; proliferation; treatment;
KW diagnosis; prevention; melanoma; breast cancer; ovarian cancer;
KW prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer;
KW lymphoma.

XX Homo sapiens.

FH Key Location/Qualifiers
FT Peptide 44..53
FT /note= "Peptide presented by MHC Class I HLA-B7"
FT Peptide 60..68
FT /note= "Peptide presented by MHC Class I HLA-B7"
FT Peptide 60..69
FT /note= "Peptide presented by MHC Class I HLA-B7"
FT Peptide 63..72
FT /note= "Peptide presented by MHC Class I HLA-B7"
FT Peptide 79..87
FT /note= "Peptide presented by MHC Class I HLA-B7, HLA-B8
FT and HLA-B35"
FT Peptide 79..88
FT /note= "Peptide presented by MHC Class I HLA-B7"
FT Peptide 82..90
FT /note= "Peptide presented by MHC Class I HLA-A1"
FT Peptide 82..91
FT /note= "Peptide presented by MHC Class I HLA-A1"
FT Peptide 83..91
FT /note= "Peptide presented by MHC Class I HLA-B44"
FT Peptide 84..92
FT /note= "Peptide presented by MHC Class I HLA-B7, HLA-B8
FT and HLA-B35"
FT Peptide 87..96
FT /note= "Peptide presented by MHC Class I HLA-A1"
FT Peptide 88..96
FT /note= "Peptide presented by MHC Class I HLA-B44"
FT Peptide 96..104
FT /note= "Peptide presented by MHC Class I HLA-B7"
FT Peptide 100..108
FT /note= "Peptide presented by MHC Class I HLA-B44"
FT Peptide 102..110
FT /note= "Peptide presented by MHC Class I HLA-B44"
FT Peptide 107..116
FT /note= "Peptide presented by MHC Class I HLA-A24"

"

FT Peptide 110..118
FT /note= "Peptide presented by MHC Class I HLA-B52"
FT Peptide 113..121
FT /note= "Peptide presented by MHC Class I HLA-B7"
FT Peptide 113..122
FT /note= "Peptide presented by MHC Class I HLA-B7 and
FT HLA-B52"
FT Peptide 115..124
FT /note= "Peptide presented by MHC Class I HLA-A3"
FT Peptide 118..126
FT /note= "Peptide presented by MHC Class I HLA-B35"
FT Peptide 124..133
FT /note= "Peptide presented by MHC Class I HLA-B52"
FT Peptide 125..133
FT /note= "Peptide presented by MHC Class I HLA-A24"
FT Peptide 138..147
FT /note= "Peptide presented by MHC Class I HLA-B8"
FT Peptide 139..147
FT /note= "Peptide presented by MHC Class I HLA-B7"
FT Peptide 145..153
FT /note= "Peptide presented by MHC Class I HLA-A24 and
FT HLA-B52"
FT Peptide 153..162
FT /note= "Peptide presented by MHC Class I HLA-B52"
FT Peptide 154..162
FT /note= "Peptide presented by MHC Class I HLA-B52"
FT Peptide 154..163
FT /note= "Peptide presented by MHC Class I HLA-B52"
FT Peptide 156..167
FT /note= "Peptide (AAV52434) presented by MHC Class I
FT HLA-A2" Peptide 158..166
FT /note= "Peptide presented by MHC Class I HLA-A3"
FT Peptide 159..167
FT /note= "Peptide presented by MHC Class I HLA-A3"
FT Peptide 162..170
FT /note= "Peptide presented by MHC Class I HLA-B52"
FT

WO9953938-A1.

28-OCT-1999.

24-MAR-1999; 99WO-US06875.

17-APR-1998; 98US-0062422.

02-OCT-1998; 98US-0165546.

(LUDW-) LUDWIG INST CANCER RES.

Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
Gure A, Ritter G;

WPI; 2000-038483/03.

N-PSDB; AAZ38380.

Novel peptides which bind to MHC class I and MHC class II molecules,
useful for therapeutic and diagnostic purposes -

Claim 30; Fig 3; 49pp; English.

This sequence represents a human tumour antigen, NY-ESO-1, the cDNA
encoding which was isolated from an oesophagus squamous cell cancer cDNA
library. Tissue localisation studies revealed it to be expressed at
high levels in normal ovary and testis but not in normal colon, kidney,
liver, brain, oesophagus and skin. It was expressed in certain tumours
and tumour cell lines with some degree of frequency - these included
melanoma specimens and cell lines, and breast and bladder cancer
specimens, with expression in other tumour types being sporadic.

Peptides derived from NY-ESO-1 are bound by both MHC (major
histocompatibility complex) Class I and Class II molecules for
presentation to T-cells. Peptides AAV52431-Y52434 bind to Class I HLA-A2
molecules, thereby stimulating proliferation of cytotoxic T-cells, while
peptides AAV52435-Y52440 bind to Class II HLA-DR53 molecules, stimulating
helper T-cell proliferation. The peptides derived from NY-ESO-1 may be

CC used in methods and compositions used for the treatment, diagnosis and
CC prevention of cancers (such as melanoma, breast cancer, prostate cancer,
CC lung cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer,
CC or lymphoma) and to stimulate the proliferation of T cells.
XX

SQ Sequence 180 AA;

Query Match 100.0%; Score 88; DB 21; Length 180;
Best Local Similarity 100.0%; Pred. No. 9.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNILTIRLTAADHRQ 18
|||||
Db 127 tvsgniltirltaadhrq 144

RESULT 11
AAG67164
ID AAG67164 standard; Protein; 180 AA.

XX
AC AAG67164;

XX
DT 13-NOV-2001 (first entry)

XX Amino acid sequence of cancer testis tumour antigen NY-ESO-1.

KW Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;
KW HLA; HLA binding peptide; major histocompatibility complex; MHC;
KW tumour; cancer; testis tumour.

XX Homo sapiens.

XX WO200162917-A1.

XX 30-AUG-2001.

XX 22-JAN-2001; 2001WO-US02126.

XX 22-FEB-2000; 2000US-0510635.

XX (LUDW-) LUDWIG INST CANCER RES.

PI Lethe B, Boon-Falleur T;

XX WPI; 2001-550091/61.

DR N-PSDB; AAH75118.

XX Genomic sequences of tumour associated antigen EY-ESO-1 (LAGE-2) useful
PT for diagnosing testicular tumours -

XX Example 5; Fig 3; 50pp; English.

CC The present sequence represents cancer testis tumour antigen NY-ESO-1
CC (also called LAGE-2). NY-ESO-1 is a molecule that is processed to at
CC least one human leukocyte antigen (HLA) binding peptide, which binds
CC to Class I and Class II major histocompatibility complex (MHC).
CC NY-ESO-1 is expressed in tumour mRNA and in testis, but not normal
CC colon, kidney, liver or brain tissue. The presence or level of expression
CC of NY-ESO-1 may be assayed for the diagnosis of cancer, especially
CC testis tumours.

XX Sequence 180 AA;

Query Match 100.0%; Score 88; DB 22; Length 180;
Best Local Similarity 100.0%; Pred. No. 9.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNILTIRLTAADHRQ 18
|||||
Db 127 tvsgniltirltaadhrq 144

RESULT 12
AAE07714
ID AAE07714 standard; Protein; 180 AA.

XX
AC AAE07714;

XX
DT 06-NOV-2001 (first entry)

XX Human NY ESO-1 protein.

KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.

XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers

FT Misc-difference 45..47
FT /note= "Encoded by CCCGGGGC"

XX WO200155393-A2.

XX 02-AUG-2001.

XX 26-JAN-2001; 2001WO-US02765.

XX 28-JAN-2000; 2000US-0179004.

XX 29-SEP-2000; 2000US-0237107.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang R, Rosenberg SA, Zeng G;

XX WPI; 2001-496851/54.

DR N-PSDB; AAD14179, AAD14180.

XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -

XX Example 1; Fig 1; 134pp; English.

XX The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or haptens and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is
CC human NY ESO-1 protein.

XX Sequence 180 AA;

Query Match 100.0%; Score 88; DB 22; Length 180;
Best Local Similarity 100.0%; Pred. No. 9.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNILTIRLTAADHRQ 18
|||||
Db 127 tvsgniltirltaadhrq 144

RESULT 13
AAU01535
ID AAU01535 standard; Protein; 180 AA.
XX
AC AAU01535;
XX
DT 18-JUL-2001 (first entry)
DE
DE Human NY-ESO-1 tumour rejection antigen precursor protein.
XX
KW NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
KW human leukocyte antigen-determining region; disease progression;
KW disease regression; disease onset; body tissue; body fluid; enzyme label;
KW radioactive label; monoclonal antibody.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 7 /note= "Myristoylated"
FT Modified-site 9 /note= "Myristoylated"
FT Modified-site 11 /note= "Phosphorylated"
FT Modified-site 98 /note= "Phosphorylated"
FT Modified-site 134 /note= "Phosphorylated"
FT Modified-site 138 /note= "Phosphorylated"
FT Modified-site 138 /note= "Phosphorylated"
XX
PN WO200123560-A2.
XX
PD 05-APR-2001.
XX
PF 26-SEP-2000; 2000WO-US26411.
XX
PR 29-SEP-1999; 99US-0408036.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PI Tureci O, Sahin U, Pfreundschuh M;
XX
DR WPI; 2001-266156/27.
DR N-PSDB; AAS02254.
XX
PT Polypeptides binding to major histocompatibility complex class II human
PT leukocyte antigen-determining region molecule having amino acid
PT sequence found in tumour rejection antigen precursor used for
PT stimulating proliferation of helper T cells -
XX
PS Claim 4; Fig 3; 62pp; English.
XX
CC The sequence represents a human NY-ESO-1 tumour rejection antigen
CC precursor. NY-ESO-1 and SSX-2 polypeptides, or fragments of, bind to
CC major histocompatibility complex (MHC) Class II molecules such as human
CC leukocyte antigen-determining region (HLA-DR) molecules and stimulate
CC proliferation of helper T cells. The peptides can be administered to an
CC HLA-DR positive subject in order to stimulate the helper T cells. An MHC
CC Class II HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell
CC or present in free form is useful for this stimulation. The nucleic acid
CC is useful for screening for a cancerous condition, which involves
CC contacting a subject sample to a cell line transfected with the
CC immunoreactive cell (helper T cell), where interaction is indicative of
CC cancer. In addition, a sample from a patient (for example, a body fluid
CC or tissue) can be monitored for the amount of the complex present in the
CC bloodstream. This is useful for determining regression, progression or
CC onset of a cancerous condition. The method involves contacting the sample
CC with a radioactive labelled or enzyme labelled monoclonal antibody which
CC specifically binds with the complex.

XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 88; DB 22; Length 180;
Best Local Similarity 100.0%; Pred. No. 9.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLTAAADHRQ 18
Db 127 tvsgnltirltaadhrq 144
|||||

RESULT 14
AAB69946
ID AAB69946 standard; Protein; 180 AA.
XX
AC AAB69946;
XX
DT 27-APR-2001 (first entry)
XX
DE Human NY-ESO-1 protein.
XX
KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW non-small cell lung carcinoma; tumour status determination.
XX
OS Homo sapiens.
XX
PN WO200107917-A1.
XX
PD 01-FEB-2001.
XX
PF 14-JUL-2000; 2000WO-US19220.
XX
PR 23-JUL-1999; 99US-0359503.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.
XX
PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
XX
DR WPI; 2001-182822/18.
DR N-PSDB; AAF58634.
XX
PT Method useful for determining the status (e.g. progression, regression
PT or stability of the disease) of a cancerous condition, involves
PT determining the levels of NY-ESO-1 specific antibodies in a sample
PT taken from a patient -
XX
PS Example 5; Fig 3; 50pp; English.
XX
CC The present sequence is human NY-ESO-1 protein. It is provided in a
CC specification relating to a method for determining the status of a
CC cancerous condition in a patient with a tumour that expresses NY-ESO-1.
CC The method comprises assaying a sample taken from the patient for
CC antibodies that specifically bind to the NY-ESO-1 and comparing the
CC value obtained to a prior value obtained from assay of a prior sample
CC taken from the patient. Any difference between the values is indicative
CC of a change in status of the cancerous condition. The method is useful
CC for determining whether a cancerous condition is progressing, regressing
CC or remaining stable, in particular in patients receiving treatment for a
CC melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder
CC carcinoma.
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 88; DB 22; Length 180;
Best Local Similarity 100.0%; Pred. No. 9.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNILTIRLTAADHRQ 18
| | | | | | | | | | | | | |
Db 127 tvsgniltirltaadhrq 144

RESULT 15
AAE13122
ID AAE13122 standard; Protein; 397 AA.
XX
AC AAE13122;
XX
DT 28-JAN-2002 (first entry)
XX
DE NY-ESO-IC-HER-2 membrane distal intracellular domain fusion protein.
XX
KW Immunostimulatory fusion protein; IFP; antigen component; therapy;
KW immunostimulatory component; T-cell mediated immune response; DC;
KW dendritic cell; colon cancer; breast carcinoma; ovarian cancer;
KW human; HER-2 membrane distal intracellular domain; NY-ESO-IC;
KW autoimmunogenic cancer/testis antigen.
XX

OS Homo sapiens.
XX
PN WO200174855-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US10515.
XX
PR 30-MAR-2000; 2000US-193504P.
XX
PA (DEND-) DENDREON CORP.
XX
PI Laus R, Vidovic D, Graddis T;
XX
DR WPI; 2001-662965/76.
DR N-PSDB; AAD21573.
XX

An immunostimulatory fusion protein comprising the intracellular domain of HER-2 and an antigen elicits an immune response to the antigen and is useful for the treatment of associated cancer associated -

PS Disclosure; Page 54-55; 59pp; English.
XX
CC The invention relates to immunostimulatory fusion proteins (IFP) and
CC nucleic acid molecules encoding such proteins. The IFPs comprise a
CC polypeptide antigen component and an immunostimulatory component derived
CC from the intracellular domain of HER-2 protein which is effective to
CC elicit a protective dendritic cell (DC)-induced T-cell mediated cellular
CC immune response to the antigen. IFP or superactivated dendritic cells
CC are used to treat cancer e.g. breast carcinoma, ovarian and colon cancer
CC associated with a particularly antigen. The present sequence is a
CC fusion protein which comprises human autoimmunogenic
CC cancer/testis antigen, NY-ESO-IC and mature human HER-2 membrane distal
CC intracellular domain.
XX
SQ Sequence 397 AA;

Query Match 100.0%; Score 88; DB 22; Length 397;
Best Local Similarity 100.0%; Pred. NO. 2.7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNILTIRLTAADHRQ 18
| | | | | | | | | | | | | |
Db 127 tvsgniltirltaadhrq 144

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:21:01 ; Search time 599.92 Seconds
(without alignments)
10.561 Million cell updates/sec

Title: US-09-165-546A-13

Perfect score: 88

Sequence: 1 TVSGNLTIRLTAAADHRQ 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

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- 2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US080_COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US081_COMB.pep.*
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- 7: /cgn2_6/ptodata/2/paa/US083_COMB.pep.*
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- 9: /cgn2_6/ptodata/2/paa/US085_COMB.pep.*
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- 25: /cgn2_6/ptodata/2/paa/US101_COMB.pep.*
- 26: /cgn2_6/ptodata/2/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	100.0	18	15	US-09-165-546A-13
2	88	100.0	18	18	US-09-408-036B-12
3	88	100.0	180	11	US-08-791-495-9
4	88	100.0	180	17	US-09-341-829A-9
5	88	100.0	180	17	US-09-392-714-25
6	88	100.0	180	19	US-09-529-206-4
7	88	100.0	180	19	US-09-529-206A-3

8	88	100.0	180	19	US-09-529-206B-3	Sequence 3, Appli
9	88	100.0	180	19	US-09-561-571-3	Sequence 3, Appli
10	88	100.0	180	21	US-09-751-798-8	Sequence 8, Appli
11	88	100.0	180	24	US-10-005-905-3	Sequence 3, Appli
12	88	100.0	180	24	US-10-023-182-8	Sequence 8, Appli
13	88	100.0	180	24	US-10-026-066-3	Sequence 3, Appli
14	88	100.0	180	26	US-60-336-968-11	Sequence 11, Appli
15	88	100.0	397	22	US-09-821-883-27	Sequence 27, Appli
16	79	89.8	180	11	US-08-791-495-7	Sequence 7, Appli
17	79	89.8	180	17	US-09-341-829A-7	Sequence 7, Appli
18	71.5	81.2	122	26	US-60-336-968-17	Sequence 17, Appli
19	56	63.6	18	15	US-09-165-546A-9	Sequence 9, Appli
20	56	63.6	18	18	US-09-408-036B-8	Sequence 8, Appli
21	51	58.0	61	19	US-09-529-206-55	Sequence 55, Appli
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24	50	56.8	10	19	US-09-529-206-16	Sequence 16, Appli
25	50	56.8	10	19	US-09-529-206-85	Sequence 85, Appli
26	50	56.8	10	19	US-09-529-206A-16	Sequence 16, Appli
27	50	56.8	10	19	US-09-529-206A-85	Sequence 85, Appli
28	50	56.8	10	19	US-09-529-206B-16	Sequence 16, Appli
29	50	56.8	10	19	US-09-529-206B-85	Sequence 85, Appli
30	50	56.8	86	26	US-60-170-346-1371	Sequence 1371, Ap
31	50	56.8	108	26	US-60-164-763-893	Sequence 893, App
32	50	56.8	108	26	US-60-169-842-4570	Sequence 4570, Ap
33	49	55.7	10	19	US-09-529-206-104	Sequence 104, App
34	49	55.7	10	19	US-09-529-206A-104	Sequence 104, App
35	49	55.7	10	19	US-09-529-206B-104	Sequence 104, App
36	47	53.4	10	19	US-09-529-206-15	Sequence 15, Appli
37	47	53.4	10	19	US-09-529-206-84	Sequence 84, Appli
38	47	53.4	10	19	US-09-529-206A-15	Sequence 15, Appli
39	47	53.4	10	19	US-09-529-206A-84	Sequence 84, Appli
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41	47	53.4	10	19	US-09-529-206B-84	Sequence 84, Appli
42	47	53.4	99	26	US-60-196-713-2482	Sequence 2482, Ap
43	47	53.4	188	26	US-60-169-867-5669	Sequence 5669, Ap
44	47	53.4	190	26	US-60-160-189-8335	Sequence 8335, Ap
45	47	53.4	190	26	US-60-160-202-3599	Sequence 3599, Ap

ALIGNMENTS

RESULT 1

US-09-165-546A-13

; Sequence 13, Application US/09165546A

; GENERAL INFORMATION:

; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao,

; Canlan, Matt; Gure, Ali, Old, Lloyd, Ritter, Gerd

; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO

; AMINO ACID SEQUENCES OF NY-ESO-1, WHICH BIND TO

; MHC CLASS I AND MHC CLASS II MOLECULES, AND

; USES THEREOF

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FULBRIGHT & JAWORSKI LLP

; STREET: 666 Fifth Avenue

; CITY: New York City

; STATE: New York

; COUNTRY: USA

; ZIP: 10158

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage

; COMPUTER: IBM

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: WordPerfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/165,546A

; FILING DATE: 02-Oct-1998

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/062,422

; FILING DATE: April 17, 1998

APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
APPLICATION NUMBER: US 08/752,182
FILING DATE: 03-October-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, Norman D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-165-546A-13

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Query Match      100.0%; Score 88; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. NO. 9.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 TVSGNLTIRLTAADHRQ 18
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Dd 1 TVSGNLTIRLTAADHRQ 18

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RESULT      2
US-09-408-036B-12
; Sequence 12, Application US/09408036B
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Isolated Peptides Which
; FILE REFERENCE: LUD 5624
; CURRENT APPLICATION NUMBER: US/09/408,036B
; CURRENT FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/165,546
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 12
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-408-036B-12

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Query Match	100.0%;	Score 88;	DB 18;	Length 18;
Best Local Similarity	100.0%;	Pred. No. 9.3e-09;		
Matches 18;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 TVSGNILTIRLTAADHRQ 18
 | | | | | | | | | | | | | | | |
Db 1 TVSGNILTIRLTAADHRQ 18

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RESULT      3
US-08-791-495-9
; Sequence 9, Application US/08791495
; GENERAL INFORMATION:
; APPLICANT: Leth , Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:

```

```

;
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-791-495-9

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Query Match	100.0%;	Score 88;	DB 11;	Length 180;
Best Local Similarity	100.0%;	Pred. No. 1.5e-07;		
Matches 18; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 TVSGNLTIRLTAADHRQ 18
 |||||
Dd 127 TVSGNLTIRLTAADHRQ 144

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RESULT      4
US-09-341-829A-9
; Sequence 9, Application US/09341829A
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-341-829A-9

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Query Match	100.0%;	Score 88;	DB 17;	Length 180;
Best Local Similarity	100.0%;	Pred. No. 1.5e-07;		
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QY 1 TVSGNLTIRLTAAADHRQ 18
 |||||
 Db 127 TVSGNLTIRLTAAADHRQ 144


```
RESULT 5
US-09-392-714-25
; Sequence 25, Application US/09392714A
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Gure, Ali O.
; APPLICANT: Williamson, Barbara
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Cancer Associated Antigens and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: L0461/7062
; CURRENT APPLICATION NUMBER: US/09/392,714A
; EARLIER FILING DATE: 1999-09-09
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-392-714-25

Query Match      100.0%; Score 88; DB 17; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNILTIRLTAADHRQ 18
Db 127 TVSGNILTIRLTAADHRQ 144

RESULT 6
US-09-529-206-4
; Sequence 4, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-4

Query Match      100.0%; Score 88; DB 19; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNILTIRLTAADHRQ 18
Db 127 TVSGNILTIRLTAADHRQ 144

RESULT 7
US-09-529-206A-3
; Sequence 3, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
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; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206A-3

Query Match      100.0%; Score 88; DB 19; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNILTIRLTAADHRQ 18
Db 127 TVSGNILTIRLTAADHRQ 144

RESULT 8
US-09-529-206B-3
; Sequence 3, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-3

Query Match      100.0%; Score 88; DB 19; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNILTIRLTAADHRQ 18
Db 127 TVSGNILTIRLTAADHRQ 144

RESULT 9
US-09-561-571-3
; Sequence 3, Application US/09561571
; GENERAL INFORMATION:
; APPLICANT: CTL Immunotherapies Corp.
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; TITLE OF INVENTION: EPITOPE CLUSTERS
; FILE REFERENCE: CTLIMM.010A
; CURRENT APPLICATION NUMBER: US/09/561,571
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
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; ORGANISM: homo sapiens
US-09-561-571-3

Query Match      100.0%; Score 88; DB 19; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLTAAADHRQ 18
Db 127 TVSGNLTIRLTAAADHRQ 144

RESULT 10
US-09-751-798-8
; Sequence 8, Application US/09751798
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
; APPLICANT: Knuth, Alexander; Old, Lloyd J.
; TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
; TITLE OF INVENTION: Associated Proteins, Uses Thereof,
; TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
; TITLE OF INVENTION: Binding Peptides Derived Therefrom
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09751,798
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
US-09-751-798-8

Query Match      100.0%; Score 88; DB 21; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLTAAADHRQ 18
Db 127 TVSGNLTIRLTAAADHRQ 144

RESULT 11
US-10-005-905-3
; Sequence 3, Application US/10005905
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; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; TITLE OF INVENTION: EPITOPE SYNCHRONIZATION IN ANTIGEN
; TITLE OF INVENTION: PRESENTING CELLS
; FILE REFERENCE: CTLIMM.021CPI
; CURRENT APPLICATION NUMBER: US/10/005,905
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 09/561,074
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/560,465
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,572
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,571
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US01/13806
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-005-905-3

Query Match      100.0%; Score 88; DB 24; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLTAAADHRQ 18
Db 127 TVSGNLTIRLTAAADHRQ 144

RESULT 12
US-10-023-182-8
; Sequence 8, Application US/10023182
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; Chen, Yao-tseng; Scanlan, Matthew;
; Knuth, Alexander; Old, Lloyd J.
; TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
; Associated Proteins, Uses Thereof,
; Truncated Forms of NY-ESO-1, and HLA
; Binding Peptides Derived Therefrom
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/023,182
; FILING DATE: 17-Dec-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/751,798
; FILING DATE: December 29, 2000
; APPLICATION NUMBER: 09/062,422
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
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;; REFERENCE/DOCKET NUMBER: LUD 5466.3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 318-3168
;; TELEFAX: (212) 752-5958
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 180
;; TYPE: amino acid
;; TOPOLOGY: linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-023-182-8

Query Match 100.0%; Score 88; DB 24; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNILTIRLTAADHRQ 18
|||
Db 127 TVSGNILTIRLTAADHRQ 144

RESULT 13
US-10-026-066-3
; Sequence 3, Application US/10026066
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; TITLE OF INVENTION: EPITOPE SYNCHRONIZATION IN ANTIGEN
; TITLE OF INVENTION: PRESENTING CELLS
; FILE REFERENCE: CTIMM.21CP1C
; CURRENT APPLICATION NUMBER: US/10/026,066
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 09/561,074
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/560,465
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,572
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,571
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US01/13806
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-026-066-3

Query Match 100.0%; Score 88; DB 24; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNILTIRLTAADHRQ 18
|||
Db 127 TVSGNILTIRLTAADHRQ 144

RESULT 14
US-60-336-968-11
; Sequence 11, Application US/60336968
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: CTIMM.022PR
; CURRENT APPLICATION NUMBER: US/60/336,968

; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-336-968-11

Query Match 100.0%; Score 88; DB 26; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNILTIRLTAADHRQ 18
|||
Db 127 TVSGNILTIRLTAADHRQ 144

RESULT 15
US-09-821-883-27
; Sequence 27, Application US/09821883
; GENERAL INFORMATION:
; APPLICANT: Laus, Reiner
; APPLICANT: Vidovic, Damir
; APPLICANT: Graddis, Thomas
; TITLE OF INVENTION: Compositions and Methods for Dendritic
; TITLE OF INVENTION: Cell-Based Immunotherapy
; FILE REFERENCE: 7636-0022.30
; CURRENT APPLICATION NUMBER: US/09/821,883
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/193,504
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: NY-ESO-IC tumor antigen
US-09-821-883-27

Query Match 100.0%; Score 88; DB 22; Length 397;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNILTIRLTAADHRQ 18
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Db 127 TVSGNILTIRLTAADHRQ 144

Search completed: July 3, 2002, 11:21:02
Job time: 889 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:22:13 ; Search time 64.42 Seconds
(without alignments)
28.270 Million cell updates/sec

Title: US-09-165-546A-13
Perfect score: 88
Sequence: 1 TVSGNILTIRLTAAADHRQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 308740 seqs, 101176262 residues

Total number of hits satisfying chosen parameters: 308740

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
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3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
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7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	88	100.0	180	1	PCT-US02-13994-30	Sequence 30, Appl
2	88	100.0	180	5	US-09-807-512-8	Sequence 8, Appl
3	88	100.0	180	6	US-10-117-937-74	Sequence 74, Appl
4	79	89.8	180	5	US-09-807-512-4	Sequence 4, Appl
5	79	89.8	180	6	US-10-117-937-75	Sequence 75, Appl
6	79	89.8	180	6	US-10-146-473-69	Sequence 69, Appl
7	46	52.3	28	6	US-10-117-937-254	Sequence 254, App
8	45	51.1	386	7	US-60-360-039-9815	Sequence 9815, Ap
9	44	50.0	309	5	US-09-907-218-69	Sequence 69, Appl
10	44	50.0	309	6	US-10-002-945-99	Sequence 99, Appl
11	44	50.0	327	6	US-10-125-459-8	Sequence 8, Appl
12	44	50.0	453	5	US-09-978-403A-69	Sequence 69, Appl
13	44	50.0	453	5	US-09-978-544A-69	Sequence 69, Appl
14	44	50.0	453	5	US-09-978-681A-69	Sequence 69, Appl
15	44	50.0	453	5	US-09-978-757A-69	Sequence 69, Appl
16	44	50.0	453	5	US-09-978-564A-69	Sequence 69, Appl
17	44	50.0	453	5	US-09-999-831A-69	Sequence 69, Appl
18	44	50.0	453	5	US-09-999-829A-69	Sequence 69, Appl
19	44	50.0	453	5	US-09-978-375A-69	Sequence 69, Appl
20	44	50.0	453	5	US-09-978-423A-69	Sequence 69, Appl
21	44	50.0	453	6	US-10-013-921A-69	Sequence 69, Appl
22	44	50.0	453	6	US-10-013-929A-69	Sequence 69, Appl
23	44	50.0	453	6	US-10-013-918A-69	Sequence 69, Appl
24	44	50.0	453	6	US-10-017-082A-69	Sequence 69, Appl
25	44	50.0	453	6	US-10-121-062-64	Sequence 64, Appl
26	44	50.0	453	6	US-10-017-085A-69	Sequence 69, Appl

27	44	50.0	453	6	US-10-013-916A-69	Sequence 69, Appl
28	44	50.0	453	6	US-10-017-086A-69	Sequence 69, Appl
29	44	50.0	453	6	US-10-013-925A-69	Sequence 69, Appl
30	44	50.0	453	6	US-10-017-081A-69	Sequence 69, Appl
31	44	50.0	453	6	US-10-016-177A-69	Sequence 69, Appl
32	44	50.0	453	6	US-10-017-084A-69	Sequence 69, Appl
33	44	50.0	453	6	US-10-013-923A-69	Sequence 69, Appl
34	43	48.9	130	6	US-10-152-780-247	Sequence 247, App
35	43	48.9	652	1	PCT-US02-09671-942	Sequence 942, App
36	43	48.9	652	1	PCT-US02-09671-971	Sequence 971, App
37	43	48.9	652	1	PCT-US02-09671-975	Sequence 975, App
38	42	47.7	9	5	US-09-344-040C-125	Sequence 125, App
39	42	47.7	9	6	US-10-117-937-185	Sequence 185, App
40	42	47.7	10	6	US-10-117-937-186	Sequence 186, App
41	42	47.7	314	7	US-60-360-039-13230	Sequence 13230, A
42	41	46.6	9	5	US-09-344-040C-121	Sequence 121, App
43	41	46.6	308	1	PCT-US02-09923-40	Sequence 40, Appl
44	41	46.6	315	5	US-09-981-566A-92	Sequence 92, Appl
45	41	46.6	620	7	US-60-360-039-4071	Sequence 4071, Ap

ALIGNMENTS

RESULT 1
PCT-US02-13994-30
; Sequence 30, Application PC/TUS0213994
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research
; APPLICANT: Cornell Research Foundation, Inc.
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd
; APPLICANT: Scanlan, Matthew
; APPLICANT: Stockert, Elisabeth
; TITLE OF INVENTION: COLON CANCER ANTIGEN PANEL
; FILE REFERENCE: L00461/70105WO(JRV)
; CURRENT APPLICATION NUMBER: PCT/US02/13994
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US 09/849,602
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-13994-30

Query Match 100.0%; Score 88; DB 1; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNILTIRLTAAADHRQ 18
|||||
Db 127 TVSGNILTIRLTAAADHRQ 144

RESULT 2
US-09-807-512-8
; Sequence 8, Application US/09807512
; GENERAL INFORMATION:
; APPLICANT: Schrier, Peter I.
; APPLICANT: Aarnoudse, Corlien
; APPLICANT: Heider, Karl-Heinz
; APPLICANT: Klade, Christoph
; TITLE OF INVENTION: Camel, An Alternative Translation Product of the Tumor
; TITLE OF INVENTION: Antigen-Lage 1
; FILE REFERENCE: 0652.220000
; CURRENT APPLICATION NUMBER: US/09/807,512
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: PCT/EP99/07832
; PRIOR FILING DATE: 1999-10-15

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; PRIOR APPLICATION NUMBER: EP 98119583.7
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-807-512-8

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Query Match 100.0%; Score 88; DB 5; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNILTIRLTAAADHRQ 18
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 Db 127 TVSGNILTIRLTAAADHRO 144

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RESULT      3
US-10-117-937-74
; Sequence 74, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-74

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Query Match 100.0%; Score 88; DB 6; Length 180;
Best Local Similarity 100.0%; Pred. NO. 1.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNILTIRLTAAADHRQ 18
 |||||
 Db 127 TVSGNILTIRLTAAADHRQ 144

RESULT 4
US-09-807-512-4
; Sequence 4, Application US/09807512
; GENERAL INFORMATION:
; APPLICANT: Schrier, Peter I.
; APPLICANT: Aarnoudse, Corlien
; APPLICANT: Heider, Karl-Heinz
; APPLICANT: Klade, Christoph
; TITLE OF INVENTION: Camel, An Alternative Translation Product of the Tumor
; TITLE OF INVENTION: Antigen-Lage 1
; FILE REFERENCE: 0652.2200000
; CURRENT APPLICATION NUMBER: US/09/807,512
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: PCT/EP99/07832
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: EP 98119583.7

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; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 180
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-807-512-4

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Query Match 89.8%; Score 79; DB 5; Length 180;
Best Local Similarity 88.9%; Pred. No. 5.8e-07;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY      1 TVSGNLTIRLTAAADHRQ 18
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Db     127 TVSGNLLFIRLTAAADHRO 144
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RESULT          5
US-10-117-937-75
; Sequence 75, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-75

```

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Query Match      89.8%; Score 79; DB 6; Length 180;
Best Local Similarity 88.9%; Pred. No. 5.8e-07;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
Qy 1 TVSGNLTIRLTAAADHRQ 18
    ||||:| |||||
Db 127 TVSGNLLFIRLTAAADHRQ 144
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```

RESULT      6
US-10-146-473-69
; Sequence 69, Application US/10146473
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Gout, Ivan
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Gure, Ali
; APPLICANT: Chen, Yao-Tsung
; APPLICANT: Old, Lloyd
; TITLE OF INVENTION: Breast Cancer Antigens
; FILE REFERENCE: L00461/70130(JRV)
; CURRENT APPLICATION NUMBER: US/10/146,473
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/291,150
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 82

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 69
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-473-69

Query Match 89.8%; Score 79; DB 6; Length 180;
Best Local Similarity 88.9%; Pred. No. 5.8e-07;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLTAADHRQ 18
|||||:| |||||
Db 127 TVSGNLLFIRLTAADHRQ 144

RESULT 7
US-10-117-937-254
; Sequence 254, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 254
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-254

Query Match 52.3%; Score 46; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.082;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 RLTAADHRQ 18
|||||
Db 1 RLTAADHRQ 9

RESULT 8
US-60-360-039-9815
; Sequence 9815, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 9815
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Desulfitobacterium hafniense

US-60-360-039-9815

Query Match 51.1%; Score 45; DB 7; Length 386;
Best Local Similarity 43.8%; Pred. No. 2.8;
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLTAADH 16
|::|||:::| |
Db 250 TLSGVMTVSVTTAEH 265

RESULT 9
US-09-907-218-69
; Sequence 69, Application US/09907218
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Patturajan, Meera
; APPLICANT: Taillon, Bruce
; APPLICANT: Casman, Stacie J
; APPLICANT: Wolenc, Adam Ryan
; APPLICANT: Li, Li
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly Ann
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-061
; CURRENT APPLICATION NUMBER: US/09/907,218
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/218,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/260,977
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/263,801
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/268,226
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/271,622
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 69
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-907-218-69

Query Match 50.0%; Score 44; DB 5; Length 309;
Best Local Similarity 43.8%; Pred. No. 3.3;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLTAADH 16
|::|||:::| |
Db 38 TLAGNIIIVTITHIDH 53

RESULT 10
US-10-002-945-99
; Sequence 99, Application US/10002945
; GENERAL INFORMATION:
; APPLICANT: Grosse, William
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Alsobrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Edinger, Shlomit


```
; APPLICANT: Gangolli, Esha A
; APPLICANT: Gorman, Linda
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Fernandes, Elma R
; APPLICANT: Vernet, Corine A M
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Casman, Stacie J
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Mishra, Vishnu
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Baumgartner, Jason C
; APPLICANT: Colman, Steven D
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-206
; CURRENT APPLICATION NUMBER: US/10/002,945
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 60/245,291
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: 60/245,317
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: 60/246,562
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: 60/246,871
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/264,389
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/264,423
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/264,799
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-002-945-99
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Query Match 50.0%; Score 44; DB 6; Length 309;
Best Local Similarity 43.8%; Pred. No. 3.3;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLTAAHD 16
I::I::: : : I I
Db 38 TLAGNIIIVTITHIDH 53

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RESULT 11
US-10-125-459-8
; Sequence 8, Application US/10125459
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Serine proteases
; CURRENT APPLICATION NUMBER: US/10/125,459
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US/09/597,839
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: 60/133,239
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/135,163
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 60/147,005
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/152,935
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 60/162,979
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 8
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-459-8
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Query Match 50.0%; Score 44; DB 6; Length 327;
Best Local Similarity 43.8%; Pred. No. 3.5;
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 3 SGNLTIRLTAAADHRQ 18
I::I::: I I
Db 69 SGHVVTLQCTACGHR 84

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RESULT 12
US-09-978-403A-69
; Sequence 69, Application US/09978403A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC17
; CURRENT APPLICATION NUMBER: US/09/978,403A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
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Query Match 50.0%; Score 44; DB 5; Length 453;
Best Local Similarity 43.8%; Pred. No. 5.1;
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 3 SGNLTIRLTAAADHRQ 18
||::|::|||
Db 196 SGHVVTLOCTACGHR 211

RESULT 13

US-09-978-544A-69
; Sequence 69, Application US/09978544A

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2630P1C13

; CURRENT APPLICATION NUMBER: US/09/978,544A

; CURRENT FILING DATE: 2002-03-19

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/064249

; PRIOR FILING DATE: 1997-11-03

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066364

; PRIOR FILING DATE: 1997-11-21

; PRIOR APPLICATION NUMBER: 60/077450

; PRIOR FILING DATE: 1998-03-10

; PRIOR APPLICATION NUMBER: 60/077632

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077641

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077649

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077791

; PRIOR FILING DATE: 1998-03-12

; PRIOR APPLICATION NUMBER: 60/078004

; PRIOR FILING DATE: 1998-03-13

; PRIOR APPLICATION NUMBER: 60/078886

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/078936

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/078910

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/083336

; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083392
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083554
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083558
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15

Query Match 50.0%; Score 44; DB 5; Length 453;
Best Local Similarity 43.8%; Pred. No. 5.1;
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 3 SGNILTRLTAADHRQ 18

||||:|:|

Db 196 SGHVVTLQCTACGHR 211

RESULT 14

US-09-978-681A-69
; Sequence 69, Application US/09978681A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C18
; CURRENT APPLICATION NUMBER: US/09/978,681A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
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; PRIOR APPLICATION NUMBER: 60/077632
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; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664

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; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/079923
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/080105
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081071
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081952
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082700
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
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; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: 60/083336
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
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; PRIOR FILING DATE: 1998-04-29
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; PRIOR FILING DATE: 1998-05-15

Query Match 50.0%; Score 44; DB 5; Length 453;
Best Local Similarity 43.8%; Pred. No. 5.1;
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 3 SGNILTIRLTAADHRQ 18
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Db 196 SGHVVTLOCTACGHR 211

RESULT 15
US-09-978-757A-69
; Sequence 69, Application US/09978757A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C26
; CURRENT APPLICATION NUMBER: US/09/978,757A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15

Query Match 50.0%; Score 44; DB 5; Length 453;
Best Local Similarity 43.8%; Pred. No. 5.1;
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 3 SGNILTIRLTAADHRQ 18
|::|::| |
Db 196 SGHVVTLQCTACGHR 211

Search completed: July 3, 2002, 11:22:14
Job time: 946 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:09:48 ; Search time 49.27 Seconds
(without alignments)
8.923 Million cell updates/sec

Title: US-09-165-546A-13
Perfect score: 88
Sequence: 1 TVSGNILTIRLFAADHRQ 18

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Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	88	100.0	180	4	US-08-937-263B-8
4	79	89.8	180	2	US-08-791-495-7
5	56	63.6	18	4	US-09-359-503-9
6	46	52.3	327	4	US-08-748-506-14
7	46	52.3	327	4	US-08-748-506-22
8	46	52.3	327	4	US-08-748-506-23
9	44	50.0	294	4	US-09-518-046-4
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11	44	50.0	455	4	US-09-261-416-2
12	42	47.7	327	4	US-08-748-506-24
13	39	44.3	597	2	US-08-883-534-6
14	39	44.3	597	3	US-09-204-764-6
15	38	43.2	479	1	US-08-416-788-2
16	37	42.0	4928	4	US-09-036-987A-5
17	37	42.0	4928	4	US-09-370-700-5
18	36	40.9	134	1	US-08-328-152A-13
19	36	40.9	222	1	US-08-328-152A-8
20	36	40.9	240	1	US-07-940-861-12
21	36	40.9	240	1	US-08-459-512-12
22	36	40.9	240	2	US-08-459-657-12
23	36	40.9	240	2	US-08-460-132-12
24	36	40.9	240	4	US-08-466-465-4
25	36	40.9	240	5	PCT-US92-02050-12
26	36	40.9	240	6	5185441-36
27	36	40.9	240	6	5223394-4

28	36	40.9	240	6	5223394-6	Patent No. 5223394
29	36	40.9	250	1	US-07-940-861-10	Sequence 10, Appl
30	36	40.9	250	1	US-08-459-512-10	Sequence 10, Appl
31	36	40.9	250	2	US-08-459-657-10	Sequence 10, Appl
32	36	40.9	250	2	US-08-460-132-10	Sequence 10, Appl
33	36	40.9	250	4	US-08-466-465-2	Sequence 2, Appl
34	36	40.9	250	5	PCT-US92-02050-10	Sequence 10, Appl
35	36	40.9	250	6	5223394-1	Patent No. 5223394
36	36	40.9	251	6	5185441-38	Patent No. 5185441
37	36	40.9	291	2	US-08-560-098A-55	Sequence 55, Appl
38	36	40.9	313	1	US-08-592-411-15	Sequence 15, Appl
39	36	40.9	314	1	US-08-592-411-17	Sequence 17, Appl
40	36	40.9	347	1	US-07-940-861-43	Sequence 43, Appl
41	36	40.9	347	1	US-08-459-512-43	Sequence 43, Appl
42	36	40.9	347	2	US-08-459-657-43	Sequence 43, Appl
43	36	40.9	347	2	US-08-460-132-43	Sequence 43, Appl
44	36	40.9	347	4	US-08-466-465-8	Sequence 8, Appl
45	36	40.9	347	5	PCT-US92-02050-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-09-359-503-13
; Sequence 13, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid

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; TOPOLOGY: linear
US-09-359-503-13

Query Match 100.0%; Score 88; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 7e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNILTIRLTAADHRQ 18
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Db 1 TVSGNILTIRLTAADHRQ 18

RESULT 2
US-08-791-495-9
; Sequence 9, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth , Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-9

Query Match 100.0%; Score 88; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNILTIRLTAADHRQ 18
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Db 127 TVSGNILTIRLTAADHRQ 144

RESULT 3
US-08-937-263B-8
; Sequence 8, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
; APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
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; APPLICANT: Alexander, Knuth; Drijfhout, Jan W.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
; TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
; TITLE OF INVENTION: ITSELF, AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,263B
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sinn, Eric, Patent Agent
; REGISTRATION NUMBER: 40,177
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
US-08-937-263B-8

Query Match 100.0%; Score 88; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNILTIRLTAADHRQ 18
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RESULT 4
US-08-791-495-7
; Sequence 7, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth , Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-9

Query Match 100.0%; Score 88; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
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QY 1 TVSGNILTIRLTAADHRQ 18
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Db 127 TVSGNILTIRLTAADHRQ 144

RESULT 3
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; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
; APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
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;; FILING DATE: 435
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Van Amsterdam, John R.
;; REGISTRATION NUMBER: 40,212
;; REFERENCE/DOCKET NUMBER: L0461/7005
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-720-3500
;; TELEFAX: 617-720-2441
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 180 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-791-495-7

Query Match 89.8%; Score 79; DB 2; Length 180;
Best Local Similarity 88.9%; Pred. No. 5.7e-07;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLTAAADHRQ 18
 |||||:|||||
Db 127 TVSGNLTIRLTAAADHRQ 144

RESULT 5
US-09-359-503-9
; Sequence 9, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958

;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
US-09-359-503-9

Query Match 63.6%; Score 56; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLT 12
 |||||
Db 7 TVSGNLTIRLT 18

RESULT 6
US-08-748-506-14
; Sequence 14, Application US/08748506
; Patent No. 6159707
; GENERAL INFORMATION:
; APPLICANT: Ronnett et al.
; TITLE OF INVENTION: NOVEL SPERM RECEPTORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: US
; ZIP: 60601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,506
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,751
; FILING DATE: 09-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 74940
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5600
; TELEFAX: 312-616-5700
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 327 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-748-506-14

Query Match 52.3%; Score 46; DB 4; Length 327;
Best Local Similarity 47.1%; Pred. No. 1.3;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLTAAADHR 17
 ::|||:|:|
Db 44 SLGMNMLIITITCVDHR 60

RESULT 7
US-08-748-506-22
; Sequence 22, Application US/08748506
; Patent No. 6159707

```

;
; GENERAL INFORMATION:
; APPLICANT: Ronnett et al.
; TITLE OF INVENTION: NOVEL SPERM RECEPTORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: US
; ZIP: 60601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,506
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,751
; FILING DATE: 09-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 74940
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5600
; TELEFAX: 312-616-5700
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 327 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-748-506-22

Query Match 52.3%; Score 46; DB 4; Length 327;
Best Local Similarity 47.1%; Pred. No. 1.3;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLTAADHR 17
   ::||:| | :| |||
Db 44 SLMGNMLIITITCVDHR 60

RESULT 8
US-08-748-506-23
; Sequence 23, Application US/08748506
; Patent No. 6159707
; GENERAL INFORMATION:
; APPLICANT: Ronnett et al.
; TITLE OF INVENTION: NOVEL SPERM RECEPTORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: US
; ZIP: 60601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,506
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,751
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 74940
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5600
; TELEFAX: 312-616-5700
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 327 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-748-506-22
```

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;
; FILING DATE: 09-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 74940
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5600
; TELEFAX: 312-616-5700
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 327 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-748-506-23

Query Match 52.3%; Score 46; DB 4; Length 327;
Best Local Similarity 47.1%; Pred. No. 1.3;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLTAADHR 17
   ::||:| | :| |||
Db 44 SLMGNMLIITITCVDHR 60

RESULT 9
US-09-518-046-4
; Sequence 4, Application US/09518046
; Patent No. 6294663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; FILE REFERENCE: D6192CIP
; CURRENT APPLICATION NUMBER: US/09/518,046
; CURRENT FILING DATE: 2000-03-02
; EARLIER APPLICATION NUMBER: 09/261,416
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 4
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: complete amino acid sequence of TADG-12
; OTHER INFORMATION: variant protein
; US-09-518-046-4

Query Match 50.0%; Score 44; DB 4; Length 294;
Best Local Similarity 43.8%; Pred. No. 2.7;
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 3 SGNILTIRLTAADHRQ 18
   ||::||:| | ||:
Db 197 SGHVVTLOCTACGHR 212

RESULT 10
US-09-518-046-2
; Sequence 2, Application US/09518046
; Patent No. 6294663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; FILE REFERENCE: D6192CIP
; CURRENT APPLICATION NUMBER: US/09/518,046
; CURRENT FILING DATE: 2000-03-02
; EARLIER APPLICATION NUMBER: 09/261,416
; EARLIER FILING DATE: 1999-03-03
```

; NUMBER OF SEQ ID NOS: 153
;-SEQ ID NO 2
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: complete amino acid sequence of TADG-12
; OTHER INFORMATION: protein
US-09-518-046-2

Query Match 50.0%; Score 44; DB 4; Length 454;
Best Local Similarity 43.8%; Pred. No. 4.6;
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 3 SGNILTRLTAADHRQ 18
||::||: || ||:
Db 197 SGHVVTLQCTACGHR 212

RESULT 11

US-09-261-416-2
; Sequence 2, Application US/09261416A
; Patent No. 6291663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: TADG-12: A No. 6291663el Transmembrane Serine Protease
; TITLE OF INVENTION: Overexpressed in Ovarian Carcinoma
; FILE REFERENCE: D6192
; CURRENT APPLICATION NUMBER: US/09/261,416A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 14
;-SEQ ID NO 2
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of TADG-12 encoded by nucleotides
; OTHER INFORMATION: 144 to 1511 of Sequence 1
; Patent No. 6291663
US-09-261-416-2

Query Match 50.0%; Score 44; DB 4; Length 455;
Best Local Similarity 43.8%; Pred. No. 4.7;
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 3 SGNILTRLTAADHRQ 18
||::||: || ||:
Db 197 SGHVVTLQCTACGHR 212

RESULT 12

US-08-748-506-24
; Sequence 24, Application. US/08748506
; Patent No. 6159707
; GENERAL INFORMATION:
; APPLICANT: Ronnett et al.
; TITLE OF INVENTION: NOVEL SPERM RECEPTORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: US
; ZIP: 60601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,506
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,751
; FILING DATE: 09-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 74940
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5600
; TELEFAX: 312-616-5700
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 327 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-748-506-24

Query Match 47.7%; Score 42; DB 4; Length 327;
Best Local Similarity 57.1%; Pred. No. 7.1;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 GNILTRLTAADHR 17
||:| | | |||
Db 47 GNMLIITYTCVDHR 60

RESULT 13

US-08-883-534-6
; Sequence 6, Application US/08883534
; Patent No. 5846777
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: TWO NEW WD-40 PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/883,534
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0332 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 597 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1384131
US-08-883-534-6

Query Match 44.3%; Score 39; DB 2; Length 597;
Best Local Similarity 52.9%; Pred. No. 54;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLTAAADHR 17
|:||||| | :||
Db 466 TLSGNNLTASHTLDNHR 482

RESULT 14
US-09-204-764-6
; Sequence 6, Application US/09204764
; Patent No. 6025464
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: TWO NEW WD-40 PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS:
; STREET:
; CITY: *171 0116*
; STATE: *10450, BAS*
; COUNTRY: *Inc.*
; ZIP: *78*
; COMPUTER: compatible
; MEDIUM TYPE: DOS
; OPERATING SYSTEM: fastseq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/204,764
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/883,534
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0332 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 597 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1384131
US-09-204-764-6

Query Match 44.3%; Score 39; DB 3; Length 597;
Best Local Similarity 52.9%; Pred. No. 54;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLTAAADHR 17
|:||||| | :||
Db 466 TLSGNNLTASHTLDNHR 482

RESULT 15
US-08-416-788-2
; Sequence 2, Application US/08416788
; Patent No. 5780245
; GENERAL INFORMATION:
; APPLICANT: Maroteaux, Luc
; TITLE OF INVENTION: No. 5780245el Polypeptides Having a Serotonin
; TITLE OF INVENTION: Receptor Activity, Nucleic Acids Coding for These
; TITLE OF INVENTION: Polypeptides and Uses
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426-0107
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/416,788
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR93/01012
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92-12280
; FILING DATE: 14-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Julie K.
; REGISTRATION NUMBER: 38,619
; REFERENCE/DOCKET NUMBER: EX92008-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610)454-3839
; TELEFAX: (610)454-3808
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 479 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-416-788-2

Query Match 43.2%; Score 38; DB 1; Length 479;
Best Local Similarity 47.1%; Pred. NO. 62;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLTAAADHR 17
|:||||| | :||
Db 67 TIGGNILVILAVALEKR 83

Search completed: July 3, 2002, 11:09:49
Job time: 271 sec

; NUMBER OF SEQ ID NOS: 153
;-SEQ ID NO 2
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: complete amino acid sequence of TADG-12
; OTHER INFORMATION: protein
US-09-518-046-2

Query Match 50.0%; Score 44; DB 4; Length 454;
Best Local Similarity 43.8%; Pred. No. 4.6;
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 3 SGNILTIRLTAADHRQ 18
||::||::||
Db 197 SGHVVTLQCTACGHR 212

RESULT 11
US-09-261-416-2
; Sequence 2, Application US/09261416A
; Patent No. 6291663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: TADG-12: A No. 6291663el Transmembrane Serine Protease
; TITLE OF INVENTION: Overexpressed in Ovarian Carcinoma
; FILE REFERENCE: D6192
; CURRENT APPLICATION NUMBER: US/09/261,416A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 2
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of TADG-12 encoded by nucleotides
; OTHER INFORMATION: 144 to 1511 of Sequence 1
; Patent No. 6291663
US-09-261-416-2

Query Match 50.0%; Score 44; DB 4; Length 455;
Best Local Similarity 43.8%; Pred. No. 4.7;
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 3 SGNILTIRLTAADHRQ 18
||::||::||
Db 197 SGHVVTLQCTACGHR 212

RESULT 12
US-08-748-506-24
; Sequence 24, Application. US/08748506
; Patent No. 6159707
; GENERAL INFORMATION:
; APPLICANT: Ronnett et al.
; TITLE OF INVENTION: NOVEL SPERM RECEPTORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: US
; ZIP: 60601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,506
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,751
; FILING DATE: 09-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 74940
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5600
; TELEFAX: 312-616-5700
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 327 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-748-506-24

Query Match 47.7%; Score 42; DB 4; Length 327;
Best Local Similarity 57.1%; Pred. No. 7.1;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 GNILTIRLTAADHR 17
||::||::||
Db 47 GNMLIITYTCVDHR 60

RESULT 13
US-08-883-534-6
; Sequence 6, Application US/08883534
; Patent No. 5846777
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: TWO NEW WD-40 PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/883,534
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0332 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 597 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

;
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1384131
US-08-883-534-6

Query Match 44.3%; Score 39; DB 2; Length 597;
Best Local Similarity 52.9%; Pred. No. 54;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TVSGNLTIRLTAADHR 17
|:||||| | :||
Db 466 TLSGNNLTASHTLDNHR 482

RESULT 14
US-09-204-764-6
; Sequence 6, Application US/09204764
; Patent No. 6025464
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: TWO NEW WD-40 PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/204,764
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/883,534
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0332 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 597 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1384131
US-09-204-764-6

Query Match 44.3%; Score 39; DB 3; Length 597;
Best Local Similarity 52.9%; Pred. No. 54;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TVSGNLTIRLTAADHR 17
|:||||| | :||
Db 466 TLSGNNLTASHTLDNHR 482

RESULT 15
US-08-416-788-2
; Sequence 2, Application US/08416788
; Patent No. 5780245
; GENERAL INFORMATION:
; APPLICANT: Maroteaux, Luc
; TITLE OF INVENTION: No. 5780245el Polypeptides Having a Serotonin
; TITLE OF INVENTION: Receptor Activity, Nucleic Acids Coding for These
; TITLE OF INVENTION: Polypeptides and Uses
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426-0107
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/416,788
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR93/01012
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92-12280
; FILING DATE: 14-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Julie K.
; REGISTRATION NUMBER: 38,619
; REFERENCE/DOCKET NUMBER: EX92008-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610)454-3839
; TELEFAX: (610)454-3808
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 479 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-416-788-2

Query Match 43.2%; Score 38; DB 1; Length 479;
Best Local Similarity 47.1%; Pred. NO. 62;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 TVSGNLTIRLTAADHR 17
|:||||| | :||
Db 67 TIGGNILVILAVALEKR 83

Search completed: July 3, 2002, 11:09:49
Job time: 271 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 11:27:56 ; Search time 47.88 Seconds
(without alignments)
9.183 Million cell updates/sec

Title: US-09-165-546A-13

Perfect score: 88

Sequence: 1 TVSGNLTFLRLTAADHRQ 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 113617

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	88	100.0	18	4	US-09-359-503-13	Sequence 13, Appl
2	56	63.6	18	4	US-09-359-503-9	Sequence 9, Appli
3	32	36.4	18	4	US-09-359-503-8	Sequence 8, Appli
4	29	33.0	17	6	5185441-3	Patent No. 5185441
5	29	33.0	18	4	US-09-359-503-10	Sequence 10, Appl
6	26	29.5	16	1	US-08-036-555B-121	Sequence 121, App
7	26	29.5	16	1	US-08-469-569-121	Sequence 121, App
8	26	29.5	16	1	US-08-249-322A-121	Sequence 121, App
9	26	29.5	16	1	US-08-469-526A-121	Sequence 121, App
10	26	29.5	16	2	US-08-734-591A-121	Sequence 121, App
11	26	29.5	16	2	US-08-469-660-121	Sequence 121, App
12	26	29.5	16	4	US-08-470-335-121	Sequence 121, App
13	26	29.5	16	4	US-08-735-021-121	Sequence 121, App
14	26	29.5	16	4	US-08-734-664A-121	Sequence 121, App
15	26	29.5	16	4	US-08-470-339-121	Sequence 121, App
16	26	29.5	16	5	PCT-US94-05083C-117	Sequence 117, App
17	26	29.5	16	5	PCT-US95-06846A-121	Sequence 121, App
18	26	29.5	18	2	US-08-702-105A-15	Sequence 15, Appl
19	26	29.5	18	3	US-08-702-110A-15	Sequence 15, Appl
20	26	29.5	18	4	US-09-325-571-15	Sequence 15, Appl
21	25	28.4	9	4	US-09-258-754-253	Sequence 253, App
22	25	28.4	9	4	US-09-042-107-253	Sequence 253, App
23	25	28.4	11	1	US-08-665-966-4	Sequence 4, Appli
24	25	28.4	11	3	US-09-041-780-4	Sequence 4, Appli
25	25	28.4	13	4	US-09-484-114B-33	Sequence 33, Appl
26	25	28.4	16	4	US-09-514-302-5	Sequence 5, Appli
27	24	27.3	13	2	US-08-771-602D-32	Sequence 32, Appl

28	24	27.3	13	4	US-09-484-114B-34	Sequence 34, Appl
29	24	27.3	15	4	US-09-476-482-13	Sequence 13, Appl
30	24	27.3	16	1	US-08-318-200-8	Sequence 8, Appli
31	24	27.3	16	1	US-08-318-200-9	Sequence 9, Appli
32	24	27.3	17	4	US-09-227-357-383	Sequence 383, App
33	23	26.1	8	1	US-08-146-886-19	Sequence 19, Appl
34	23	26.1	8	4	US-09-109-613-19	Sequence 19, Appl
35	23	26.1	10	6	5428134-7	Patent No. 5428134
36	23	26.1	10	6	5436320-8	Patent No. 5436320
37	23	26.1	11	2	US-08-801-301A-1	Sequence 1, Appli
38	23	26.1	16	2	US-07-894-063A-12	Sequence 12, Appl
39	23	26.1	17	2	US-08-466-860-27	Sequence 27, Appl
40	23	26.1	17	3	US-08-472-040A-27	Sequence 27, Appl
41	23	26.1	17	4	US-08-276-776-27	Sequence 27, Appl
42	23	26.1	17	4	US-08-471-209-27	Sequence 27, Appl
43	22.5	25.6	16	1	US-07-940-861-7	Sequence 7, Appli
44	22.5	25.6	16	1	US-08-459-512-7	Sequence 7, Appli
45	22.5	25.6	16	2	US-08-459-657-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-359-503-13
; Sequence 13, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
US-09-359-503-13

Query Match 100.0%; Score 88; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 7e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLTAADHRQ 18
| | | | | | | | | | | | | | | | | |
Db 1 TVSGNLTIRLTAADHRQ 18

RESULT 2
US-09-359-503-9
; Sequence 9, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-359-503-9

Query Match 63.6%; Score 56; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLT 12
| | | | | | | | | | | | | | | | | |

Db 7 TVSGNLTIRLT 18

RESULT 3
US-09-359-503-8
; Sequence 8, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS: 18 amino acids
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-359-503-8

Query Match 36.4%; Score 32; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AADHRQ 18
| | | | | | | | | | | | | | | | | |
Db 1 AADHRQ 6

RESULT 4
5185441-3
; Patent No. 5185441
; APPLICANT: WALLNER, BARBARA P.; HESSIONS, CATHERINE
; TITLE OF INVENTION: DNA SEQUENCES, RECOMBINANT DNA
; MOLECULES AND PROCESSES FOR PRODUCING PI-LINKED LYMPHOCYTE
; FUNCTION ASSOCIATED ANTIGEN-3

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; NUMBER OF SEQUENCES: 41
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/237,309
; FILING DATE: 26-AUG-1988
; SEQ ID NO:3:
; LENGTH: 17
5185441-3

Query Match      33.0%; Score 29; DB 6; Length 17;
Best Local Similarity 46.2%; Pred. No. 40;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLTA 13
   ||||: ||:
Db 5 TVSGSLTIYNLTS 17

RESULT 5
US-09-359-503-10
; Sequence 10, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-359-503-10
to NY-
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Query Match 33.0%; Score 29; DB 4; Length 18;

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Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNI 6
   |||||
Db 13 TVSGNI 18

RESULT 6
US-08-036-555B-121
; Sequence 121, Application US/08036555B
; Patent No. 5530109
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew; Stroobant, Paul;
; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
; APPLICANT: Chen, Maio Su; Hiles, Ian
; TITLE OF INVENTION: Glial Mitogenic Factors, Their
; TITLE OF INVENTION: Preparation and Use
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/036,555B
; FILING DATE: 24-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APRIL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsai, Christine H.
; REGISTRATION NUMBER: 34,266
; REFERENCE/DOCKET NUMBER: LUD 5250.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 121:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-036-555B-121

Query Match      29.5%; Score 26; DB 1; Length 16;
Best Local Similarity 55.6%; Pred. No. 1.3e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 NLTIRLTA 13
   ::||:| |
Db 7 SLTVRLGA 15
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RESULT 7
US-08-469-569-121
; Sequence 121, Application US/08469569
; Patent No. 5606032
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew; Stroobant, Paul;
; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
; APPLICANT: Chen, Maio Su; Hiles, Ian
; TITLE OF INVENTION: Glial Mitogenic Factors, Their
; PREPARATION AND USE
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,569
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APRIL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsai, Christine H.
; REGISTRATION NUMBER: 34,266
; REFERENCE/DOCKET NUMBER: LUD 5250.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 121:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-469-569-121

Query Match 29.5%; Score 26; DB 1; Length 16;
Best Local Similarity 55.6%; Pred. No. 1.3e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 NILTIRLTA 13
::||:| |
Db 7 SLLTVRLGA 15

RESULT 8
US-08-249-322A-121

; Sequence 121, Application US/08249322A
; Patent No. 5716930
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew; Stroobant, Paul;
; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
; APPLICANT: Chen, Maio Su; Hiles, Ian
; TITLE OF INVENTION: Glial Mitogenic Factors, Their
; PREPARATION AND USE
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/249,322A
; FILING DATE: 26-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APRIL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsai, Christine H.
; REGISTRATION NUMBER: 34,266
; REFERENCE/DOCKET NUMBER: LUD 250.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 121:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-249-322A-121

Query Match 29.5%; Score 26; DB 1; Length 16;
Best Local Similarity 55.6%; Pred. No. 1.3e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 NILTIRLTA 13
::||:| |
Db 7 SLLTVRLGA 15

RESULT 9
US-08-469-526A-121
; Sequence 121, Application US/08469526A
; Patent No. 5792849
; GENERAL INFORMATION:

;; APPLICANT: Goodearl, Andrew
;; APPLICANT: Stroobant, Paul
;; APPLICANT: Minghetti, Luisa
;; APPLICANT: Waterfield, Michael
;; APPLICANT: Marchionni, Mark
;; APPLICANT: Chen, Maio Su
;; APPLICANT: Hiles, Ian
;; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
;; TITLE OF INVENTION: PREPARATION AND USE
;; NUMBER OF SEQUENCES: 187
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Clark & Elbing LLP
;; STREET: 176 Federal Street
;; CITY: Boston
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02110
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/469,526A
;; FILING DATE: 06 June 1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/036,555
;; FILING DATE: 24-MAR-1993
;; APPLICATION NUMBER: 07/965,173
;; FILING DATE: 23-OCT-1992
;; APPLICATION NUMBER: 07/940,389
;; FILING DATE: 03-SEP-1992
;; APPLICATION NUMBER: 07/907,138
;; FILING DATE: 03-JUN-1992
;; APPLICATION NUMBER: 07/863,703
;; FILING DATE: 03-APRIL-1992
;; APPLICATION NUMBER: U.K. 91 07566.3
;; FILING DATE: 10-APR-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Bieker-Brady, Kristina
;; REGISTRATION NUMBER: 39,109
;; REFERENCE/DOCKET NUMBER: 04585/00200A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-428-0200
;; TELEFAX: 617-428-7045
;; INFORMATION FOR SEQ ID NO: 121:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-469-526A-121

Query Match 29.5%; Score 26; DB 1; Length 16;
Best Local Similarity 55.6%; Pred. No. 1.3e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 NILTIRLTA 13
: :||:| |
Db 7 SLLTVRLGA 15

RESULT 10
US-08-734-591A-121
; Sequence 121, Application US/08734591A
; Patent No. 5854220
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew
; APPLICANT: Stroobant, Paul
; APPLICANT: Minghetti, Luisa
; APPLICANT: Waterfield, Michael

;; APPLICANT: Hiles, Ian
;; APPLICANT: Marchionni, Mark
;; APPLICANT: Chen, Mario
;; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
;; TITLE OF INVENTION: PREPARATION AND USE
;; NUMBER OF SEQUENCES: 187
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Clark & Elbing LLP
;; STREET: 176 Federal Street
;; CITY: Boston
;; STATE: Massachusetts
;; COUNTRY: U.S.A.
;; ZIP: 02110
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; COMPUTER: IBM Compatible Pentium
;; OPERATING SYSTEM: Windows95
;; SOFTWARE: WordPerfect (Version 7.0)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/734,591A
;; FILING DATE: 22-OCT-1996
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/470,335
;; FILING DATE: 06-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/036,555
;; FILING DATE: 03-MAR-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/965,173
;; FILING DATE: 23-OCT-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/940,389
;; FILING DATE: 03-SEP-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/907,138
;; FILING DATE: 30-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/863,703
;; FILING DATE: 03-APR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: UK 91 07566.3
;; FILING DATE: 10-APR-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Bieker-Brady, Kristina
;; REGISTRATION NUMBER: 39,109
;; REFERENCE/DOCKET NUMBER: 04585/00200P
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 428-0200
;; TELEFAX: (617) 428-7045
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 121:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; US-08-734-591A-121

Query Match 29.5%; Score 26; DB 2; Length 16;
Best Local Similarity 55.6%; Pred. No. 1.3e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 NILTIRLTA 13
: :||:| |
Db 7 SLLTVRLGA 15

RESULT 11
US-08-469-660-121
; Sequence 121, Application US/08469660
; Patent No. 5876973

; GENERAL INFORMATION:
; APPLICANT: Gwynne, David I.; Marchionni, Mark;
; APPLICANT: McBurney, Robert N.
; TITLE OF INVENTION: INHIBITORS OF CELL PROLIFERATION,
; TITLE OF INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; ZIP: 02111-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,660
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/011,396
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/984,085
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/951,747
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/927,337
; FILING DATE: 10-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04585/017004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: 200154
; INFORMATION FOR SEQ ID NO: 121:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-469-660-121

Query Match 29.5%; Score 26; DB 2; Length 16;
Best Local Similarity 55.6%; Pred. No. 1.3e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 NILTIRLTA 13
::||:| |
Db 7 SLLTVRLGA 15

- RESULT 12
US-08-470-335-121
; Sequence 121, Application US/08470335F
; Patent No. 6147190
; GENERAL INFORMATION:
; APPLICANT: GOODEARL, ANDREW
; APPLICANT: STROOBANT, PAUL
; APPLICANT: MINGHETTI, LUISA
; APPLICANT: WATERFIELD, MICHAEL
; APPLICANT: MARCHIONNI, MARK
; APPLICANT: CHEN, MARIO S.
; APPLICANT: HILES, IAN
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; PREPARATION AND USE
; FILE REFERENCE: 04585/00200B

; CURRENT APPLICATION NUMBER: US/08/470,335F
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/036,555
; EARLIER FILING DATE: 1993-03-24
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 121
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Bos taurus
; US-08-470-335-121

Query Match 29.5%; Score 26; DB 4; Length 16;
Best Local Similarity 55.6%; Pred. No. 1.3e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 NILTIRLTA 13
::||:| |
Db 7 SLLTVRLGA 15

RESULT 13
US-08-735-021-121
; Sequence 121, Application US/08735021B
; Patent No. 6194377
; GENERAL INFORMATION:
; APPLICANT: GOODEARL, ANDREW
; APPLICANT: STROOBANT, PAUL
; APPLICANT: MINGHETTI, LUISA
; APPLICANT: WATERFIELD, MICHAEL
; APPLICANT: MARCHIONNI, MARK
; APPLICANT: CHEN, MARIO S.
; APPLICANT: HILES, IAN
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; PREPARATION AND USE
; FILE REFERENCE: 04585/00200L
; CURRENT APPLICATION NUMBER: US/08/735,021B
; CURRENT FILING DATE: 1996-10-22
; EARLIER APPLICATION NUMBER: 08/472,065
; EARLIER FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/036,555
; EARLIER FILING DATE: 1993-03-24
; EARLIER APPLICATION NUMBER: 07/965,173
; EARLIER FILING DATE: 1992-10-23
; EARLIER APPLICATION NUMBER: 07/940,389
; EARLIER FILING DATE: 1992-09-03
; EARLIER APPLICATION NUMBER: 07/907,138
; EARLIER FILING DATE: 1992-06-30
; EARLIER APPLICATION NUMBER: 07/863,703
; EARLIER FILING DATE: 1992-04-03
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 121
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Bos taurus
; US-08-735-021-121

Query Match 29.5%; Score 26; DB 4; Length 16;
Best Local Similarity 55.6%; Pred. No. 1.3e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 NILTIRLTA 13
::||:| |
Db 7 SLLTVRLGA 15

RESULT 14
US-08-734-664A-121
; Sequence 121, Application US/08734664A
; Patent No. 6204241


```

;
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew
; APPLICANT: Stroobant, Paul
; APPLICANT: Minghetti, Luisa
; APPLICANT: Waterfield, Michael
; APPLICANT: Marchionni, Mark
; APPLICANT: Chen, Mario
; APPLICANT: Hiles, Ian
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 187
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible Pentium
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734.664A
; FILING DATE: 22-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,322
; FILING DATE: 26-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 91 07556.3
; FILING DATE: 10-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bleker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 04585/00200J
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 428-0200
; TELEFAX: (617) 428-7045
; TELEX:
;
; INFORMATION FOR SEQ ID NO: 121:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
; US-08-734-664A-121

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Query Match      29.5%; Score 26; DB 4; Length 16;
Best Local Similarity 55.6%; Pred. No. 1.3e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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QY 5 NILTIRLTA 13
:|:|:| |
Db 7 SLLTVRLGA 15

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RESULT 15
US-08-470-339-121
; Sequence 121, Application US/08470339C
; Patent No. 6232286
; GENERAL INFORMATION:
; APPLICANT: GOODEARL, ANDREW
; APPLICANT: STROOBANT, PAUL
; APPLICANT: MINGHETTI, LUISA
; APPLICANT: WATERFIELD, MICHAEL
; APPLICANT: MARCHIONNI, MARK
; APPLICANT: CHEN, MARIO S.
; APPLICANT: HILES, IAN
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; FILE REFERENCE: 04585/002008
; CURRENT APPLICATION NUMBER: US/08/470,339C
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/036,555
; EARLIER FILING DATE: 1993-03-24
; EARLIER APPLICATION NUMBER: 07/940,389
; EARLIER FILING DATE: 1992-09-03
; EARLIER APPLICATION NUMBER: 07/907,138
; EARLIER FILING DATE: 1992-06-30
; EARLIER APPLICATION NUMBER: 07/863,703
; EARLIER FILING DATE: 1992-04-03
; EARLIER APPLICATION NUMBER: 91 07566.3 GB
; EARLIER FILING DATE: 1999-04-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 121
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Bos taurus
;
; US-08-470-339-121

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Query Match 29.5%; Score 26; DB 4; Length 16;
Best Local Similarity 55.6%; Pred. No. 1.3e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 NILTIRLTA 13
:|:|:| |
Db 7 SLLTVRLGA 15

Search completed: July 3, 2002, 11:27:56
Job time: 412 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 11:27:55 ; Search time 47.88 Seconds
(without alignments)
9.183 Million cell updates/sec

Title: US-09-165-546A-12
Perfect score: 91
Sequence: 1 SRLLFYLAMPPFATPMEA 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 113617

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA: *
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep: *
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep: *
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep: *
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep: *
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep: *
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	91	100.0	18	4	US-09-359-503-12
2	32	35.2	17	2	US-08-480-190-18
3	32	35.2	17	2	US-08-488-379-18
4	32	35.2	17	5	PCT-US93-07545-18
5	31	34.1	16	1	US-08-258-851-8
6	30	33.0	12	1	US-08-190-788A-159
7	30	33.0	12	1	US-08-383-474B-162
8	30	33.0	12	1	US-08-465-391A-159
9	30	33.0	12	2	US-08-464-538B-159
10	30	33.0	12	2	US-08-463-076E-211
11	30	33.0	14	4	US-07-963-329A-76
12	30	33.0	14	5	PCT-US92-09443A-76
13	28	30.8	10	1	US-08-190-788A-140
14	28	30.8	10	1	US-08-383-474B-145
15	28	30.8	10	1	US-08-465-391A-140
16	28	30.8	10	2	US-08-464-538B-140
17	28	30.8	10	2	US-08-463-076E-190
18	27	29.7	10	1	US-08-190-788A-61
19	27	29.7	10	1	US-08-190-788A-240
20	27	29.7	10	1	US-08-383-474B-66
21	27	29.7	10	1	US-08-383-474B-243
22	27	29.7	10	1	US-08-465-391A-61
23	27	29.7	10	1	US-08-465-391A-240
24	27	29.7	10	2	US-08-464-538B-61
25	27	29.7	10	2	US-08-464-538B-240
26	27	29.7	10	2	US-08-463-076E-105
27	27	29.7	10	2	US-08-463-076E-292

28	27	29.7	11	1	US-08-190-788A-227	Sequence 227, App
29	27	29.7	11	1	US-08-383-474B-230	Sequence 230, App
30	27	29.7	11	1	US-08-465-391A-227	Sequence 227, App
31	27	29.7	11	2	US-08-464-538B-227	Sequence 227, App
32	27	29.7	11	2	US-08-463-076E-281	Sequence 281, App
33	27	29.7	12	1	US-08-190-788A-119	Sequence 119, App
34	27	29.7	12	1	US-08-190-788A-198	Sequence 198, App
35	27	29.7	12	1	US-08-190-788A-215	Sequence 215, App
36	27	29.7	12	1	US-08-383-474B-124	Sequence 124, App
37	27	29.7	12	1	US-08-383-474B-201	Sequence 201, App
38	27	29.7	12	1	US-08-383-474B-218	Sequence 218, App
39	27	29.7	12	1	US-08-465-391A-119	Sequence 119, App
40	27	29.7	12	1	US-08-465-391A-198	Sequence 198, App
41	27	29.7	12	1	US-08-465-391A-215	Sequence 215, App
42	27	29.7	12	2	US-08-464-538B-119	Sequence 119, App
43	27	29.7	12	2	US-08-464-538B-198	Sequence 198, App
44	27	29.7	12	2	US-08-464-538B-215	Sequence 215, App
45	27	29.7	12	2	US-08-463-076E-167	Sequence 167, App

ALIGNMENTS

RESULT 1
US-09-359-503-12
; Sequence 12, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
US-09-359-503-12

Query Match 100.0%; Score 91; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLLFYLPMPFATPMEA 18
| | | | | | | | | | | | | | | | | |
Db 1 SRLLFYLPMPFATPMEA 18

RESULT 2

US-08-480-190-18
; Sequence 18, Application US/08480190
; Patent No. 5827516

; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,190
; FILING DATE:
; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.

; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-480-190-18

Query Match 35.2%; Score 32; DB 2; Length 17;
Best Local Similarity 26.7%; Pred. NO. 19;
Matches 4; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 4 LEFYLPMPFATPMEA 18
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Db 4 VEYHFLSPYVSPKES 16

RESULT 3

US-08-488-379-18
; Sequence 18, Application US/08488379
; Patent No. 5880103

; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,379
; FILING DATE:
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.

; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-488-379-18

Query Match 35.2%; Score 32; DB 2; Length 17;
Best Local Similarity 26.7%; Pred. No. 19;
Matches 4; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 4 LEFYLPMPFATPMEA 18
| | | | | | | | | | | | | | | | | |
Db 2 VEYHFLSPYVSPKES 16

RESULT 4

PCT-US93-07545-18
; Sequence 18, Application PC/TUS9307545
; GENERAL INFORMATION:

; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07545
FILING DATE: 19930811
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 17
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US93-07545-18

Query Match 35.2%; Score 32; DB 5; Length 17;
Best Local Similarity 26.7%; Pred. No. 19;
Matches 4; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 4 LEFYLAMPFATPMEA 18
:|:: |: :| |:
Db 2 VEYHFLSPYVSPKES 16

RESULT 5
US-08-258-851-8
Sequence 8, Application US/08258851
Patent No. 5585244
GENERAL INFORMATION:
APPLICANT: Elizabeth A. Allegretto
APPLICANT: J. Wesley Pike
TITLE OF INVENTION: DETECTION OF RETINOID
TITLE OF INVENTION: RECEPTOR SUBTYPE
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/258,851
FILING DATE: 10 June 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application

PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 207/199
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
FEATURE:
OTHER INFORMATION:
US-08-258-851-8

Query Match 34.1%; Score 31; DB 1; Length 16;
Best Local Similarity 50.0%; Pred. No. 26;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 RLLEYFLAMP 11
:|::| | | | |
Db 4 QILDFYTASP 13

RESULT 6
US-08-190-788A-159
Sequence 159, Application US/08190788A
Patent No. 5608035
GENERAL INFORMATION:
APPLICANT: Yanofsky, Stephen D.
APPLICANT: Barrett, Ronald W.
APPLICANT: Baldwin, David N.
APPLICANT: Jacobs, Jeff W.
TITLE OF INVENTION: Peptides and Compounds That Bind to the
TITLE OF INVENTION: IL-1 Receptor
NUMBER OF SEQUENCES: 312
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies N.V.
STREET: 4001 Miranda Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,788A
FILING DATE: 02-FEB-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,567
FILING DATE: 05-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 1019.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 159:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-190-788A-159

Query Match 33.0%; Score 30; DB 1; Length 12;
Best Local Similarity 57.1%; Pred. No. 28;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFATPME 17
I:||||:
Db 5 PYATPLD 11

RESULT 7

US-08-383-474B-162
Sequence 162, Application US/08383474B
Patent No. 5767234

GENERAL INFORMATION:

APPLICANT: Yanofsky, Stephen D.
APPLICANT: Barrett, Ronald W.
APPLICANT: Baldwin, David N.
APPLICANT: Jacobs, Jeff W.
TITLE OF INVENTION: Peptides and Compounds That Bind to
TITLE OF INVENTION: the IL-1 Receptor
NUMBER OF SEQUENCES: 314

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend & Townsend & Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/383,474B
FILING DATE: 01-FEB-1995
CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 1019.3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832

INFORMATION FOR SEQ ID NO: 162:

SEQUENCE CHARACTERISTICS:

LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-383-474B-162

Query Match 33.0%; Score 30; DB 1; Length 12;
Best Local Similarity 57.1%; Pred. No. 28;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFATPME 17
I:||||:
Db 5 PYATPLD 11

RESULT 8

US-08-465-391A-159
Sequence 159, Application US/08465391A
Patent No. 5786331

GENERAL INFORMATION:

APPLICANT: Barrett, Ronald W.
APPLICANT: Yanofsky, Stephen D.
APPLICANT: Baldwin, David
APPLICANT: Jacobs, Jeff W.
APPLICANT: Bovy, Phillipe R.
APPLICANT: Leahy, Ellen M.
APPLICANT: Pottorf, Richard S.
TITLE OF INVENTION: Peptides and Compounds That Bind to the
TITLE OF INVENTION: IL-1 Receptor
NUMBER OF SEQUENCES: 405

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/465,391A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/373,474
FILING DATE: 01-FEB-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: No. 5786331viel, Vern
REGISTRATION NUMBER: 32,483
REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 159:

SEQUENCE CHARACTERISTICS:

LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-465-391A-159

Query Match 33.0%; Score 30; DB 1; Length 12;
Best Local Similarity 57.1%; Pred. No. 28;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFATPME 17
I:||||:
Db 5 PYATPLD 11

RESULT 9

US-08-464-538B-159
Sequence 159, Application US/08464538B
Patent No. 5861476

GENERAL INFORMATION:

APPLICANT: Barrett, Ronald W.
APPLICANT: Yanofsky, Stephen D.
APPLICANT: Baldwin, David

APPLICANT: Jacobs, Jeff W.
APPLICANT: Bovy, Phillippe R.
APPLICANT: Leahy, Ellen M.
APPLICANT: Pottorf, Richard S.
TITLE OF INVENTION: Peptides and Compounds That Bind to the
TITLE OF INVENTION: IL-1 Receptor
NUMBER OF SEQUENCES: 402
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,538B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,474
FILING DATE: 01-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 16528A-001810
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 159:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-464-538B-159
Query Match 33.0%; Score 30; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 28;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 11 PFATPME 17
Db 5 PYATPLD 11
RESULT 10
US-08-463-076E-211
Sequence 211, Application US/08463076E
Patent No. 580096
GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Yanofsky, Stephen D.
TITLE OF INVENTION: Peptides and Compounds That Bind to the
TITLE OF INVENTION: IL-1 Receptor
NUMBER OF SEQUENCES: 392
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA

ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,076E
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Snyder, Joseph R.
REGISTRATION NUMBER: 39,381
REFERENCE/DOCKET NUMBER: 16528A-001850US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 211:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-463-076E-211
Query Match 33.0%; Score 30; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 28;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 11 PFATPME 17
Db 5 PYATPLD 11
RESULT 11
US-07-963-329A-76
Sequence 76, Application US/07963329A
Patent No. 6310040
GENERAL INFORMATION:
APPLICANT: Bozyczko-Coyne, Donna
APPLICANT: Neff, Nicola
APPLICANT: Lewis, Michael E.
APPLICANT: Iqbal, Mohamed
TITLE OF INVENTION: TREATING RETINAL NEURONAL DISORDERS
TITLE OF INVENTION: BY THE APPLICATION OF INSULIN-LIKE
TITLE OF INVENTION: GROWTH FACTORS AND ANALOGS
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/963,329A
FILING DATE: 19921015
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/790,690
FILING DATE: No. 6310040ember 8, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 02655/012002
TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-07-963-329A-76

Query Match 33.0%; Score 30; DB 4; Length 14;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 0;

QY 3 LLEFYLAMP 11
||| |:
Db 2 LLETYMATP 10

RESULT 12
PCT-US92-09443A-76
; Sequence 76, Application PC/TUS9209443A
; GENERAL INFORMATION:
; APPLICANT: Bozyczko-Coyne, Donna
; APPLICANT: Neff, Nicola
; APPLICANT: Lewis, Michael E.
; APPLICANT: Iqbal, Mohamed
; TITLE OF INVENTION: TREATING RETINAL NEURONAL
; TITLE OF INVENTION: DISORDERS BY THE APPLICATION OF
; TITLE OF INVENTION: INSULIN-LIKE GROWTH FACTORS AND
; TITLE OF INVENTION: ANALOGS
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09443A
; FILING DATE: 19921103
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/790,690
; FILING DATE: November 8, 1991
; APPLICATION NUMBER: 07/963,329
; FILING DATE: October 15, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 02655/012WO2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14
; TYPE: AMINO ACID
; STRANDEDNESS: N/A
; TOPOLOGY: N/A
PCT-US92-09443A-76

Query Match 33.0%; Score 30; DB 5; Length 14;

Best Local Similarity 66.7%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 0;

QY 3 LLEFYLAMP 11
||| |:
Db 2 LLETYMATP 10

RESULT 13
US-08-190-788A-140
; Sequence 140, Application US/08190788A
; Patent No. 5608035
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David N.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 312
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies N.V.
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,788A
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,567
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1019.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 140:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-190-788A-140

Query Match 30.8%; Score 28; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 52;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFATPM 16
|:|:
Db 5 PYATPL 10

RESULT 14
US-08-383-474B-145
; Sequence 145, Application US/08383474B
; Patent No. 5767234
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David N.

APPLICANT: Jacobs, Jeff W.
TITLE OF INVENTION: Peptides and Compounds That Bind to
TITLE OF INVENTION: the IL-1 Receptor
NUMBER OF SEQUENCES: 314
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend & Townsend & Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,474B
FILING DATE: 01-FEB-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 1019.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-383-474B-145

Query Match 30.8%; Score 28; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 52;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 11 PFATPM 16
Db 5 PYATPL 10

RESULT 15
US-08-465-391A-140
Sequence 140, Application US/08465391A
Patent No. 5786331
GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Yanofsky, Stephen D.
APPLICANT: Baldwin, David
APPLICANT: Jacobs, Jeff W.
APPLICANT: Bovy, Phillipe R.
APPLICANT: Leahy, Ellen M.
APPLICANT: Pottorf, Richard S.
TITLE OF INVENTION: Peptides and Compounds That Bind to the
TITLE OF INVENTION: IL-1 Receptor
NUMBER OF SEQUENCES: 405
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,391A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,474
FILING DATE: 01-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: No. 5786331viel, Vern
REGISTRATION NUMBER: 32,483
REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-465-391A-140

Query Match 30.8%; Score 28; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 52;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 11 PFATPM 16
Db 5 PYATPL 10

Search completed: July 3, 2002, 11:27:56
Job time: 412 sec

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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:38:25 ; Search time 560.51 Seconds
(without alignments)
11.303 Million cell updates/sec

Title: US-09-165-546A-11
Perfect score: 105
Sequence: 1 GAASGLNGCCRCGARGPE 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 451056

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*
1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US080_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	63	60.0	10	19 US-09-529-206-24	Sequence 24, Appl
4	63	60.0	10	19 US-09-529-206A-24	Sequence 24, Appl
5	63	60.0	10	19 US-09-529-206A-122	Sequence 122, Appl
6	63	60.0	10	19 US-09-529-206B-24	Sequence 24, Appl
7	63	60.0	10	19 US-09-529-206B-122	Sequence 122, Appl

8	59	56.2	9	19	US-09-529-206-81	Sequence 81, Appl
9	59	56.2	9	19	US-09-529-206A-81	Sequence 81, Appl
10	59	56.2	9	19	US-09-529-206B-81	Sequence 81, Appl
11	57	54.3	10	19	US-09-529-206-21	Sequence 21, Appl
12	57	54.3	10	19	US-09-529-206A-21	Sequence 21, Appl
13	57	54.3	10	19	US-09-529-206A-119	Sequence 119, Appl
14	57	54.3	10	19	US-09-529-206B-21	Sequence 21, Appl
15	57	54.3	10	19	US-09-529-206B-119	Sequence 119, Appl
16	53	50.5	9	19	US-09-529-206-83	Sequence 83, Appl
17	53	50.5	9	19	US-09-529-206A-83	Sequence 83, Appl
18	53	50.5	9	19	US-09-529-206B-83	Sequence 83, Appl
19	48	45.7	9	19	US-09-529-206-100	Sequence 100, Appl
20	48	45.7	9	19	US-09-529-206A-100	Sequence 100, Appl
21	48	45.7	9	19	US-09-529-206B-100	Sequence 100, Appl
22	47	44.8	10	19	US-09-529-206-20	Sequence 20, Appl
23	47	44.8	10	19	US-09-529-206A-20	Sequence 20, Appl
24	47	44.8	10	19	US-09-529-206A-118	Sequence 118, Appl
25	47	44.8	10	19	US-09-529-206B-20	Sequence 20, Appl
26	47	44.8	10	19	US-09-529-206B-118	Sequence 118, Appl
27	42	40.0	10	11	US-08-753-781B-16	Sequence 16, Appl
28	41	39.0	11	13	US-08-982-981-16	Sequence 16, Appl
29	41	39.0	11	1	PCT-US00-03021-14	Sequence 14, Appl
30	41	39.0	11	18	US-09-497-491-14	Sequence 14, Appl
31	40	38.1	11	17	US-09-362-731-15	Sequence 15, Appl
32	40	38.1	12	1	PCT-US99-05804-292	Sequence 292, App
33	40	38.1	12	17	US-09-397-945-313	Sequence 313, App
34	39	37.1	12	1	PCT-US00-29426-18	Sequence 18, Appl
35	37	35.2	15	1	PCT-US99-02405-51	Sequence 51, Appl
36	37	35.2	15	20	US-09-601-558-51	Sequence 51, Appl
37	37	35.2	15	22	US-09-894-594-51	Sequence 51, Appl
38	36	34.3	10	1	PCT-US00-25559-148	Sequence 148, App
39	36	34.3	10	20	US-09-664-225-148	Sequence 148, App
40	36	34.3	14	1	PCT-US00-25559-155	Sequence 155, App
41	36	34.3	14	20	US-09-664-225-155	Sequence 155, App
42	36	34.3	15	1	PCT-US94-11927-22	Sequence 22, Appl
43	36	34.3	15	1	PCT-US97-02298B-308	Sequence 308, App
44	36	34.3	15	19	US-09-500-124-308	Sequence 308, App
45	36	34.3	15	21	US-09-786-681-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-165-546A-11
; Sequence 11, Application US/09165546A
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao,
; Canlan, Matt; Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO
; AMINO ACID SEQUENCES OF NY-ESO-1, WHICH BIND TO
; MHC CLASS I AND MHC CLASS II MOLECULES, AND
; USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,546A
; FILING DATE: 02-Oct-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998

APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
APPLICATION NUMBER: US 08/752,182
FILING DATE: 03-October-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, Norman D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-165-546A-11

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Best Local Similarity 100.0%; Pred. No. 6.4e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
Db 1 GAASGLNGCCRCGARGPE 18

RESULT 2

US-09-408-036B-10
Sequence 10, Application US/09408036B
GENERAL INFORMATION:
APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: pfreundschuh, Michael
TITLE OF INVENTION: Isolated Peptides Which Bind to MHC Class II Molecules and Uses Thereof
FILE REFERENCE: LUD 5624
CURRENT APPLICATION NUMBER: US/09/408,036B
CURRENT FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 09/344,040
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 09/165,546
PRIOR FILING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 38
SEQ ID NO 10
LENGTH: 18
TYPE: PRT
ORGANISM: Homo sapiens
US-09-408-036B-10

Query Match 100.0%; Score 105; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.4e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
Db 1 GAASGLNGCCRCGARGPE 18

RESULT 3

US-09-529-206-24
Sequence 24, Application US/09529206
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America as represented by the Secretary of Health and Human Services
TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene Thereof
FILE REFERENCE: 20264269PC
CURRENT APPLICATION NUMBER: US/09/529,206
CURRENT FILING DATE: 2000-06-13
PRIOR APPLICATION NUMBER: US60/061,428
PRIOR FILING DATE: 1997-10-08

NUMBER OF SEQ ID NOS: 106
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 24
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-09-529-206-24

Query Match 60.0%; Score 63; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LNGCCRCGAR 15
Db 1 LNGCCRCGAR 10

RESULT 4

US-09-529-206A-24
Sequence 24, Application US/09529206A
GENERAL INFORMATION:
APPLICANT: Wang Rong, Fu
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene Thereof
FILE REFERENCE: 20264269US1
CURRENT APPLICATION NUMBER: US/09/529,206A
CURRENT FILING DATE: 2000-06-13
PRIOR APPLICATION NUMBER: PCT/US98/19609
PRIOR FILING DATE: 1998-09-21
PRIOR APPLICATION NUMBER: US60/061,428
PRIOR FILING DATE: 1997-10-08
NUMBER OF SEQ ID NOS: 127
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 24
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-09-529-206A-24

Query Match 60.0%; Score 63; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LNGCCRCGAR 15
Db 1 LNGCCRCGAR 10

RESULT 5

US-09-529-206A-122
Sequence 122, Application US/09529206A
GENERAL INFORMATION:
APPLICANT: Wang Rong, Fu
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene Thereof
FILE REFERENCE: 20264269US1
CURRENT APPLICATION NUMBER: US/09/529,206A
CURRENT FILING DATE: 2000-06-13
PRIOR APPLICATION NUMBER: PCT/US98/19609
PRIOR FILING DATE: 1998-09-21
PRIOR APPLICATION NUMBER: US60/061,428
PRIOR FILING DATE: 1997-10-08
NUMBER OF SEQ ID NOS: 127
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 122
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-09-529-206A-122

Query Match 60.0%; Score 63; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LNGCCRCGAR 15
Db 1 LNGCCRCGAR 10

RESULT 6
US-09-529-206B-24
; Sequence 24, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-24

Query Match 60.0%; Score 63; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LNGCCRCGAR 15
Db 1 LNGCCRCGAR 10

RESULT 7
US-09-529-206B-122
; Sequence 122, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 122
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-122

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Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LNGCCRCGAR 15

Db 1 LNGCCRCGAR 10
RESULT 8
US-09-529-206-81
; Sequence 81, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 81
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-81

Query Match 56.2%; Score 59; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NGCCRCGAR 15
Db 1 NGCCRCGAR 9

RESULT 9
US-09-529-206A-81
; Sequence 81, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206A-81

Query Match 56.2%; Score 59; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NGCCRCGAR 15
Db 1 NGCCRCGAR 9

RESULT 10
US-09-529-206B-81
; Sequence 81, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven

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; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-81

Query Match      56.2%; Score 59; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NGCCRCGAR 15
Db 1 NGCCRCGAR 9

RESULT 11
US-09-529-206-21
; Sequence 21, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-21

Query Match      54.3%; Score 57; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AASGLNGCCR 11
Db 1 AASGLNGCCR 10

RESULT 12
US-09-529-206A-21
; Sequence 21, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206A-21

Query Match      54.3%; Score 57; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AASGLNGCCR 11
Db 1 AASGLNGCCR 10

RESULT 13
US-09-529-206A-119
; Sequence 119, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 119
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206A-119

Query Match      54.3%; Score 57; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AASGLNGCCR 11
Db 1 AASGLNGCCR 10

RESULT 14
US-09-529-206B-21
; Sequence 21, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-21
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Query Match 54.3%; Score 57; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AASGLNGCCR 11
Db 1 AASGLNGCCR 10

RESULT 15
US-09-529-206B-119
; Sequence 119, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 119
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-119

Query Match 54.3%; Score 57; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AASGLNGCCR 11
Db 1 AASGLNGCCR 10

Search completed: July 3, 2002, 11:38:25
Job time: 851 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:27:54 ; Search time 47.88 Seconds
(without alignments)
9.183 Million cell updates/sec

Title: US-09-165-546A-10
Perfect score: 92
Sequence: 1 PLPVPGVLLKFTVSGNI 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	92	100.0	18	4	US-09-359-503-10	Sequence 10, Appl
2	57	62.0	18	4	US-09-359-503-9	Sequence 9, Appli
3	37	40.2	15	4	US-08-981-392-59	Sequence 59, Appl
4	32	34.8	15	3	US-08-630-916A-91	Sequence 91, Appl
5	32	34.8	15	4	US-08-602-999A-321	Sequence 321, App
6	32	34.8	15	4	US-08-630-915A-147	Sequence 147, App
7	31	33.7	11	2	US-08-769-745-24	Sequence 24, Appl
8	31	33.7	15	3	US-09-195-868-4	Sequence 4, Appli
9	31	33.7	16	1	US-08-447-010-14	Sequence 14, Appl
10	30	32.6	13	4	US-08-602-999A-64	Sequence 64, Appl
11	30	32.6	13	4	US-08-278-865-64	Sequence 64, Appl
12	30	32.6	13	4	US-08-630-915A-4	Sequence 4, Appli
13	30	32.6	13	4	US-08-630-915A-178	Sequence 178, App
14	30	32.6	17	4	US-08-630-915A-42	Sequence 42, Appl
15	30	32.6	18	4	US-08-604-365-1	Sequence 1, Appli
16	29	31.5	7	1	US-08-230-047-37	Sequence 37, Appl
17	29	31.5	10	3	US-08-159-339A-772	Sequence 772, App
18	29	31.5	12	1	US-08-230-047-36	Sequence 36, Appl
19	29	31.5	15	1	US-08-230-047-28	Sequence 28, Appl
20	29	31.5	15	4	US-08-602-999A-306	Sequence 306, App
21	29	31.5	18	4	US-09-177-249-285	Sequence 285, App
22	29	31.5	18	4	US-09-359-503-13	Sequence 13, Appl
23	28	30.4	7	2	US-08-417-174-28	Sequence 28, Appl
24	28	30.4	7	2	US-08-231-565A-28	Sequence 28, Appl
25	28	30.4	7	2	US-09-007-961-28	Sequence 28, Appl
26	28	30.4	7	4	US-09-267-439-28	Sequence 28, Appl
27	28	30.4	8	2	US-08-482-651-49	Sequence 49, Appl

28	28	30.4	8	4	US-08-660-092-52	Sequence 52, Appl
29	28	30.4	10	2	US-08-482-651-61	Sequence 61, Appl
30	28	30.4	10	4	US-08-660-092-214	Sequence 214, App
31	28	30.4	12	1	US-07-778-233B-13	Sequence 13, Appl
32	28	30.4	12	1	US-07-963-321-13	Sequence 13, Appl
33	28	30.4	12	1	US-08-290-641-13	Sequence 13, Appl
34	28	30.4	12	1	US-08-548-540-13	Sequence 13, Appl
35	28	30.4	12	5	PCT-US96-09809-13	Sequence 13, Appl
36	28	30.4	13	4	US-08-602-999A-73	Sequence 73, Appl
37	28	30.4	13	4	US-08-278-865-73	Sequence 73, Appl
38	28	30.4	13	4	US-09-319-730-2	Sequence 2, Appli
39	28	30.4	16	5	PCT-US91-09152-13	Sequence 13, Appl
40	28	30.4	16	5	PCT-US91-09152-23	Sequence 23, Appl
41	28	30.4	18	2	US-08-809-267-12	Sequence 12, Appl
42	28	30.4	18	5	PCT-US95-13662A-12	Sequence 12, Appl
43	27	29.3	12	1	US-08-186-364-2	Sequence 2, Appli
44	27	29.3	12	1	US-08-064-271-7	Sequence 7, Appli
45	27	29.3	12	3	US-08-930-589A-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-359-503-10
; Sequence 10, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid

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; TOPOLOGY: linear
US-09-359-503-10

Query Match 100.0%; Score 92; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
   |||||
Db 1 PLPVPGVLLKEFTVSGNI 18

RESULT 2
US-09-359-503-9
; Sequence 9, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-359-503-9

Query Match 62.0%; Score 57; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VLLKEFTVSGNI 18
   |||||
to NY-
```

```

Db 1 VLLKEFTVSGNI 12

RESULT 3
US-08-981-392-59
; Sequence 59, Application US/08981392
; Patent No. 6262025
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; APPLICANT: Henrique, Domingos Manuel Pinto
; APPLICANT: Lewis, Julian Hart
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
; TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,392
; FILING DATE: 22-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Antler, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-981-392-59

Query Match 40.2%; Score 37; DB 4; Length 15;
Best Local Similarity 63.6%; Pred. No. 3.4;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKE 11
   |:|:|:|:|
Db 3 PVPLPGRLLGE 13

RESULT 4
US-08-630-916A-91
; Sequence 91, Application US/08630916A
; Patent No. 6011137
; GENERAL INFORMATION:
; APPLICANT: Pirozzi, Gregorio
; APPLICANT: Kay, Brian K.
; APPLICANT: Fowlkes, Dana M.
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
; TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
```


;
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,916A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-203
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 896-8864/9741
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-630-916A-91

Query Match 34.8%; Score 32; DB 3; Length 15;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 PLPVPGV 7
 | | | | |
Db 9 PLDPGV 15

RESULT 5
US-08-602-999A-321
; Sequence 321, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872

;
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 321:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-321

Query Match 34.8%; Score 32; DB 4; Length 15;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 PLPVPGV 7
 | | | | |
Db 9 PLDPGV 15

RESULT 6
US-08-630-915A-147
; Sequence 147, Application US/08630915A
; Patent No. 6309820
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. 6309820h
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; TITLE OF INVENTION: USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,915A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 147:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-630-915A-147

Query Match 34.8%; Score 32; DB 4; Length 15;
Best Local Similarity 85.7%; Pred. No. 25;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLPVPGV 7
 | | | | |
Db 9 PLPDPGV 15

RESULT 7

US-08-769-745-24
; Sequence 24, Application US/08769745
; Patent No. 5955259
; GENERAL INFORMATION:
; APPLICANT: Holmes, Todd C.
; APPLICANT: Levitan, Irwin B.
; APPLICANT: Brandeis University
; TITLE OF INVENTION: Mechanism for the Regulation of Ion
; FILE REFERENCE: BRU96-02
; CURRENT APPLICATION NUMBER: US/08/769,745
; CURRENT FILING DATE: 1996-12-19
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Rat
US-08-769-745-24

Query Match 33.7%; Score 31; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLPVPG 6
 | | | | |
Db 2 PLPAPG 7

RESULT 8

US-09-195-868-4
; Sequence 4, Application US/09195868
; Patent No. 6090621
; GENERAL INFORMATION:
; APPLICANT: KAVANAUGH MD, MICHAEL
; APPLICANT: POT PH.D., DAVID
; APPLICANT: WILLIAMS MDPHD, LEWIS T.
; TITLE OF INVENTION: SIGNALING INOSITOL POLYPHOSPHATE
; TITLE OF INVENTION: 5-PHOSPHATASES (SIPs)
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: 4560 HORTON STREET
; CITY: EMERYVILLE
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/195,868
; FILING DATE:
; CLASSIFICATION:
; APPLICATION NUMBER: US/09/195,868
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FIRESTONE, LEIGH H.
; REGISTRATION NUMBER: 36,831
; REFERENCE/DOCKET NUMBER: 1182.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-923-2707

; TELEFAX: 510-655-3542
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-195-868-4

Query Match 33.7%; Score 31; DB 3; Length 15;
Best Local Similarity 62.5%; Pred. No. 36;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLPVPGV 8
 | | | | |
Db 4 PCPEPGIL 11

RESULT 9

US-08-447-010-14
; Sequence 14, Application US/08447010
; Patent No. 5770718
; GENERAL INFORMATION:
; APPLICANT: MOFFATT, BARBARA
; TITLE OF INVENTION: GENE FOR APRT FROM PLANT TISSUE
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 330 University Avenue, Suite 701
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,010
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/888,132
; FILING DATE: 26-MAY-1992
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1811-183 MIS:vg
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; TELEX: 065-24567 SIMBAS
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-447-010-14

Query Match 33.7%; Score 31; DB 1; Length 16;
Best Local Similarity 36.4%; Pred. No. 39;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 PVPGVLLKEFT 13
| | | : : |
Db 6 PKPGIMFQDIT 16

RESULT 10

US-08-602-999A-64
; Sequence 64, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-64

Query Match 32.6%; Score 30; DB 4; Length 13;
Best Local Similarity 71.4%; Pred. No. 46;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLPVPVG 7
| | | : |
Db 5 PLPIPPV 11

RESULT 11

US-08-278-865-64
; Sequence 64, Application US/08278865
; Patent No. 6303574
; GENERAL INFORMATION:
; APPLICANT: KAY, BRIAN K.
; APPLICANT: SPARKS, ANDREW B.
; APPLICANT: THORN, JUDITH M.
; APPLICANT: QUILLIAM, LAWRENCE A.
; APPLICANT: DER, CHANNING J.

; TITLE OF INVENTION: Src SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/278,865
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-007-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-278-865-64

Query Match 32.6%; Score 30; DB 4; Length 13;
Best Local Similarity 71.4%; Pred. No. 46;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLPVPVG 7
| | | : |
Db 5 PLPIPPV 11

RESULT 12

US-08-630-915A-4
; Sequence 4, Application US/08630915A
; Patent No. 6309820
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. 6309820h
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; TITLE OF INVENTION: USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/630,915A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Other
; OTHER INFORMATION: May or may not have carboxy-terminal
; OTHER INFORMATION: amide and/or biotinylated N-terminal
US-08-630-915A-4

Query Match 32.6%; Score 30; DB 4; Length 13;
Best Local Similarity 71.4%; Pred. No. 46;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLPVPVGV 7
|||:| |
Db 5 PLPIPPV 11

RESULT 13
US-08-630-915A-178
; Sequence 178, Application US/08630915A
; Patent No. 6309820
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. 6309820h
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; TITLE OF INVENTION: USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,915A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 178:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-630-915A-178

Query Match 32.6%; Score 30; DB 4; Length 13;
Best Local Similarity 71.4%; Pred. No. 46;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLPVPVGV 7
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Db 5 PLPIPPV 11

RESULT 14
US-08-630-915A-42
; Sequence 42, Application US/08630915A
; Patent No. 6309820
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. 6309820h
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; TITLE OF INVENTION: USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,915A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Other
; OTHER INFORMATION: Biotinylated N-terminal
US-08-630-915A-42

Query Match 32.6%; Score 30; DB 4; Length 17;
Best Local Similarity 71.4%; Pred. No. 63;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Job time: 410 sec

QY 1 PLPVPGV 7
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Db 9 PLPIPPV 15

RESULT 15
US-08-604-365-1
; Sequence 1, Application US/08604365
; Patent No. 6183949
; GENERAL INFORMATION:
; APPLICANT: Seidel, Christoph; Ehrlich-Weinreich,
; APPLICANT: Gertraud; Bayer, Hubert; Wienhues, Ursula; Jung,
; APPLICANT: G nther-Gerhard; Ihlenfeldt, Hans Georg
; TITLE OF INVENTION: HCV Peptide Antigens and Methods for
; TITLE OF INVENTION: the Determination of HCV
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/604,365
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/977,398
; FILING DATE: 11-MARCH-1993
; APPLICATION NUMBER: PCT/EP92/01468
; FILING DATE: 30-JUNE-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 41 22 160.5
; FILING DATE: 04-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 41 41 304.0
; FILING DATE: 14-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 42 09 216.9
; FILING DATE: 21-MARCH-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsai, Christine H.
; REGISTRATION NUMBER: 34,266
; REFERENCE/DOCKET NUMBER: BOER 1010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-604-365-1

Query Match 32.6%; Score 30; DB 4; Length 18;
Best Local Similarity 54.5%; Pred. No. 67;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 LPVPGVLLKEF 12
: | | | : | |
Db 7 IPDRGVLYREF 17

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:38:24 ; Search time 560.51 Seconds
(without alignments)
11.303 Million cell updates/sec

Title: US-09-165-546A-10
Perfect score: 92
Sequence: 1 PLPVPGVLLKEFTVSGNI 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 451056

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	100.0	18	15 US-09-165-546A-10	Sequence 10, Appl
2	92	100.0	18	18 US-09-408-036B-9	Sequence 9, Appli
3	57	62.0	18	15 US-09-165-546A-9	Sequence 9, Appli
4	57	62.0	18	18 US-09-408-036B-8	Sequence 8, Appli
5	52	56.5	10	19 US-09-529-206-88	Sequence 88, Appl
6	52	56.5	10	19 US-09-529-206A-88	Sequence 88, Appl
7	52	56.5	10	19 US-09-529-206B-88	Sequence 88, Appl

8	45	48.9	9	19	US-09-529-206-65	Sequence 65, Appl
9	45	48.9	9	19	US-09-529-206A-65	Sequence 65, Appl
10	45	48.9	9	19	US-09-529-206B-65	Sequence 65, Appl
11	43	46.7	9	19	US-09-529-206-66	Sequence 66, Appl
12	43	46.7	9	19	US-09-529-206A-66	Sequence 66, Appl
13	43	46.7	9	19	US-09-529-206B-66	Sequence 66, Appl
14	37	40.2	9	6	US-08-234-784B-27	Sequence 27, Appl
15	37	40.2	9	10	US-08-682-768-27	Sequence 27, Appl
16	37	40.2	9	12	US-08-816-454-27	Sequence 27, Appl
17	37	40.2	9	12	US-08-816-454A-27	Sequence 27, Appl
18	37	40.2	9	12	US-08-816-454B-27	Sequence 27, Appl
19	37	40.2	15	21	US-09-783-931-59	Sequence 59, Appl
20	37	40.2	15	23	US-09-908-322-59	Sequence 59, Appl
21	35	38.0	9	18	US-09-409-455A-120	Sequence 120, App
22	35	38.0	9	22	US-09-833-039-120	Sequence 120, App
23	35	38.0	10	19	US-09-529-206-91	Sequence 91, Appl
24	35	38.0	10	19	US-09-529-206A-91	Sequence 91, Appl
25	35	38.0	10	19	US-09-529-206B-91	Sequence 91, Appl
26	33	35.9	9	6	US-08-234-784B-26	Sequence 26, Appl
27	33	35.9	9	10	US-08-682-768-26	Sequence 26, Appl
28	33	35.9	9	12	US-08-816-454-26	Sequence 26, Appl
29	33	35.9	9	12	US-08-816-454A-26	Sequence 26, Appl
30	33	35.9	9	12	US-08-816-454B-26	Sequence 26, Appl
31	33	35.9	10	6	US-08-234-784B-69	Sequence 69, Appl
32	33	35.9	10	10	US-08-682-768-69	Sequence 69, Appl
33	33	35.9	10	12	US-08-816-454-69	Sequence 69, Appl
34	33	35.9	10	12	US-08-816-454A-69	Sequence 69, Appl
35	33	35.9	10	12	US-08-816-454B-69	Sequence 69, Appl
36	32	34.8	15	1	PCT-US97-02298B-321	Sequence 321, App
37	32	34.8	15	12	US-08-826-516B-91	Sequence 91, Appl
38	32	34.8	15	12	US-08-826-516-91	Sequence 91, Appl
39	32	34.8	15	19	US-09-500-124-321	Sequence 321, App
40	32	34.8	15	22	US-09-879-957-147	Sequence 147, App
41	32	34.8	17	24	US-10-029-386-33100	Sequence 33100, A
42	31	33.7	12	24	US-10-007-649-92	Sequence 92, Appl
43	31	33.7	15	9	US-08-569-578-4	Sequence 4, Appli
44	31	33.7	15	10	US-08-624-190-4	Sequence 4, Appli
45	31	33.7	15	11	US-08-759-397A-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-165-546A-10
; Sequence 10, Application US/09165546A
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao,
; Canlan, Matt; Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO
; AMINO ACID SEQUENCES OF NY-ESO-1, WHICH BIND TO
; MHC CLASS I AND MHC CLASS II MOLECULES, AND
; USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,546A
; FILING DATE: 02-Oct-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998


```

;
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-165-546A-10

Query Match      100.0%; Score 92; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PLPVPGVLLKKEFTVSGNI 18
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Db      1 PLPVPGVLLKKEFTVSGNI 18

RESULT 2
US-09-408-036B-9
; Sequence 9, Application US/09408036B
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Isolated Peptides Which Bind to MHC Class II Molecules and Uses T
; FILE REFERENCE: LUD 5624
; CURRENT APPLICATION NUMBER: US/09/408,036B
; CURRENT FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/165,546
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 9
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-408-036B-9

Query Match      100.0%; Score 92; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PLPVPGVLLKKEFTVSGNI 18
      |||||
Db      1 PLPVPGVLLKKEFTVSGNI 18

RESULT 3
US-09-165-546A-9
; Sequence 9, Application US/09165546A
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao,
; Canlan, Matt; Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO
; AMINO ACID SEQUENCES OF NY-ESO-1, WHICH BIND TO
; MHC CLASS I AND MHC CLASS II MOLECULES, AND
; USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
```

```

;
; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,546A
; FILING DATE: 02-Oct-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-165-546A-9

Query Match      62.0%; Score 57; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 VLLKEFTVSGNI 18
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Db      1 VLLKEFTVSGNI 12

RESULT 4
US-09-408-036B-8
; Sequence 8, Application US/09408036B
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Isolated Peptides Which Bind to MHC Class II Molecules and Use
; FILE REFERENCE: LUD 5624
; CURRENT APPLICATION NUMBER: US/09/408,036B
; CURRENT FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/165,546
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-408-036B-8

Query Match      62.0%; Score 57; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 7 VLLKFTVSGNI 18
| | | | | | | | | |
Db 1 VLLKFTVSGNI 12

RESULT 5
US-09-529-206-88
; Sequence 88, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-88

Query Match 56.5%; Score 52; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLK 10
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Db 1 PLPVPGVLLK 10

RESULT 6
US-09-529-206A-88
; Sequence 88, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206A-88

Query Match 56.5%; Score 52; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLK 10
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Db 1 PLPVPGVLLK 10

RESULT 7
US-09-529-206B-88
; Sequence 88, Application US/09529206B
; GENERAL INFORMATION:

; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-88

Query Match 56.5%; Score 52; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLK 10
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Db 1 PLPVPGVLLK 10

RESULT 8
US-09-529-206-65
; Sequence 65, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-65

Query Match 48.9%; Score 45; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPVPGVLLK 10
| | | | | | | | | |
Db 1 LPVPGVLLK 9

RESULT 9
US-09-529-206A-65
; Sequence 65, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428

; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206A-65

Query Match 48.9%; Score 45; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPVPGVLLK 10
|
Db 1 LPVPGVLLK 9

RESULT 10
US-09-529-206B-65
; Sequence 65, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-65

Query Match 48.9%; Score 45; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPVPGVLLK 10
|
Db 1 LPVPGVLLK 9

RESULT 11
US-09-529-206-66
; Sequence 66, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-66

Query Match 46.7%; Score 43; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GVLLKEFTV 14
|
Db 1 GVLLKEFTV 9

RESULT 12
US-09-529-206A-66
; Sequence 66, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206A-66

Query Match 46.7%; Score 43; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GVLLKEFTV 14
|
Db 1 GVLLKEFTV 9

RESULT 13
US-09-529-206B-66
; Sequence 66, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-66

Query Match 46.7%; Score 43; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GVLLKEFTV 14
|
Db 1 GVLLKEFTV 9

RESULT 14
US-08-234-784B-27
; Sequence 27, Application US/08234784B
; GENERAL INFORMATION:
; APPLICANT: Slingsluff, Craig L, Jr.
; APPLICANT: Engelhard, Victor H.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Shabanowitz, Jeffrey
; APPLICANT: Cox, Andrea L.
; TITLE OF INVENTION: PEPTIDES RECOGNIZED BY MELANOMA-SPECIFIC
; TITLE OF INVENTION: CYTOTOXIC LYMPHOCYTES, AND USES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,784B
; FILING DATE: 29-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/197,399
; FILING DATE: 16-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: SLINGSLUFF=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: amino acids
; STRANDEDNESS: n/a
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal fragment
; ORIGINAL SOURCE: not applicable
; IMMEDIATE SOURCE: not applicable
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 12
; MAP POSITION: unknown
; UNITS: unknown
; FEATURE:
; NAME/KEY: SEQ ID NO: 27
; LOCATION: Precursor protein Pmel-17 (PIR database, accession
; LOCATION: number A41234), residues 585-593.
; IDENTIFICATION METHOD: This peptide was identified, from the
; IDENTIFICATION METHOD: Pmel-17 molecule, as fitting the consensus sequence for P
; IDENTIFICATION METHOD: ing to human HLA-A2.1. Pmel-17 was identified because of
; IDENTIFICATION METHOD: to the Seq ID No. 14 which has biologic activity.
; OTHER INFORMATION: None
; PUBLICATION INFORMATION: Unpublished.
US-08-234-784B-27

Query Match 40.2%; Score 37; DB 6; Length 9;
Best Local Similarity 75.0%; Pred. No. 3.2e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LPVPGVLL 9
; :|||:|
Db 2 MPVPGILL 9
; :|||:|
RESULT 15
US-08-682-768-27
; Sequence 27, Application US/08682768
; GENERAL INFORMATION:
; APPLICANT: SLINGSLUFF, Craig L.
; APPLICANT: ENGELHARD, Victor H.
; APPLICANT: HUNT, Donald F.
; APPLICANT: SHABANOWITZ, Jeffrey
; TITLE OF INVENTION: PEPTIDES RECOGNIZED BY MELANOMA-SPECIFIC
; TITLE OF INVENTION: CYTOTOXIC LYMPHOCYTES, AND USES THEREFOR
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,768
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01991
; FILING DATE: 16-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/234,784
; FILING DATE: 29-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,399
; FILING DATE: 16-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: SLINGSLUFF=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: amino acids
; STRANDEDNESS: n/a
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal fragment
; ORIGINAL SOURCE: not applicable
; IMMEDIATE SOURCE: not applicable
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 12
; MAP POSITION: unknown
; UNITS: unknown
; FEATURE:
; NAME/KEY: SEQ ID NO: 27
; LOCATION: Precursor protein Pmel-17 (PIR database, accession
; LOCATION: number A41234), residues 585-593.
; IDENTIFICATION METHOD: This peptide was identified, from the
; IDENTIFICATION METHOD: Pmel-17 molecule, as fitting the consensus sequence fo
; IDENTIFICATION METHOD: ing to human HLA-A2.1. Pmel-17 was identified because
; IDENTIFICATION METHOD: to the Seq ID No. 14 which has biologic activity.
; OTHER INFORMATION: None
; PUBLICATION INFORMATION: Unpublished.

US-08-682-768-27

Query Match 40.2%; Score 37; DB 10; Length 9;
Best Local Similarity 75.0%; Pred. No. 3.2e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPVPGVLL 9
:||||:
Db 2 MPVPGILL 9

Search completed: July 3, 2002, 11:38:25
Job time: 851 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:27:53 ; Search time 47.88 Seconds
(without alignments)
9.183 Million cell updates/sec

Title: US-09-165-546A-9

Perfect score: 84
Sequence: 1 VLLKEFTVSGNLTIRLT 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 113617

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84	100.0	18	4	US-09-359-503-9
2	57	67.9	18	4	US-09-359-503-10
3	56	66.7	18	4	US-09-359-503-13
4	33	39.3	18	4	US-09-177-249-285
5	28	33.3	12	1	US-07-778-233B-13
6	28	33.3	12	1	US-07-963-321-13
7	28	33.3	12	1	US-08-290-641-13
8	28	33.3	12	1	US-08-548-540-13
9	28	33.3	12	5	PCT-US96-09809-13
10	28	33.3	17	6	5185441-3
11	26	31.0	14	2	US-08-764-640-92
12	26	31.0	14	3	US-08-973-225-92
13	26	31.0	14	3	US-08-973-225-217
14	26	31.0	14	3	US-09-244-298A-92
15	26	31.0	14	4	US-09-516-704-92
16	26	31.0	17	4	US-09-227-357-383
17	26	31.0	18	2	US-08-702-105A-15
18	26	31.0	18	3	US-08-702-110A-15
19	26	31.0	18	4	US-09-325-571-15
20	25	29.8	9	4	US-09-258-754-253
21	25	29.8	9	4	US-09-042-107-253
22	25	29.8	11	1	US-08-665-966-4
23	25	29.8	11	3	US-09-041-780-4
24	25	29.8	16	4	US-09-514-302-5
25	24	28.6	15	4	US-09-336-447A-36
26	24	28.6	16	1	US-08-036-555B-121
27	24	28.6	16	1	US-08-469-569-121

28	24	28.6	16	1	US-08-249-322A-121	Sequence 121, App
29	24	28.6	16	1	US-08-469-526A-121	Sequence 121, App
30	24	28.6	16	2	US-08-734-591A-121	Sequence 121, App
31	24	28.6	16	2	US-08-469-660-121	Sequence 121, App
32	24	28.6	16	4	US-08-470-335-121	Sequence 121, App
33	24	28.6	16	4	US-08-735-021-121	Sequence 121, App
34	24	28.6	16	4	US-08-734-664A-121	Sequence 121, App
35	24	28.6	16	4	US-08-470-339-121	Sequence 121, App
36	24	28.6	16	5	PCT-US94-05083C-117	Sequence 117, App
37	24	28.6	16	5	PCT-US95-06846A-121	Sequence 121, App
38	24	28.6	18	3	US-09-100-414B-24	Sequence 24, Appl
39	24	28.6	18	4	US-09-303-323-24	Sequence 24, Appl
40	23	27.4	8	1	US-08-146-886-19	Sequence 19, Appl
41	23	27.4	8	4	US-09-109-613-19	Sequence 19, Appl
42	23	27.4	11	2	US-08-801-301A-1	Sequence 1, Appli
43	23	27.4	12	1	US-08-290-301-67	Sequence 67, Appl
44	23	27.4	12	2	US-08-480-190-248	Sequence 248, App
45	23	27.4	12	2	US-08-488-379-248	Sequence 248, App

ALIGNMENTS

RESULT 1
US-09-359-503-9
; Sequence 9, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid


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; TOPOLOGY: linear
US-09-359-503-9

Query Match 100.0%; Score 84; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNLTIRLT 18
   |||
Db 1 VLLKEFTVSGNLTIRLT 18
   |||

RESULT 2
US-09-359-503-10
; Sequence 10, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-359-503-10

Query Match 67.9%; Score 57; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNI 12
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```

Db 7 VLLKEFTVSGNI 18

RESULT 3
US-09-359-503-13
; Sequence 13, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-359-503-13

Query Match 66.7%; Score 56; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TVSGNLTIRLT 18
   |||
Db 1 TVSGNLTIRLT 12
   |||

RESULT 4
US-09-177-249-285
; Sequence 285, Application US/09177249
; Patent No. 6229064
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir

```

APPLICANT: Kiyosue, Tomohiro
APPLICANT: Yadegari, Ramin
APPLICANT: Margossian, Linda
APPLICANT: Harada, John
APPLICANT: Goldberg, Robert B.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
TITLE OF INVENTION: Development in Plants
FILE REFERENCE: 023070-086120US
CURRENT APPLICATION NUMBER: US/09/177,249
CURRENT FILING DATE: 1998-10-22
EARLIER APPLICATION NUMBER: US 09/071,838
EARLIER FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 324
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 285
LENGTH: 18
TYPE: PRT
ORGANISM: Arabidopsis sp.
US-09-177-249-285

Query Match 39.3%; Score 33; DB 4; Length 18;
Best Local Similarity 58.3%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LLKEFTVSGNIL 13
| | | : | | | |
Db 5 LLKRMSISENIL 16

RESULT 5
US-07-778-233B-13
; Sequence 13, Application US/07778233B
; Patent No. 5270170
; GENERAL INFORMATION:
; APPLICANT: Schatz, Peter J.
; APPLICANT: Cull, Millard G.
; APPLICANT: Miller, Jeff F.
; TITLE OF INVENTION: Peptide Library and Screening Method
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/778,233B
; FILING DATE: 19911016
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11509-50
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: 57 3 0.9

US-07-778-233B-13
Query Match 33.3%; Score 28; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 72;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 2 LLKEFTVSG 10
| : | | | |
Db 3 LRREFKVSG 11
RESULT 6
US-07-963-321-13
; Sequence 13, Application US/07963321
; Patent No. 5338665
; GENERAL INFORMATION:
; APPLICANT: Schatz, Peter J.
; APPLICANT: Cull, Millard G.
; APPLICANT: Miller, Jeff F.
; APPLICANT: Stemmer, Willem P.C.
; TITLE OF INVENTION: Peptide Library and Screening Method
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/963,321
; FILING DATE: 19921015
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/778,223
; FILING DATE: 16-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11509-50-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: 57 3 0.9
US-07-963-321-13
Query Match 33.3%; Score 28; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 72;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 2 LLKEFTVSG 10
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Db 3 LRREFKVSG 11
RESULT 7
US-08-290-641-13
; Sequence 13, Application US/08290641

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; Patent No. 5498530
; GENERAL INFORMATION:
; APPLICANT: Schatz, Peter J.
; APPLICANT: Cull, Millard G.
; APPLICANT: Miller, Jeff F.
; APPLICANT: Stemmer, Willem P.C.
; TITLE OF INVENTION: Peptide Library and Screening Method
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,641
; FILING DATE: 15-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,321
; FILING DATE: 15-OCT-1992
; APPLICATION NUMBER: US 07/778,223
; FILING DATE: 16-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11509-50-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: 57 3 0.9
;
US-08-290-641-13

Query Match 33.3%; Score 28; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 72;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LLKEFTVSG 10
   | :||| |||
Db 3 LRREFKVS 11

RESULT 8
US-08-548-540-13
; Sequence 13, Application US/08548540
; Patent No. 5733731
; GENERAL INFORMATION:
; APPLICANT: Schatz, Peter J.
; APPLICANT: Cull, Millard G.
; APPLICANT: Miller, Jeff F.
; APPLICANT: Stemmer, Willem P.C.
; APPLICANT: Gates, Christian M.
; TITLE OF INVENTION: Peptide Library and Screening Method
; NUMBER OF SEQUENCES: 162
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
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; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/548,540
; FILING DATE: 26-OCT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/290,641
; FILING DATE: 15-AUG-1994
; APPLICATION NUMBER: US 07/963,321
; FILING DATE: 15-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 16528J-001240US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: 57 3 0.9
;
US-08-548-540-13

Query Match 33.3%; Score 28; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 72;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LLKEFTVSG 10
   | :||| |||
Db 3 LRREFKVS 11

RESULT 9
PCT-US96-09809-13
; Sequence 13, Application PC/TUS9609809
; GENERAL INFORMATION:
; APPLICANT: Schatz, Peter J.
; APPLICANT: Cull, Millard G.
; APPLICANT: Miller, Jeff F.
; APPLICANT: Stemmer, Willem P.C.
; APPLICANT: Gates, Christian M.
; TITLE OF INVENTION: Peptide Library and Screening Method
; NUMBER OF SEQUENCES: 162
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09809
; FILING DATE:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,540
; FILING DATE: 26-OCT-1995
; APPLICATION NUMBER: US 08/290,641
; FILING DATE: 15-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,321
; FILING DATE: 15-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 16528J-001240US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: 57 3 0.9
; PCT-US96-09809-13

Query Match 33.3%; Score 28; DB 5; Length 12;
Best Local Similarity 66.7%; Pred. No. 72;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LLKEFTVSG 10
| : || |||
Db 3 LRREFKVS 11

RESULT 10
5185441-3
; Patent No. 5185441
; APPLICANT: WALLNER, BARBARA P.; HESSIONS, CATHERINE
; TITLE OF INVENTION: DNA SEQUENCES, RECOMBINANT DNA
; MOLECULES AND PROCESSES FOR PRODUCING PI-LINKED LYMPHOCYTE
; FUNCTION ASSOCIATED ANTIGEN-3
; NUMBER OF SEQUENCES: 41
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/237,309
; FILING DATE: 26-AUG-1988
; SEQ ID NO: 3:
; LENGTH: 17
; 5185441-3

Query Match 33.3%; Score 28; DB 6; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 7 TVSGNLTIRLT 18
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Db 5 TVSGSLTIYNLT 16

RESULT 11
US-08-764-640-92
; Sequence 92, Application US/08764640
; Patent No. 5869451
; Patent No. 5869451 5837683
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Gates, Christian
; APPLICANT: Schatz, Peter J.
; APPLICANT: Balasubramanian, Palaniappan

;
; APPLICANT: Wagstrom, Christopher R.
; APPLICANT: Hendren, Richard W.
; APPLICANT: Deprince, Randolph B.
; APPLICANT: Podduturi, Surekha
; APPLICANT: Yin, Qun
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; NUMBER OF SEQUENCES: 244
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,640
; FILING DATE: 11-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-764-640-92

Query Match 31.0%; Score 26; DB 2; Length 14;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LKEFTVSG 10
| | | | |
Db 3 LKEFLHSG 10

RESULT 12
US-08-973-225-92
; Sequence 92, Application US/08973225A
; Patent No. 6083913
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; Barrett, Ronald W.
; Cwirla, Steven E.
; Duffin, David J.
; Gates, Christian
; Haselden, Sherril S.
; Mattheakis, Larry C.
; Schatz, Peter J.
; Wagstrom, Christopher R.
; Wrighton, Nicholas C.
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA

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; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,225A
; FILING DATE: 04-Dec-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3065USW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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US-08-973-225-92

Query Match      31.0%; Score 26; DB 3; Length 14;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 LKEFTVSG 10
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Db      3 LKEFLHSG 10

RESULT 13
US-08-973-225-217
; Sequence 217, Application US/08973225A
; Patent No. 6083913
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; Barrett, Ronald W.
; Cwirla, Steven E.
; Duffin, David J.
; Gates, Christian
; Haselden, Sherril S.
; Mattheakis, Larry C.
; Schatz, Peter J.
; Wagstrom, Christopher R.
; Wrighton, Nicholas C.
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; THROMBOPOIETIN RECEPTOR
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,225A
; FILING DATE: 04-Dec-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3065USW
; TELECOMMUNICATION INFORMATION:
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; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 217:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 217:
US-08-973-225-217

Query Match      31.0%; Score 26; DB 3; Length 14;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 LKEFTVSG 10
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Db      3 LKEFLHSG 10

RESULT 14
US-09-244-298A-92
; Sequence 92, Application US/09244298A
; Patent No. 6121238
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Gates, Christian
; APPLICANT: Schatz, Peter J.
; APPLICANT: Balasubramanian, Palaniappan
; APPLICANT: Wagstrom, Christopher R.
; APPLICANT: Hendren, Richard W.
; APPLICANT: Depreince, Randolph B.
; APPLICANT: Podduturi, Surekha
; APPLICANT: Yin, Qun
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; RECEPTOR
; NUMBER OF SEQUENCES: 244
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/244,298A
; FILING DATE: 11-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-244-298A-92

Query Match      31.0%; Score 26; DB 3; Length 14;
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Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LKEFTVSG 10
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Db 3 LKEFLHSG 10

RESULT 15
US-09-516-704-92
; Sequence 92, Application US/09516704
; Patent No. 6251864
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; Barrett, Ronald W.
; Cwirla, Steven E.
; Gates, Christian
; Schatz, Peter J.
; Balasubramanian, Palaniappan
; Wagstrom, Christopher R.
; Hendren, Richard W.
; Deprince, Randolph B.
; Poddaturi, Surekha
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; RECEPTOR
; NUMBER OF SEQUENCES: 244
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/516,704
; FILING DATE: 01-Mar-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 92:

Query Match 31.0%; Score 26; DB 4; Length 14;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LKEFTVSG 10
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Db 3 LKEFLHSG 10

Search completed: July 3, 2002, 11:27:54
Job time: 410 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:21:04 ; Search time 47.88 Seconds
(without alignments)
9.183 Million cell updates/sec

Title: US-09-165-546A-8
Perfect score: 88
Sequence: 1 AADHRQLQLSISSCLQQL 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 113617

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	32	36.4	18	4 US-09-359-503-13	Sequence 13, Appl
3	29	33.0	12	1 US-07-721-761A-12	Sequence 12, Appl
4	29	33.0	12	1 US-07-978-687-12	Sequence 12, Appl
5	29	33.0	12	5 PCT-US91-05801-12	Sequence 12, Appl
6	29	33.0	13	3 US-08-159-339A-1119	Sequence 1119, Ap
7	27	30.7	17	2 US-08-640-847C-23	Sequence 23, Appl
8	26.5	30.1	13	2 US-08-771-602D-32	Sequence 32, Appl
9	26	29.5	13	4 US-09-484-114B-34	Sequence 34, Appl
10	25	28.4	11	1 US-08-127-351-16	Sequence 16, Appl
11	25	28.4	11	1 US-08-480-367B-16	Sequence 16, Appl
12	25	28.4	11	1 US-08-487-221A-16	Sequence 16, Appl
13	25	28.4	11	1 US-08-480-370-16	Sequence 16, Appl
14	25	28.4	12	1 US-08-511-662-6	Sequence 6, Appli
15	25	28.4	12	5 PCT-US96-12632-6	Sequence 6, Appl
16	25	28.4	14	2 US-08-764-640-93	Sequence 93, Appl
17	25	28.4	14	3 US-08-973-225-93	Sequence 93, Appl
18	25	28.4	14	3 US-09-244-298A-93	Sequence 93, Appl
19	25	28.4	14	4 US-09-516-704-93	Sequence 93, Appl
20	25	28.4	15	1 US-08-208-181A-19	Sequence 16, Appl
21	25	28.4	15	3 US-08-701-582D-16	Sequence 16, Appl
22	25	28.4	16	1 US-08-318-200-9	Sequence 9, Appli
23	25	28.4	16	1 US-08-519-777-3	Sequence 3, Appli
24	25	28.4	16	1 US-08-519-777-49	Sequence 49, Appl
25	25	28.4	16	1 US-08-742-035-3	Sequence 3, Appli
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32	25	28.4	16	3 US-08-775-414-49	Sequence 49, Appl
33	25	28.4	16	4 US-08-931-858E-3	Sequence 3, Appli
34	25	28.4	16	4 US-08-981-739-3	Sequence 3, Appli
35	25	28.4	16	4 US-08-981-739-49	Sequence 49, Appl
36	25	28.4	17	2 US-08-640-847C-26	Sequence 26, Appl
37	24	27.3	7	4 US-08-428-711A-5	Sequence 5, Appli
38	24	27.3	13	1 US-08-471-791-5	Sequence 5, Appli
39	24	27.3	13	5 PCT-US91-01746-5	Sequence 5, Appli
40	24	27.3	14	2 US-08-997-080-8	Sequence 8, Appli
41	24	27.3	14	2 US-08-997-362-8	Sequence 8, Appli
42	24	27.3	14	3 US-08-873-970-8	Sequence 8, Appli
43	24	27.3	14	4 US-09-095-855-8	Sequence 8, Appli
44	24	27.3	14	4 US-08-705-347A-8	Sequence 8, Appli
45	24	27.3	14	4 US-09-324-542-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-359-503-8
; Sequence 8, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status Of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS: 18 amino acids
; LENGTH: 18 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
US-09-359-503-8

Query Match 100.0%; Score 88; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.1e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQQL 18
|||||
Db 1 AADHRQLQLSISSCLQQL 18

RESULT 2
US-09-359-503-13
; Sequence 13, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-359-503-13

to NY-

Query Match 36.4%; Score 32; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQ 6
|||||

Db 13 AADHRQ 18

RESULT 3
US-07-721-761A-12
; Sequence 12, Application US/07721761A
; Patent No. 5475099
; GENERAL INFORMATION:
; APPLICANT: Vic. C. Knauf
; APPLICANT: Gregory A. Thompson
; TITLE OF INVENTION: Plant Fatty Acid Synthases
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: CA
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.7
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/721,761A
; FILING DATE: 19910626
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/568,493
; FILING DATE: 15-AUGUST-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Lassen
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; REFERENCE/DOCKET NUMBER: CGNE 76-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (916) 753-6313
; TELEFAX: (916) 753-1510
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-721-761A-12

Query Match 33.0%; Score 29; DB 1; Length 12;
Best Local Similarity 44.4%; Pred. No. 26;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 9 LSISSCLQ 17
|:||||:
Db 4 LGVSSCIER 12

RESULT 4
US-07-978-687-12
; Sequence 12, Application US/07978687
; Patent No. 5510255
; GENERAL INFORMATION:
; APPLICANT: Vic. C. Knauf
; APPLICANT: Gregory A. Thompson
; TITLE OF INVENTION: Plant Fatty Acid Synthases
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: CA
; COUNTRY: USA

;
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.7
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/978,687
; FILING DATE: FEBRUARY 1, 1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/05801
; FILING DATE: 15-AUGUST-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/568,493
; FILING DATE: 15-AUGUST-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/721,761
; FILING DATE: 26-JUNE-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Lassen
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; REFERENCE/DOCKET NUMBER: CGNE 76-2 WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (916) 753-6313
; TELEFAX: (916) 753-1510
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-978-687-12

Query Match 33.0%; Score 29; DB 1; Length 12;
Best Local Similarity 44.4%; Pred. No. 26;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 9 LSISSCLQ 17
Db 4 LGVSSCIER 12

RESULT 5
PCT-US91-05801-12
; Sequence 12, Application PC/TUS9105801
; GENERAL INFORMATION:
; APPLICANT: Vic. C. Knauf
; APPLICANT: Gregory A. Thompson
; TITLE OF INVENTION: Plant Fatty Acid Synthases
; NUMBER OF SEQUENCES:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: CA
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.7
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/05801
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/568,493
; FILING DATE: 15-AUGUST-1990

;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/721,761
; FILING DATE: 26-JUNE-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Lassen
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; REFERENCE/DOCKET NUMBER: CGNE 76-2 WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (916) 753-6313
; TELEFAX: (916) 753-1510
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US91-05801-12

Query Match 33.0%; Score 29; DB 5; Length 12;
Best Local Similarity 44.4%; Pred. No. 26;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 9 LSISSCLQ 17
Db 4 LGVSSCIER 12

RESULT 6
US-08-159-339A-1119
; Sequence 1119, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:

; INFORMATION FOR SEQ ID NO: 1119:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-1119

Query Match 33.0%; Score 29; DB 3; Length 13;
Best Local Similarity 75.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

QY 10 SISSCLQQ 17
| | | | |
Db 1 STSSCLHQ 8

RESULT 7
US-08-640-847C-23
; Sequence 23, Application US/08640847C
; Patent No. 5993865
; GENERAL INFORMATION:
; APPLICANT: BECH, Lene M.
; APPLICANT: SORENSEN, Steen B.
; APPLICANT: VAAG, Pia
; APPLICANT: MULDBJERG, Marianne
; APPLICANT: BEENFELDT, Thorkild
; APPLICANT: LEAH, Robert
; APPLICANT: BREDDAM, Klaus
; TITLE OF INVENTION: BEVERAGE AND A METHOD OF PREPARING IT
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LADAS & PARRY
; STREET: 26 WEST 61 STREET
; CITY: NEW YORK
; STATE: NY
; ZIP: 10023
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3-1/4" Disk 1.44 MB
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11
; SOFTWARE: WordPerfect 8 for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/640,847C
; FILING DATE: 26-JUN-1996
; CLASSIFICATION: 426
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK94/00420
; FILING DATE: 08-NOV-1994
; APPLICATION NUMBER: DK001266/93
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: MASS, Clifford J.
; REGISTRATION NUMBER: 30,086
; REFERENCE/DOCKET NUMBER: U-010781-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 708-1890
; TELEFAX: (212) 246-8959
; TELEX: 233288
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 Amino Acids
; TYPE: Amino Acids
; TOPOLOGY: Linear
US-08-640-847C-23

Query Match 30.7%; Score 27; DB 2; Length 17;
Best Local Similarity 38.5%; Pred. No. 92;
Matches 5; Conservative 4; Mismatches 4; Indels 4; Gaps 0;

QY 3 DHRQLQLSISSCL 15
| | | | |
Db 2 DCGQVNSSLASCI 14

RESULT 8
US-08-771-602D-32
; Sequence 32, Application US/08771602D
; Patent No. 5976795
; GENERAL INFORMATION:
; APPLICANT: Voytas, Daniel F.
; APPLICANT: Zou, Sigé
; TITLE OF INVENTION: Retrotransposon and Methods
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/771,602D
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/010,869
; FILING DATE: 31-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 8-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
US-08-771-602D-32

Query Match 30.1%; Score 26.5; DB 2; Length 13;
Best Local Similarity 46.2%; Pred. No. 82;
Matches 6; Conservative 2; Mismatches 0; Indels 5; Gaps 1;

QY 2 ADHRQLQLSISSC 14
| | | | |
Db 6 ADHR-----LSNC 13

RESULT 9
US-09-484-114B-34
; Sequence 34, Application US/09484114B
; Patent No. 6329178
; GENERAL INFORMATION:
; APPLICANT: Patel, Premal H.
; APPLICANT: Loeb, Lawrence A.
; TITLE OF INVENTION: DNA POLYMERASE MUTANT HAVING ONE OR MORE
; MUTATIONS IN THE ACTIVE SITE
; FILE REFERENCE: 74890002US00
; CURRENT APPLICATION NUMBER: US/09/484,114B
; CURRENT FILING DATE: 2000-01-14

; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Eschericia coli
US-09-484-114B-34

Query Match 29.5%; Score 26; DB 4; Length 13;
Best Local Similarity 57.1%; Pred. No. 1e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 DHRQLQL 9
|:|:|:
Db 6 DYRQIEL 12

RESULT 10
US-08-127-351-16
; Sequence 16, Application US/08127351
; Patent No. 5449761
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; TITLE OF INVENTION: CONSTRUCTS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
; ADDRESSEE: NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,351
; FILING DATE: 28-SEP-1993
; CLASSIFICATION: 534
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-004-44
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-127-351-16

Query Match 28.4%; Score 25; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 QLQLSISS 13
| | | | | |
Db 1 QLQLSAES 8

RESULT 11
US-08-480-367B-16
; Sequence 16, Application US/08480367B
; Patent No. 5578288
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; TITLE OF INVENTION: CONSTRUCTS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE, PRICE, LeBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,367B
; FILING DATE: 07-06-95
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 2654-002A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 684-1111
; TELEFAX: (703) 684-1124
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-480-367B-16

Query Match 28.4%; Score 25; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 QLQLSISS 13
| | | | | |
Db 1 QLQLSAES 8

RESULT 12
US-08-487-221A-16
; Sequence 16, Application US/08487221A
; Patent No. 5593656
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; TITLE OF INVENTION: CONSTRUCTS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
; ADDRESSEE: NEUSTADT, P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia

```
;
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,221A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,351
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-004-44
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-487-221A-16

Query Match 28.4%; Score 25; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 QLQLSISS 13
Db 1 QLQLSAES 8

RESULT 13
US-08-480-370-16
; Sequence 16, Application US/08480370
; Patent No. 5609847
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; TITLE OF INVENTION: CONSTRUCTS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
; ADDRESSEE: NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,370
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,351
; FILING DATE: 28-SEP-1993
```

```
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-004-44
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-480-370-16

Query Match 28.4%; Score 25; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 QLQLSISS 13
Db 1 QLQLSAES 8

RESULT 14
US-08-511-662-6
; Sequence 6, Application US/08511662
; Patent No. 5807552
; GENERAL INFORMATION:
; APPLICANT: Stanton, G. John
; APPLICANT: Hughes, Jr., Thomas K.
; APPLICANT: Smith, Eric M.
; TITLE OF INVENTION: Compositions for Conferring Immunogenicity
; TITLE OF INVENTION: to a Substance and Uses Thereof
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,662
; FILING DATE: Concurrently herewith
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hodgins, Daniel S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTSG:162/HOD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 515/418-3000
; TELEFAX: 512/474-7577
; TELEX: NA
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-511-662-6

Query Match 28.4%; Score 25; DB 1; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.4e+02;
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Matches 3; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Search completed: July 3, 2002, 11:27:53
Job time: 409 sec

QY 4 HRQLQLSIS 12
| |::|::
Db 4 HAQIEVSV 12

RESULT 15
PCT-US96-12632-6
; Sequence 6, Application PC/TUS9612632
; GENERAL INFORMATION:
; APPLICANT: BOARD OF REGENTS, THE UNIVERSITY OF
; APPLICANT: NAME: TEXAS SYSTEM
; APPLICANT: STREET: 201 West 7th Street
; APPLICANT: CITY: Austin
; APPLICANT: STATE: Texas
; APPLICANT: COUNTRY: United States of America
; APPLICANT: POSTAL CODE: 78701
; APPLICANT: TELEPHONE NO: (512) 499-4462
; APPLICANT: TELEFAX: (512) 499-4523
; TITLE OF INVENTION: COMPOSITIONS FOR CONFERRING
; TITLE OF INVENTION: IMMUNOGENICITY TO A SUBSTANCE AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/12632
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/511,662
; FILING DATE: 04 August 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: HODGINS, DANIEL S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTFG162P--
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 515/418-3000
; TELEFAX: 512/474-7577
; TELEX: NA
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US96-12632-6

Query Match 28.4%; Score 25; DB 5; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.4e+02;
Matches 3; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 HRQLQLSIS 12
| |::|::
Db 4 HAQIEVSV 12

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:22:19 ; Search time 57.51 Seconds
(without alignments)
30.075 Million cell updates/sec

Title: US-09-165-546A-8
Perfect score: 88
Sequence: 1 AADHRQLQLSISCLQQL 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 3210

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	27.3	16	2 S34444	blaZ protein - Sta
2	24	27.3	17	2 S05917	chorion class A pr
3	23	26.1	14	2 I49514	B144 protein A - m
4	23	26.1	15	2 S28873	lipid transfer pro
5	23	26.1	17	2 B23219	high-cysteine chor
6	23	26.1	17	2 A29834	trp leader peptide
7	22	25.0	14	2 I54284	C1-inhibitor - hum
8	22	25.0	15	2 D48394	major fat-globule
9	22	25.0	17	2 S05913	chorion class A pr
10	21	23.9	12	2 I57678	gene rPLP-A protei
11	21	23.9	14	2 PHI806	T cell receptor al
12	21	23.9	18	2 S63487	fibrinogenolytic p
13	21	23.9	18	2 S59490	translation elonga
14	20	22.7	6	2 S71349	beta-crystallin B2
15	20	22.7	13	2 PT0305	Ig heavy chain CRD
16	20	22.7	14	2 PHI321	Ig heavy chain DJ
17	20	22.7	15	2 PT0096	pyruvate dehydroge
18	20	22.7	17	2 S05923	chorion class A pr
19	20	22.7	17	2 S57519	T cell receptor be
20	20	22.7	18	2 A41877	LcrKc - Versinia p
21	20	22.7	18	2 S54270	GATA-2 protein - A
22	19	21.6	10	2 A47364	placental lactogen
23	19	21.6	14	2 A17150	glucose 1-dehydrog
24	19	21.6	15	2 PQ0194	Sz-glycoprotein -
25	19	21.6	15	2 PC2215	fibrinogenolytic p
26	19	21.6	15	2 S57201	basic proteinase I
27	19	21.6	18	2 PQ0022	fixA protein - Rhi
28	19	21.6	18	2 PX0081	dipeptidyl-peptida
29	18.5	21.0	16	2 A44823	synaptosomal-assoc

30	18.5	21.0	17	2	A59069	excretory gland al
31	18	20.5	6	2	I49421	laminin B1 - weste
32	18	20.5	9	2	A61364	isotocin - common
33	18	20.5	10	2	A31571	hypertrehalosemic/
34	18	20.5	10	2	A58365	neuropeptide FFRFa
35	18	20.5	11	2	B43669	hypothetical prote
36	18	20.5	11	2	PH1583	Ig H chain V-D-J r
37	18	20.5	12	4	PC2121	aminotransferase c
38	18	20.5	13	2	S09018	hemolytic protein
39	18	20.5	14	2	I56493	endothelial growth
40	18	20.5	14	2	PL0040	glycogen phosphory
41	18	20.5	14	2	S39930	S-allele-associate
42	18	20.5	15	2	PQ0195	Sf11-glycoprotein
43	18	20.5	15	2	S33781	acetolactate synth
44	18	20.5	15	2	C32521	hexokinase (EC 2.7
45	18	20.5	16	2	S30384	hypothetical prote

ALIGNMENTS

RESULT 1
S34444
blaZ protein - Staphylococcus aureus plasmid pI258 (fragment)
C;Species: Staphylococcus aureus
C;Date: 22-Nov-1993 #sequence_revision 09-Mar-1996 #text_change 07-May-1999
C;Accession: S34444
R;Wang, P.Z.; Projan, S.J.; Novick, R.P.
Nucleic Acids Res. 19, 4000, 1991
A;Title: Nucleotide sequence of beta-lactamase regulatory genes from staphylococcal p
A;Reference number: S34444; MUID:91319567
A;Accession: S34444
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-16 <WAN>
A;Cross-references: EMBL:M62650
A;Experimental source: strain RN11
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
C;Genetics:
A;Gene: blaZ
A;Genome: plasmid pI258

Query Match 27.3%; Score 24; DB 2; Length 16;
Best Local Similarity 71.4%; Pred. No. 7.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 5 RQLQLSI 11
:|||||
Db 6 KQLQLKI 12
RESULT 2
S05917
chorion class A protein L4 precursor - silkworm (fragment)
C;Species: Bombyx mori (silkworm)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Aug-1999
C;Accession: S05917
R;Spoerel, N.A.; Nguyen, H.T.; Eickbush, T.H.; Kafatos, F.C.
J. Mol. Biol. 209, 1-19, 1989
A;Title: Gene evolution and regulation in the chorion complex of Bombyx mori. Hybridi
A;Reference number: S05913; MUID:90040707
A;Accession: S05917
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-17 <SPO>
A;Cross-references: EMBL:X15560; NID:g5781; PIDN:CAA33571.1; PID:g5782
A;Note: this sequence was submitted to the EMBL Data Library, Jun-1989
C;Genetics:
A;Map position: 2
C;Superfamily: chorion class A protein pc292

Query Match 27.3%; Score 24; DB 2; Length 17;
Best Local Similarity 45.5%; Pred. No. 8.3e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 7 LQLSISSCLQQ 17
| | : | | |
Db 7 LLLCVQACLIQ 17

RESULT 3
I49514
B144 protein A - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: I49514
R;Tsuge, I.; Shen, F.
Immunogenetics 26, 378-380, 1987
A;Title: A gene in the H-2S: H-2D interval of the major histocompatibility complex which
A;Reference number: I49514; MUID:88031493
A;Accession: I49514
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-14 <RES>
A;Cross-references: GB:M18187; NID:g192097; PIDN:AAA37272.1; PID:g192098

Query Match 26.1%; Score 23; DB 2; Length 14;
Best Local Similarity 40.0%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 9 LSISSCLQQL 18
| : | | |
Db 2 LDLQACSQSL 11

RESULT 4
S28873
lipid transfer protein Cw(41) - maize (fragment)
C;Species: Zea mays (maize)
C;Date: 19-Mar-1997 #sequence_revision 17-Jul-1998 #text_change 17-Jul-1998
C;Accession: S28873
R;Molina, A.; Segura, A.; Garcia-Olmedo, F.
FEBS Lett. 316, 119-122, 1993
A;Title: Lipid transfer proteins (nsLTPs) from barley and maize leaves are potent inhibi
A;Reference number: S28871; MUID:93131027
A;Accession: S28873
A;Molecule type: protein
A;Residues: 1-15 <MOL>
A;Experimental source: etiolated leaf, cultivar INIA 1986
C;Keywords: lipid transport

Query Match 26.1%; Score 23; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 QLQLSISSCL 15
| : | | |
Db 6 QVSXAIAACL 15

RESULT 5
B23219
high-cysteine chorion protein A 13 - silkworm (fragment)
C;Species: Bombyx mori (silkworm)
C;Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 21-Jul-2000
C;Accession: B23219
R;Rodakis, G.C.; Lecanidou, R.; Eickbush, T.H.
J. Mol. Evol. 20, 265-273, 1984
A;Title: Diversity in a chorion multigene family created by tandem duplications and a pu
A;Reference number: A92960; MUID:85083111
A;Accession: B23219
A;Molecule type: DNA

A;Residues: 1-17 <ROD>
A;Cross-references: GB:X01068; NID:g5752; PIDN:CAB57790.1; PID:g6015486
C;Genetics:
A;Introns: 17/3
C;Superfamily: chorion class A protein pc292

Query Match 26.1%; Score 23; DB 2; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 7 LQLSISSCLQQ 17
| | : | | |
Db 7 LLLCVQACLIQ 17

RESULT 6
A29834
trp leader peptide - Corynebacterium glutamicum
C;Species: Corynebacterium glutamicum
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 24-Sep-1999
C;Accession: A29834; A24723; A29458; S13087; A48967
R;Matsui, K.; Miwa, K.; Sano, K.
J. Bacteriol. 169, 5330-5332, 1987
A;Title: Two single-base-pair substitutions causing desensitization to tryptophan fee
ntum.
A;Reference number: A29834; MUID:88032866
A;Contents: B. lactofermentum
A;Accession: A29834
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-17 <MAT>
A;Cross-references: GB:M17892; NID:gl44101; PIDN:AAB59110.1; PID:g1129101
R;Matsui, K.; Sano, K.; Ohtsubo, E.
Nucleic Acids Res. 14, 10113-10114, 1986
A;Title: Complete nucleotide and deduced amino acid sequences of the Brevibacterium 1
A;Reference number: A93606; MUID:87117512
A;Contents: B. lactofermentum
A;Accession: A24723
A;Molecule type: DNA
A;Residues: 1-17 <MA2>
A;Cross-references: GB:X04960; NID:g39591; PIDN:CAA28622.1; PID:g580785
R;Sano, K.; Matsui, K.
Gene 53, 191-200, 1987
A;Title: Structure and function of the trp operon control regions of Brevibacterium 1
A;Reference number: A91575; MUID:87277409
A;Contents: B. lactofermentum
A;Accession: A29458
A;Molecule type: DNA
A;Residues: 1-17 <SAN>
R;Heery, D.M.; Dunican, L.K.
Nucleic Acids Res. 18, 7138, 1990
A;Title: Nucleotide sequence of the Corynebacterium glutamicum trpE gene.
A;Reference number: S13087; MUID:91088299
A;Accession: S13087
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-17 <HEE>
A;Cross-references: EMBL:X55994; NID:g40521; PIDN:CAA39466.1; PID:g580992
R;Herry, D.M.; Dunican, L.K.
Appl. Environ. Microbiol. 59, 791-799, 1993
A;Title: Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of C
A;Reference number: A48967; MUID:93243735
A;Accession: A48967
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-13 <HER>
A;Cross-references: GB:S59299; NID:g299877; PIDN:AAB26395.1; PID:g299878
A;Experimental source: ATCC 21850
A;Note: sequence extracted from NCBI backbone (NCBIN:130455, NCBIP:130456)
C;Genetics:
A;Gene: trpL
A;Start codon: GTG

C;Superfamily: unassigned leader peptides

Query Match 26.1%; Score 23; DB 2; Length 17;
Best Local Similarity 66.7%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 SSCLQQ 17
:| | | |
Db 3 NSCLSQ 8

RESULT 7
I54284
C1-inhibitor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
C;Accession: I54284
R;Siddique, Z.; McPhaden, A.R.; McCluskey, D.; Whaley, K.
Hum. Hered. 42, 231-234, 1992
A;Title: A single base deletion from the C1-inhibitor gene causes type I hereditary angioedema
A;Reference number: I54284; MUID:92380682
A;Accession: I54284
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-14 <RES>
A;Cross-references: GB:S44615; NID:g254386; PIDN:AAB23055.1; PID:g254387

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Best Local Similarity 41.7%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 3 DHRQLQLSISSC 14
| | | | |
Db 1 DFRFLRCSTRQC 12

RESULT 8
D48394
major fat-globule membrane protein GP 55 - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997
C;Accession: D48394
R;Mather, I.H.; Banghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig II-like sequences.
A;Reference number: A48394; MUID:93250576
A;Accession: D48394
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <MAT>
A;Experimental source: milk
A;Note: sequence extracted from NCBI backbone (NCBIP:131448)
C;Superfamily: milk fat globule protein; discoidin I amino-terminal homology; EGF homology

Query Match 25.0%; Score 22; DB 2; Length 15;
Best Local Similarity 33.3%; Pred. No. 1.7e+03;
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 7 LQLSISSCLQQ 18
| : : | | |
Db 4 LGCELNGCLEPL 15

RESULT 9
S05913
Chorion class A protein L2 precursor - silkworm (fragment)
C;Species: Bombyx mori (silkworm)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Aug-1999
C;Accession: S05913

R;Spoerel, N.A.; Nguyen, H.T.; Eickbush, T.H.; Kafatos, F.C.
J. Mol. Biol. 209, 1-19, 1989
A;Title: Gene evolution and regulation in the chorion complex of Bombyx mori. Hybrid
A;Reference number: S05913; MUID:90040707
A;Accession: S05913
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-17 <SPO>
A;Cross-references: EMBL:X15558; NID:g5771; PIDN:CAA33567.1; PID:g5772
A;Note: this sequence was submitted to the EMBL Data Library, Jun-1989
C;Genetics:
A;Map position: 2
C;Superfamily: chorion class A protein pc292

Query Match 25.0%; Score 22; DB 2; Length 17;
Best Local Similarity 44.4%; Pred. No. 1.9e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 9 LSISSCLQQ 17
| : : | | |
Db 9 LCVQACLIQ 17

RESULT 10
I57678
gene rPLP-A protein - rat (fragment)
C;Species: Rattus sp. (rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 28-Feb-1997
C;Accession: I57678
R;Vuille, J.C.; Cattini, P.A.; Bock, M.E.; Verstuyf, A.; Schroedter, I.C.; Duckworth, M.L. Cell. Endocrinol. 96, 91-98, 1993
A;Title: Rat prolactin-like protein A partial gene and promoter structure: promoter a
A;Reference number: I57678; MUID:94102438
A;Accession: I57678
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-12 <RES>
A;Cross-references: GB:S68117; NID:g544690
C;Genetics:
A;Gene: rPLP-A

Query Match 23.9%; Score 21; DB 2; Length 12;
Best Local Similarity 45.5%; Pred. No. 2e+03;
Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 HRQLQLSISSC 14
| | | | |
Db 2 HLSLSHQWSSC 12

RESULT 11
PH1806
T cell receptor alpha chain V region (clone 4DN V alpha 24-4) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: PH1806
R;Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A;Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood lymphocytes

A;Reference number: PH1754; MUID:93301585
A;Accession: PH1806
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-14 <POR>

Query Match 23.9%; Score 21; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SSCL 15
| | | |
Db 11 SSCL 14

RESULT 12
S63487
fibrinogenolytic proteinase beta chain - horn viper (fragment)
N;Alternate names: beta-fibrinogenase
C;Species: Cerastes cerastes (horn viper)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 17-Mar-1999
C;Accession: S63487
R;Laraba-Djebari, F.; Martin-Eauclaire, M.F.; Mauco, G.; Marchot, P.
Eur. J. Biochem. 233, 756-765, 1995
A;Title: Afaacytin, an alpha-beta-fibrinogenase from Cerastes cerastes (horned viper) ve
A;Reference number: S63486; MUID:96085138
A;Accession: S63487
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-18 <LAR>

Query Match 23.9%; Score 21; DB 2; Length 18;
Best Local Similarity 57.1%; Pred. No. 3e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 DHRQLQL 9
: | | | |
Db 11 EHRSVLV 17

RESULT 13
S59490
translation elongation factor eEF-2 - rat (fragments)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S59490
R;Dumont-Miscopein, A.; Lavergne, J.P.; Reboud, J.P.
Biochim. Biophys. Acta 1263, 221-227, 1995
A;Title: Properties of elongation factor-2 fragments obtained by partial proteolysis.
A;Reference number: S59490; MUID:96004892
A;Accession: S59490
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-6;7-12;13-18 <DUM>

Query Match 23.9%; Score 21; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 3e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 11 ISSCLQQL 18
| : | | : |
Db 11 ITICLKDL 18

RESULT 14
S71349
beta-crystallin B2 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 07-May-1999
C;Accession: S71349
R;Dirks, R.P.H.; Kraft, H.J.; van Genesen, S.T.; Klok, E.J.; Pfundt, R.; Schoenmakers, J
Eur. J. Biochem. 239, 23-32, 1996
A;Title: The cooperation between two silencers creates an enhancer element that controls
A;Reference number: S71349; MUID:96305362
A;Accession: S71349
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-6 <DIR>
A;Cross-references: EMBL:X83671
A;Experimental source: strain Wistar; lens epithelial cells
C;Genetics:

A;Gene: CRYBB2

Query Match 22.7%; Score 20; DB 2; Length 6;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHR 5
| : | | :
Db 2 ASDHQ 6

RESULT 15
PT0305
Ig heavy chain CRD3 region (clone 5-121) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0305
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A;Reference number: PT0222; MUID:91108337
A;Accession: PT0305
A;Molecule type: DNA
A;Residues: 1-13 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 22.7%; Score 20; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 3.3e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 12 SSCLQQL 18
| | | : : |
Db 7 SSCHRKL 13

Search completed: July 3, 2002, 11:28:56
Job time: 397 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:27:59 ; Search time 27.94 Seconds
(without alignments)
24.945 Million cell updates/sec

Title: US-09-165-546A-8

Perfect score: 88

Sequence: 1 AADHRQLQLSISSCLQL 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 923

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	23	26.1	17	1	CHH3_BOMMO	P20729 bombyx mori
2	23	26.1	17	1	LPW_CORGL	P06556 corynebacte
3	20	22.7	9	1	OXYT_RAJCL	P42994 raja clavate
4	19	21.6	17	1	TPIS_PINPS	P81666 pinus pinas
5	19	21.6	18	1	FIXA_RHILE	P14313 rhizobium l
6	18	20.5	9	1	ISOT_CYPCA	P42993 cyprinus ca
7	18	20.5	10	1	FARP_MYTED	P42560 mytilus edu
8	18	20.5	10	1	HTF_HELZE	P16353 heliothis z
9	18	20.5	13	1	HPAL_RANES	P32415 rana escul
10	18	20.5	15	1	48KD_BACCE	P80173 bacillus ce
11	18	20.5	16	1	BAIL_EUBSU	P32371 eubacterium
12	18	20.5	16	1	YMOR_PSEPU	Q02210 pseudomonas
13	17	19.3	9	1	OXYT_BUFRE	P42995 bufo regula
14	17	19.3	12	1	UH03_RAT	P56572 rattus norv
15	17	19.3	15	1	ALLS_MANSE	P42559 manduca sex
16	17	19.3	17	1	EFG_THEAQ	Q01697 thermus aqu
17	16	18.2	9	1	HUTU_KLEAE	P12381 klebsiella
18	16	18.2	11	1	LADD_ONCMY	P81018 oncorhynch
19	16	18.2	12	1	UR2_POLSP	P81022 polyodon sp
20	16	18.2	14	1	CX1A_CONBE	P58623 conus betul
21	16	18.2	15	1	KPP2_SELMI	P25934 selenastrum
22	16	18.2	18	1	A2M_OCTVU	P30800 octopus vul
23	15	17.0	7	1	UF03_MOUSE	P38641 mus musculu
24	15	17.0	9	1	DNF1_LOCFI	P16339 locusta mig
25	15	17.0	9	1	OXYA_SCYCA	P42996 scylliorhinu
26	15	17.0	9	1	OXYA_SCYAC	P42999 squalus aca
27	15	17.0	12	1	LICH_BACLI	P82907 bacillus li
28	15	17.0	12	1	RR16_GINBI	P36207 ginkgo bilo
29	15	17.0	13	1	ACT7_SOYBN	P15987 glycine max
30	15	17.0	14	1	PSAG_CUCSA	P42049 cucumis sat
31	15	17.0	14	1	SMS1_MYOSC	P20750 myoxocephal
32	15	17.0	14	1	SMS_ALLMI	P31885 alligator m
33	15	17.0	15	1	MM01_RAT	P81563 rattus norv

34	15	17.0	17	1	ACT6_SOYBN	P15986 glycine max
35	15	17.0	17	1	BOL1_MEGPE	P10521 megabombus
36	15	17.0	17	1	NU4M_TRIRU	Q36834 trichophyto
37	14	15.9	7	1	WWA2_ACHFU	P35920 achatina fu
38	14	15.9	8	1	HTF_TENMO	P25419 tenebrio mo
39	14	15.9	8	1	RPCH_PANBO	P08939 pandalus bo
40	14	15.9	9	1	OXYT_CYPCA	P23879 cyprinus ca
41	14	15.9	9	1	OXYT_RABIT	P32878 oryctolagus
42	14	15.9	9	1	OXYV_SQUAC	P43000 squalus aca
43	14	15.9	10	1	COX4_THUOB	P80971 thunnus obe
44	14	15.9	10	1	FARP_LOCFI	P38553 locusta mig
45	14	15.9	10	1	GLEM_HUMAN	P02728 homo sapien

ALIGNMENTS

RESULT 1						
CHH3_BOMMO						
ID CHH3_BOMMO	STANDARD;	PRT;	17 AA.			
AC P20729;						
DT 01-FEB-1991 (Rel. 17, Created)						
DT 01-FEB-1991 (Rel. 17, Last sequence update)						
DT 01-FEB-1991 (Rel. 17, Last annotation update)						
DE Chorion class high-cysteine HCA protein 13 precursor (HC-A.13)						
DE (Fragment).						
OS Bombyx mori (Silk moth).						
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;						
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;						
OC Bombycoidea; Bombycidae; Bombyx.						
OX NCBI_TaxID=7091;						
RN [1]						
RP SEQUENCE FROM N.A.						
RX MEDLINE=85083111; PubMed=6439880;						
RA Rodakis G.C., Lecanidou R., Eickbush T.H.;						
RT "Diversity in a chorion multigene family created by tandem						
RT duplications and a putative gene-conversion event.";						
RL J. Mol. Evol. 20:265-273(1984).						
CC -!- FUNCTION: THIS PROTEIN IS ONE OF MANY FROM THE EGGSHELL OF THE						
CC SILK MOTH.						
CC -!- SIMILARITY: MEMBER OF THE ALPHA-BRANCH OF CHORION PROTEIN TO WHICH						
CC BELONG CLASSES A, CA AND HCA.						
CC -----						
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CC or send an email to license@isb-sib.ch).						
CC -----						
CC EMBL; X01068; CAB57790.1; -.						
DR PIR; B23219; B23219.						
KW Eggshell; Chorion; Repeat; Multigene family; Signal.						
FT SIGNAL 1 >17						
FT NON_TER 17 17						
SQ SEQUENCE 17 AA; 1913 MW; 5E634508C5355C9C CRC64;						

Query Match 26.1%; Score 23; DB 1; Length 17;
Best Local Similarity 45.5%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY	7	LQLSISSCLQQ	17
		:	
Db	7	LLLCVQGCLIQ	17

RESULT 2						
LPW_CORGL						
ID LPW_CORGL	STANDARD;	PRT;	17 AA.			
AC P06556;						
DT 01-JAN-1988 (Rel. 06, Created)						

DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Trp operon leader peptide.
GN TRPL.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteriidae;
OC Actinomycetales; Corynebacterineae; Corynebacteriaceae;
OC Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87117512; PubMed=3808947;
RA Matsui K., Sano K., Ohtsubo E.;
RT "Complete nucleotide and deduced amino acid sequences of the
RT Brevibacterium lactofermentum tryptophan operon.";
RL Nucleic Acids Res. 14:10113-10114(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88032866; PubMed=3667535;
RA Matsui K., Miwa K., Sano K.;
RT "Two single-base-pair substitutions causing desensitization to
RT tryptophan feedback inhibition of anthranilate synthase and enhanced
RT expression of tryptophan genes of Brevibacterium lactofermentum.";
RL J. Bacteriol. 169:5330-5332(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=87277409; PubMed=3609747;
RA Sano K., Matsui K.;
RT "Structure and function of the trp operon control regions of
RT Brevibacterium lactofermentum, a glutamic-acid-producing bacterium.";
RL Gene 53:191-200(1987).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13059 / AS019;
RX MEDLINE=91088299; PubMed=2263476;
RA Heery D.M., Dunican L.K.;
RT "Nucleotide sequence of the Corynebacterium glutamicum trpE gene.";
RL Nucleic Acids Res. 18:7138-7138(1990).
CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
CC OF TRYPTOPHAN.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X04960; CAA28622.1; -.
DR EMBL; M17892; AAB59110.1; -.
DR EMBL; M16663; -; NOT_ANNOTATED_CDS.
DR EMBL; X55994; CAA39466.1; -.
DR PIR; A29458; A29458.
DR PIR; A29834; A29834.
DR PIR; A24723; A24723.
DR PIR; S13087; S13087.
KW Tryptophan biosynthesis; Leader peptide.
SQ SEQUENCE 17 AA; 2112 MW; 74C7E7924DAAE56B CRC64;

Query Match 26.1%; Score 23; DB 1; Length 17;
Best Local Similarity 66.7%; Pred. No. 3.7e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 SSCLOQ 17
:||||
Db 3 NSCLSQ 8

RESULT 3
OXYT_RAJCL C.
ID OXYT_RAJCL STANDARD; PRT; 9 AA.

AC P42994;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Glumitocin.
OS Raja clavata (Thornback ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalia; Hypnosqualea; Pristiogoralea; Batoidea;
OC Rajiformes; Rajidae; Raja.
OX NCBI_TaxID=7781;
RN [1]
RP SEQUENCE.
RX MEDLINE=66123415; PubMed=5880565;
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
RT "Phylogeny of neurophyophyseal peptides: isolation of a new hormone,
RT glumitocin (Ser 4-Gln 8-ocytocin) present in a cartilaginous fish,
RT the ray (Raja clavata).";
RL Biochim. Biophys. Acta 107:393-396(1965).
CC -!- FUNCTION: ANTIDIURETIC HORMONE.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurohypophys_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 984 MW; 17E9C76EB455B04B CRC64;

Query Match 22.7%; Score 20; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ISSCLQ 16
:||||
Db 3 ISNCPQ 8

RESULT 4
TPIS_PINPS
ID TPIS_PINPS STANDARD; PRT; 17 AA.
AC P81666;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Triosephosphate isomerase, cytosolic (EC 5.3.1.1) (TIM) (Fragments).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycerone
CC phosphate.
CC -!- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- INDUCTION: BY WATER STRESS.
CC -!- MISCELLANEOUS: IN PLANTS, THERE ARE TWO TYPES OF TPIS, CYTOSOLIC
CC AND PLASTID.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN
CC (SPOT N139) IS: 5.9, ITS MW IS: 24 kDa.
CC -!- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
DR InterPro; IPR000652; Trioseph_isomerase.
DR PROSITE; PS00171; TIM; PARTIAL.
KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;

```
KW Pentose shunt.
FT NON_TER 1 1
FT NON_CONS 9 10
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 2053 MW; 183DB41757AF13CB CRC64;

Query Match 21.6%; Score 19; DB 1; Length 17;
Best Local Similarity 60.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 14 CLQQL 18
Db 5 CYEQL 9

RESULT 5
FIXA_RHILE STANDARD; PRT; 18 AA.
AC P14313;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE FixA protein (Fragment).
GN FIXA.
OS Rhizobium leguminosarum.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=384;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90066358; PubMed=2555670;
RA Hontelez J.G.J., Lankhorst R.K., Katinakis P., van den Bos R.C.,
RA van Kammen A.;
RT "Characterization and nucleotide sequence of a novel gene fixw
RT upstream of the fixABC operon in Rhizobium leguminosarum.";
RL Mol. Gen. Genet. 218:536-544(1989).
CC -!- FUNCTION: MAY PLAY A ROLE IN A REDOX PROCESS INVOLVED IN NITROGEN
CC FIXATION.
CC -!- SUBUNIT: FIXA AND FIXB FORM A HETERODIMER (PROBABLE).
CC -!- SIMILARITY: BELONGS TO THE ETF BETA-SUBUNIT / FIXA FAMILY.
CC -----
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CC -----
DR EMBL; X16521; CAA34527.1; -.
DR PIR; PQ0022; PQ0022.
DR InterPro; IPR000049; ETF_beta.
DR PROSITE; PS01065; ETF_BETA; PARTIAL.
KW Electron transport; Nitrogen fixation.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2036 MW; 74973C8BA2087663 CRC64;

Query Match 21.6%; Score 19; DB 1; Length 18;
Best Local Similarity 30.0%; Pred. No. 2e+03;
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 9 LSISSCLQQL 18
Db 1 MHIVVCIKQV 10

RESULT 6
ISOT_CYPCA STANDARD; PRT; 9 AA.
ID ISOT_CYPCA
AC P42993;
DT 01-NOV-1995 (Rel. 32, Created)
```

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DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Isotocin.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary;
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
RT "Characterization of neurohypophyseal hormones from a fresh water bony
RT fish, the carp (Cyprinus carpio). Comparison with hormones from sea
RT water bony fishs.";
RL Comp. Biochem. Physiol. 14:245-254(1965).
CC -!- FUNCTION: ANTIDIURETIC HORMONE.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; A61364; A61364.
DR InterPro; IPR000981; Neurhypophys_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 969 MW; 17FF476EB455B04B CRC64;

Query Match 20.5%; Score 18; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 ISSC 14
Db 3 ISNC 6

RESULT 7
FARP_MYTED STANDARD; PRT; 10 AA.
ID FARP_MYTED
AC P42560;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE FMRFamide-like neuropeptide ALAGDHFFRF-amide.
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloida;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE.
RX MEDLINE=93047883; PubMed=1358534;
RA Walker R.J.;
RT "Neuroactive peptides with an RFamide or Famide carboxyl terminal.";
RL Comp. Biochem. Physiol. 102C:213-222(1992).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1180 MW; C2F80CC9C1EAA87D CRC64;

Query Match 20.5%; Score 18; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AADH 4
Db 3 AGDH 6

RESULT 8
HTF_HELZE
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ID HTF_HELZE STANDARD; PRT; 10 AA.
AC P16353;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Hypertrehalosaemic hormone (Hez-HRTH).
OS Heliothis zea (Corn earworm) (Bollworm).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Noctuoidae; Noctuidae; Heliothinae; Helicoverpa.
OX NCBI_TaxID=7113;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=88326324; PubMed=3415690;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Bird T.G.,
RA Tseng C.M., Zhang Y.S., Hayes D.K.;
RT "Isolation and primary structure of a neuropeptide hormone from
RT Heliothis zea with hypertrehalosemic and adipokinetic activities.";
RL Biochem. Biophys. Res. Commun. 155:344-350(1988).
CC -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
CC PIR; A31571; A31571.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1096 MW; 8E70367865A5B9D1 CRC64;

Query Match 20.5%; Score 18; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.6e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 QLSISS 13
II: II
Db 1 QLTFSS 6

RESULT 9
HPAL_RANES STANDARD; PRT; 13 AA.
AC P32415;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-OCT-1993 (Rel. 27, Last annotation update)
DE Hemolytic protein A1 (Fragment).
OS Rana esculenta (Edible frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8401;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90198965; PubMed=2317508;
RA Simmaco M., de Biase D., Severini C., Aita M., Erspamer G.F.,
RA Barra D., Bossa F.;
RT "Purification and characterization of bioactive peptides from skin
RT extracts of Rana esculenta.";
RL Biochim. Biophys. Acta 1033:318-323(1990).
CC -!- FUNCTION: SHOWS HEMOLYTIC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: SKIN.
CC PIR; S09018; S09018.
KW Amphibian skin; Amidation; Hemolysis.
FT MOD_RES 13 13 AMIDATION.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1390 MW; C6BA768B9DFE587D CRC64;
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Query Match 20.5%; Score 18; DB 1; Length 13;
Best Local Similarity 44.4%; Pred. No. 2.1e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 10 SISSCLQQL 18
II: III
Db 4 AIAGILSQL 12

RESULT 10
48KD_BACCE STANDARD; PRT; 15 AA.
AC P80173;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-OCT-1993 (Rel. 27, Last annotation update)
DE 48 kDa protein (Fragment).
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1396;
RN [1]
RP SEQUENCE.
RC STRAIN=1230-88;
RX MEDLINE=93307641; PubMed=8319899;
RA Granum P.E., Nissen H.;
RT "Sphingomyelinase is part of the 'enterotoxin complex' produced by
RT Bacillus cereus.";
RL FEMS Microbiol. Lett. 110:97-100(1993).
CC -!- FUNCTION: NOT KNOWN, PART OF THE ENTEROTOXIN COMPLEX.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1644 MW; 88442960B4B0FB62 CRC64;

Query Match 20.5%; Score 18; DB 1; Length 15;
Best Local Similarity 45.5%; Pred. No. 2.5e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 RQLQLSISSCL 15
II: IIII
Db 3 QQEGMDISSSL 13

RESULT 11
BAIL_EUBSP STANDARD; PRT; 16 AA.
AC P32371;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Bile acid-inducible operon protein I (Fragment).
GN BAI1.
OS Eubacterium sp. (strain VPI 12708).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Eubacterium.
OX NCBI_TaxID=1734;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93259945; PubMed=8491719;
RA Franklund C.V., Baron S.F., Hylemon P.B.;
RT "Characterization of the baiH gene encoding a bile acid-inducible
RT NADH:flavin oxidoreductase from Eubacterium sp. strain VPI 12708.";
RL J. Bacteriol. 175:3002-3012(1993).
CC -!- PATHWAY: Bile acid 7-alpha-dehydroxylation.
CC -----
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CC
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DR EMBL; U57489; AAC45418.1; -.
DR PIR; D36912; D36912.
KW Bile acid catabolism.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1721 MW; B9BAAE7B8746E4F4 CRC64;

Query Match      20.5%; Score 18; DB 1; Length 16;
Best Local Similarity 60.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 SISSC 14
Db 5 AISGC 9

RESULT 12
YMOB_PSEPU
ID YMOB_PSEPU STANDARD; PRT; 16 AA.
AC Q02210;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in MORA 3'region (Fragment).
OS Pseudomonas putida.
OG Plasmid pMDH7.2.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M10;
RX MEDLINE=931199531; PubMed=8452544;
RA Willey D.L., Caswell D.A., Lowe C.R., Bruce N.C.;
RT "Nucleotide sequence and over-expression of morphine dehydrogenase, a
RT plasmid-encoded gene from Pseudomonas putida M10.";
RL Biochem. J. 290:539-544(1993).
CC -----
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CC -----
DR EMBL; M94775; AAB17357.1; -.
DR PIR; S30384; S30384.
KW Hypothetical protein; Plasmid.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1962 MW; A2F1EB8C172766ED CRC64;

Query Match      20.5%; Score 18; DB 1; Length 16;
Best Local Similarity 60.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 SISSC 14
Db 11 SLRSC 15

RESULT 13
OXYT_BUFRE
ID OXYT_BUFRE STANDARD; PRT; 9 AA.
AC P42995;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Seritocin.
OS Bufo regularis (Leopard toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Bufonidae;
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OC Bufo.
OX NCBI_TaxID=8390;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary neurointermediate lobe;
RX MEDLINE=96059313; PubMed=7591488;
RA Chauvet J., Michel G., Ouedraogo Y., Chou J., Chait B.T., Acher R.;
RT "A new neurohypophysial peptide, seritocin ([Ser5,Ile8]-oxytocin),
RT identified in a dryness-resistant African toad, Bufo regularis.";
RL Int. J. Pept. Protein Res. 45:482-487(1995).
CC -!- FUNCTION: DEVOID OF OXYTOCIC ACTIVITY.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurohypophys_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9 AMIDATION.
FT SEQUENCE 9 AA; 983 MW; 17FF476EA5A6D04B CRC64;

Query Match      19.3%; Score 17; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 ISSC 14
Db 3 IQSC 6

RESULT 14
UH03_RAT
ID UH03_RAT STANDARD; PRT; 12 AA.
AC P56572;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot P3) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE.
RC STRAIN=WISTAR; TISSUE=Heart;
RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.;
RL Submitted (SEP-1998) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 8.3, ITS MW IS: 28 kDa.
FT UNSURE 2 2
FT UNSURE 9 9
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1255 MW; 46F58D101DC33053 CRC64;

Query Match      19.3%; Score 17; DB 1; Length 12;
Best Local Similarity 10.0%; Pred. No. 2.9e+03;
Matches 1; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 4 HRQLQLSISS 13
Db 3 HTKIKVAVDT 12

RESULT 15
ALLS_MANSE
ID ALLS_MANSE STANDARD; PRT; 15 AA.
AC P42559;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Allatostatin (Mas-AS).
```

OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Sphingioidea; Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RX MEDLINE=92052112; PubMed=1946359;
RA Kramer S.J., Toschi A., Miller C.A., Kataoka H., Quistad G.B.,
Li J.P., Carney R.L., Schooley D.A.;
RT "Identification of an allatostatin from the tobacco hornworm Manduca
RT sexta.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:9458-9462(1991).
CC -!- FUNCTION: STRONGLY INHIBITS JUVENILE HORMONE BIOSYNTHESIS IN VITRO
CC BY THE CORPORA ALLATA FROM FIFTH-STADIUM LARVAE AND ADULT FEMALES.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 15 AA; 1908 MW; 1605B77CDEBC838E CRC64;

Query Match 19.3%; Score 17; DB 1; Length 15;
Best Local Similarity 40.0%; Pred. No. 3.7e+03;
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 RQLQLSISSC 14
|| : ||
Db 5 RQCYFNPISC 14

Search completed: July 3, 2002, 11:41:54
Job time: 835 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:27:04 ; Search time 100.54 Seconds
(without alignments)
30.972 Million cell updates/sec

Title: US-09-165-546A-8
Perfect score: 88
Sequence: 1 AADHRQLQLSISSCLQL 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 4250

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_19.*
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mhc.*
 - 8: sp_organelle.*
 - 9: sp_phage.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp_vertebrate.*
 - 14: sp_unclassified.*
 - 15: sp_rvirus.*
 - 16: sp_bacteriap.*
 - 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	31.8	18	13 O57600	Q57600 gallus gall
2	25	28.4	17	10 Q9S919	Q9S919 petunia hyb
3	24	27.3	12	11 Q9QZY4	Q9qzy4 mus musculu
4	24	27.3	17	5 Q9TVX7	Q9tvx7 bombyx mori
5	23	26.1	14	11 Q9Z1H4	Q9z1h4 mus musculu
6	23	26.1	17	2 Q45304	Q45304 corynebacte
7	22	25.0	14	5 Q9I809	Q9i809 drosophila
8	22	25.0	15	3 Q9UR64	Q9ur64 pleurotus o
9	22	25.0	16	5 Q95V73	Q95v73 mytilus edu
10	22	25.0	17	5 Q17203	Q17203 bombyx mori
11	21.5	24.4	16	4 O00497	O00497 homo sapien
12	21	23.9	17	2 O34216	O34216 sphingomona
13	21	23.9	18	2 Q9F581	Q9f581 escherichia
14	21	23.9	18	13 Q9PRM8	Q9prm8 cerastes ce
15	20	22.7	9	4 Q99887	Q99887 homo sapien
16	20	22.7	9	6 Q9XT05	Q9xt05 macropus ru

17	20	22.7	11	3 Q9UR95	Q9ur95 pichia angu
18	20	22.7	11	4 Q9UNL8	Q9unl8 homo sapien
19	20	22.7	12	3 Q9UR22	Q9ur22 cryptococcu
20	20	22.7	12	9 Q9T1J4	Q9t1j4 bacterioph
21	20	22.7	14	11 Q91Y24	Q91y24 mus musculu
22	20	22.7	15	4 Q9UCC9	Q9ucc9 homo sapien
23	20	22.7	16	2 P70990	P70990 bacillus su
24	20	22.7	17	2 Q9APU5	Q9apu5 pseudomonas
25	20	22.7	17	5 Q27269	Q27269 bombyx mori
26	20	22.7	18	2 P77033	P77033 escherichia
27	19	21.6	10	2 Q47651	Q47651 escherichia
28	19	21.6	11	11 Q9QXN6	Q9qxn6 mus musculu
29	19	21.6	13	4 Q16392	Q16392 homo sapien
30	19	21.6	14	4 Q9GZP5	Q9gzp5 homo sapien
31	19	21.6	15	4 Q9UC60	Q9uc60 homo sapien
32	19	21.6	15	13 Q9PRW3	Q9prw3 crotalus at
33	19	21.6	15	13 Q9PRW2	Q9prw2 crotalus at
34	19	21.6	16	2 Q9LAP2	Q9lap2 enterococcu
35	19	21.6	16	6 P79137	P79137 cercopithe
36	19	21.6	16	11 Q9QV11	Q9qv11 rattus sp.
37	19	21.6	17	2 Q9WW21	Q9ww21 enterococcu
38	19	21.6	17	2 Q9WW20	Q9ww20 enterococcu
39	19	21.6	17	2 Q9X5I5	Q9x5i5 enterococcu
40	19	21.6	17	8 Q9G468	Q9g468 brassica ju
41	19	21.6	17	10 Q9S7E8	Q9s7e8 arabidopsis
42	19	21.6	18	5 Q9TWS7	Q9tws7 lamellibrac
43	19	21.6	18	8 Q95CN9	Q95cn9 isotropis c
44	19	21.6	18	10 Q9S7E5	Q9s7e5 arabidopsis
45	18	20.5	10	2 Q50032	Q50032 mycobacteri

ALIGNMENTS

RESULT 1
O57600 PRELIMINARY; PRT; 18 AA.
ID O57600
AC O57600;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE THROMBOMUCIN (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97444372; PubMed=9298993;
RA McNaghy K.M., Pettersson I., Rossi F., Flamme I., Shevchenko A.,
RA Mann M., Graf T.;
RT "Thrombomucin, a novel cell surface protein that defines thrombocytes
RT and multipotent hematopoietic progenitors.";
RL J. Cell Biol. 138:1395-1407(1997).
DR EMBL; Y13976; CAA74309.1; -.
FT NON_TER 1
SQ SEQUENCE 18 AA; 1973 MW; CA71002CD77FE4F9 CRC64;

Query Match 31.8%; Score 28; DB 13; Length 18;
Best Local Similarity 55.6%; Pred. No. 2.9e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 8 QLSISSCLQ 16
| : ||||
Db 7 QVDAASCLQ 15

RESULT 2
Q9S919 PRELIMINARY; PRT; 17 AA.
ID Q9S919
AC Q9S919;


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DE 01-MAY-2000 (TReMBLrel. 13, Created)
DN 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)
DE SO-PROTEIN-31 KDA.
OS Petunia hybrida (Petunia).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
OX NCBI_TaxID=4102;
RN [1]
RP SEQUENCE
RX MEDLINE=921114864; PubMed=1766433;
RA Ai Y.J., Kron E., Kao T.H.;
RT "S-alleles are retained and expressed in a self-compatible cultivar of
RT Petunia hybrida.";
RL Mol. Gen. Genet. 230:353-358(1991).
DR InterPro; IPR001568; RNase_T2.
DR Pfam; PF00445; ribonuclease_T2; 1.
SQ SEQUENCE 17 AA; 2035 MW; 59270B606B574F63 CRC64;

Query Match 28.4%; Score 25; DB 10; Length 17;
Best Local Similarity 60.0%; Pred. No. 9.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AADHRQLQLS 10
Db 1 AFDHWQLVLT 10

RESULT 3
Q9QZY4 PRELIMINARY; PRT; 12 AA.
AC Q9QZY4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE PROTEIN KINASE LKB1 (FRAGMENT).
GN LKB1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=99330555; PubMed=10400995;
RA Smith D.P., Spicer J., Smith A., Swift S., Ashworth A.;
RT "The mouse Peutz-Jeghers syndrome gene lkb1 encodes a nuclear protein
RT kinase.";
RL Hum. Mol. Genet. 8:1479-1485(1999).
DR EMBL; AF145697; AAD55369.1; -.
KW Kinase.
FT NON_TER 1 1
SQ SEQUENCE 12 AA; 1445 MW; 6B06A6C54BC5B734 CRC64;

Query Match 27.3%; Score 24; DB 11; Length 12;
Best Local Similarity 57.1%; Pred. No. 9.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 ISSCLQQ 17
Db 6 LSACKQQ 12

RESULT 4
Q9TVX7 PRELIMINARY; PRT; 17 AA.
AC Q9TVX7;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)

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DE A.X3 PROTEIN (FRAGMENT).
GN A.X3 OR A.L4 OR A.L13 OR A.R2 OR A.R3 OR A.X1 OR A.X2.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Bombycoidea; Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=703;
RX MEDLINE=90040707; PubMed=2810362;
RA Spoerel N.A., Nguyen H.T., Eickbush T.H., Kafatos F.C.;
RT "Gene evolution and regulation in the chorion complex of Bombyx mori.
RT Hybridization and sequence analysis of multiple developmentally middle
RT A/B chorion gene pairs.";
RL J. Mol. Biol. 209:1-19(1989).
DR EMBL; X15572; CAA33595.1; -.
DR EMBL; X15560; CAA33571.1; -.
DR EMBL; X15566; CAA33583.1; -.
DR EMBL; X15568; CAA33587.1; -.
DR EMBL; X15569; CAA33589.1; -.
DR EMBL; X15570; CAA33591.1; -.
DR EMBL; X15571; CAA33593.1; -.
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1901 MW; 5FD3450433955C8C CRC64;

Query Match 27.3%; Score 24; DB 5; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 7 LQLSISSCLQQ 17
Db 7 LLLCVQACLIQ 17

RESULT 5
Q9Z1H4 PRELIMINARY; PRT; 14 AA.
ID Q9Z1H4
AC Q9Z1H4;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE B144 PROTEIN A (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88031493; PubMed=3117682;
RA Tsuge I., Shen F.-W.W., Steinmetz M., Boyse E.A.;
RT "A gene in the H-2S: H-2D interval of the major histocompatibility
RT complex which is transcribed in B cells and macrophages.";
RL Immunogenetics 26:378-380(1987).
DR EMBL; M18187; AAA37272.1; -.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1542 MW; 8D9A518F3F9C1ABE CRC64;

Query Match 26.1%; Score 23; DB 11; Length 14;
Best Local Similarity 40.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 9 LSISSSCLQQ 18
Db 2 LDLQACSQSL 11

RESULT 6
Q45304 PRELIMINARY; PRT; 17 AA.
ID Q45304
AC Q45304;

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DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)
DE HYPOTHETICAL 2.1 KDA PROTEIN.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteriidae;
OC Actinomycetales; Corynebacterineae; Corynebacteriaceae;
OC Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AJ12036;
RX MEDLINE=87277409; PubMed=3609747;
RA Sano K., Matsui K.;
RT "Structure and function of the trp operon control regions of
RT Brevibacterium lactofermentum, a glutamic-acid-producing bacterium.";
RL Gene 53:191-200(1987).
DR EMBL; M16663; AAA83988.1; -.
KW Hypothetical protein.
SQ SEQUENCE 17 AA; 2098 MW; 74C247924DAAE56B CRC64;

Query Match 26.1%; Score 23; DB 2; Length 17;
Best Local Similarity 66.7%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 SSC1QQ 17
Db :||| |
3 NSCLSQ 8

RESULT 7
Q9I809 PRELIMINARY; PRT; 14 AA.
AC Q9I809;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE CG17715 PROTEIN.
GN CG17715 OR CG18603.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
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RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE002969; AAF45324.2; -.
DR FlyBase; FBgn0041004; CG17715.
SQ SEQUENCE 14 AA; 1554 MW; 5F317A6FFEB08CB7 CRC64;

Query Match 25.0%; Score 22; DB 5; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.6e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 QLQLSISSCL 15
Db |:||| |
2 QCRLSLSDSL 11

RESULT 8
Q9UR64 PRELIMINARY; PRT; 15 AA.
AC Q9UR64;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE 46 KDA HEME-CONTAINING ASCORBATE OXIDASE (FRAGMENT).
OS Pleurotus ostreatus (Oyster mushroom) (White-rot fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Pleurotaceae; Pleurotus.
OX NCBI_TaxID=5322;
RN [1]
RP SEQUENCE.
RX MEDLINE=96216386; PubMed=8621708;
RA Kim Y.R., Yu S.W., Lee S.R., Hwang Y.Y., Kang S.O.;
RT "A heme-containing ascorbate oxidase from Pleurotus ostreatus.";
RL J. Biol. Chem. 271:3105-3111(1996).
SQ SEQUENCE 15 AA; 1738 MW; FF939C118BD30D75 CRC64;

Query Match 25.0%; Score 22; DB 3; Length 15;
Best Local Similarity 44.4%; Pred. No. 2.8e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 DHRQLQLSI 11
Db :||| |
7 EHLQLALMV 15

RESULT 9
Q95V73 PRELIMINARY; PRT; 16 AA.
AC Q95V73;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE ELONGATION FACTOR 1 ALPHA (FRAGMENT).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE FROM N.A.
RA Bierne N., Daguin C., Borsa P., Jolivet D., Viard F., Bonhomme F.,
```

RA	David P.;
RT	"Introgression patterns in the Mytilus edulis / Mytilus galloprovincialis mosaic hybrid zone along the Atlantic coasts of France.";
RT	Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AF424743; AAL24804.1; -.
FT	NON_TER 1
FT	NON_TER 16
SQ	SEQUENCE 16 AA; 1973 MW; DC4038430BCA3B17 CRC64;
Query Match 25.0%; Score 22; DB 5; Length 16;	
Best Local Similarity 33.3%; Pred. No. 3e+03;	
Matches	4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY	6 QLQLSISSCLQQ 17 : :
Dd	5 EIQKEVSSYLKK 16
RESULT	10
QI7203	PRELIMINARY; PRT; 17 AA.
AC	Q17203;
DT	01-NOV-1996 (TrEMBLrel. 01, Created)
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE	A.L2 PROTEIN (FRAGMENT).
GN	A.L2.
OS	Bombyx mori (Silk moth);
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC	Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC	Bombycoidea; Bombycidae; Bombyx.
OX	NCBI_TaxID=7091;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=703;
RX	MEDLINE=90040707; PubMed=2810362;
RA	Spoerel N.A., Nguyen H.T., Eickbush T.H., Kafatos F.C.;
RT	"Gene Evolution and Regulation in the Chorion Complex of Bombyx mori:
RT	Hybridization and Sequence Analysis of Multiple Developmentally Middle
RT	A/B Chorion Gene Pairs.";
RL	J. Mol. Biol. 209:1-19(1989).
DR	EMBL; X15558; CAA33567.1; -.
FT	NON_TER 17
SQ	SEQUENCE 17 AA; 1935 MW; 5FD34DA633955C8C CRC64;
Query Match 25.0%; Score 22; DB 5; Length 17;	
Best Local Similarity 44.4%; Pred. No. 3.2e+03;	
Matches	4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY	9 LSISSCLQQ 17 :
Dd	9 LCVQAQLIQ 17
RESULT	11
O00497	PRELIMINARY; PRT; 16 AA.
ID	O00497
AC	O00497;
DT	01-JUL-1997 (TrEMBLrel. 04, Created)
DT	01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE	DNA MISMATCH REPAIR PROTEIN (FRAGMENT).
GN	HMLH1.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Palmirotta R., Veri M.C., Curia M.C., Aceto G., D'Amico F.;

RA Furuya N., Komano T., Mizobuchi K.;
RT "Organization and diversification of plasmid genomes: complete
RT nucleotide sequence of the R721 genome.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K-12; TRANSPOSON=TN7;
RX MEDLINE=93015772; PubMed=1400257;
RA Kim S., Komano T.;
RT "Nucleotide sequence of the R721 shufflon.";
RL J. Bacteriol. 174:7053-7058(1992).
DR EMBL; AP002527; BAB12584.1; -.
KW Plasmid.
SQ SEQUENCE 18 AA; 2131 MW; EA26E4AFE5DE92C3 CRC64;

Query Match 23.9%; Score 21; DB 2; Length 18;
Best Local Similarity 44.4%; Pred. No. 5.2e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 QLQLSISSC 14
| : | | : |
Db 9 QCKLSAACC 17

RESULT 14
Q9PRM8 PRELIMINARY; PRT; 18 AA.
AC Q9PRM8;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE AFAACYTIN CHAIN RCM-BETA (FRAGMENT).
OS Cerastes cerastes (Horned desert viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Cerastes.
OX NCBI_TaxID=8697;
RN [1]
RP SEQUENCE.
RX MEDLINE=96085138; PubMed=8521839;
RA Laraba-Djebari F., Martin-Eauchlaire M.F., Maucio G., Marchot P.;
RT "Afaacytin, an alpha beta-fibrinogenase from Cerastes cerastes (horned
RT viper) venom, activates purified factor X and induces serotonin
RT release from human blood platelets.";
RL Eur. J. Biochem. 233:756-765(1995).
SQ SEQUENCE 18 AA; 1937 MW; CF680343EFE55327 CRC64;

Query Match 23.9%; Score 21; DB 13; Length 18;
Best Local Similarity 57.1%; Pred. No. 5.2e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 DHRQLQL 9
: | | | |
Db 11 EHRSVLV 17

RESULT 15
Q99887 PRELIMINARY; PRT; 9 AA.
AC Q99887;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE 11 <BETA>-HSD2 PROTEIN (FRAGMENT).
GN 11 <BETA>-HSD2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=96133030; PubMed=8538347;
RA Stewart P.M., Krozowski Z.S., Gupta A., Milford D.V., Howie A.J.,
RA Sheppard M.C., Whorwood C.B.;
RT "Hypertension in the syndrome of apparent mineralocorticoid excess due
RT to mutation of the 11 beta-hydroxysteroid dehydrogenase type 2 gene.";
RL Lancet 347:88-91(1996).
DR EMBL; S80133; AAD14324.1; -.
FT NON_TER 1
SQ SEQUENCE 9 AA; 1020 MW; CEFC2EB1F5B059C9 CRC64;

Query Match 22.7%; Score 20; DB 4; Length 9;
Best Local Similarity 80.0%; Pred. No. 5.6e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 ISSCL 15
| | | |
Db 4 ISHCL 8

Search completed: July 3, 2002, 11:41:20
Job time: 856 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:11:03 ; Search time 128.9 Seconds
(without alignments)
15.511 Million cell updates/sec

Title: US-09-165-546A-8
Perfect score: 88
Sequence: 1 AADHRQLQLSISSCLQQL 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 214377

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	88	100.0	18	21	AA52435 Human tumour antig
2	88	100.0	18	22	AAE07770 Human NY ESO-1 HLA
3	88	100.0	18	22	AAU01539 HLA-DR53 recognisi
4	88	100.0	18	22	AAB69939 Human NY-ESO-1 HLA
5	80	90.9	17	22	AAE07735 Human NY ESO-1 MHC
6	71	80.7	14	22	AAE07736 Human NY ESO-1 MHC
7	61	69.3	13	22	AAE07737 Human NY ESO-1 MHC
8	48	54.5	10	20	AA52435 Human cancer antig
9	47	53.4	10	20	AA52435 Human cancer antig
10	45	51.1	9	22	AAG67179 Cancer testis tumo
11	45	51.1	9	22	AAB69911 Human NY-ESO-1 HLA

12	45	51.1	10	22	AAG67202 Cancer testis tumo
13	45	51.1	10	22	AAB69934 Human NY-ESO-1 HLA
14	43	48.9	9	20	AA52435 Human cancer antig
15	43	48.9	9	21	AA52435 NY-ESO-1 derived p
16	42	47.7	9	20	AA52435 Human cancer antig
17	42	47.7	9	22	AAG67191 Cancer testis tumo
18	42	47.7	9	22	AAB69923 Human NY-ESO-1 HLA
19	39	44.3	9	20	AA52435 Human cancer antig
20	39	44.3	9	22	AAG67173 Cancer testis tumo
21	39	44.3	9	22	AAB69905 Human NY-ESO-1 HLA
22	36	40.9	9	21	AA52435 NY-ESO-1 derived p
23	32	36.4	18	21	AA52440 Human tumour antig
24	32	36.4	18	22	AAU01544 HLA-DR53 recognisi
25	32	36.4	18	22	AAB69944 Human NY-ESO-1 HLA
26	31	35.2	13	22	AAE07776 Human NY ESO-1 pep
27	31	35.2	14	22	AAE07775 Human NY ESO-1 pep
28	30	34.1	14	22	AAM98017 Human peptide #129
29	29	33.0	13	20	AA52435 Immunogenic peptid
30	29	33.0	18	16	AAR84751 GST-phospholipase
31	29	33.0	18	20	AAW96889 ApoB-100 nuclear 1
32	28	31.8	10	22	AAG94202 Human complementar
33	28	31.8	10	22	AAG94204 Human complementar
34	28	31.8	10	22	AAG94542 Human complementar
35	28	31.8	15	22	AAU69887 Human prostate pro
36	28	31.8	15	22	AAM01242 P703P epitope #7.
37	28	31.8	16	21	AA52435 Tyrosine phosphata
38	28	31.8	18	22	ABB29269 Peptide #1920 enco
39	28	31.8	18	22	ABB34439 Peptide #1945 enco
40	28	31.8	18	22	ABB19849 Protein #1848 enco
41	28	31.8	18	22	AAW55225 Human brain expres
42	28	31.8	18	22	AAM67621 Human bone marrow
43	28	31.8	18	22	AAM15427 Peptide #1861 enco
44	28	31.8	18	22	AAM38502 Peptide #12539 enc
45	27	30.7	9	20	AA52435 Human cancer antig

ALIGNMENTS

RESULT 1	
AA52435	AA52435 standard; Protein; 18 AA.
ID	AA52435 standard; Protein; 18 AA.
XX	
AC	AA52435;
XX	
DT	15-FEB-2000 (first entry)
XX	
DE	Human tumour antigen NY-ESO-1 peptide #8.
XX	
KW	Cancer; tumour; antigen; MHC; major histocompatibility complex; Class II;
KW	T-cell; helper; stimulation; proliferation; treatment;
KW	diagnosis; prevention; melanoma; breast cancer; ovarian cancer;
KW	prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer;
KW	lymphoma.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
PN	WO9953938-A1.
XX	
PD	28-OCT-1999.
XX	
PF	24-MAR-1999; 99WO-US06875.
XX	
PR	17-APR-1998; 98US-0062422.
PR	02-OCT-1998; 98US-0165546.
XX	
PA	(LUDW-) LUDWIG INST CANCER RES.
XX	
PI	Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
PI	Gure A, Ritter G;
XX	
DR	WPI; 2000-038483/03.

XX Novel peptides which bind to MHC class I and MHC class II molecules,
PT useful for therapeutic and diagnostic purposes -
XX Claim 4; Page 22; 49pp; English.
PS
XX Peptides #8-#13 (AAV52435-Y52440) are peptides derived from the human
CC tumour antigen, NY-ESO-1 (AAV52430) which can bind to MHC(major
CC histocompatibility Class II HLA-DR53 molecules, thereby stimulating
CC proliferation of helper T-cells. cDNA encoding NY-ESO-1 was initially
CC isolated from an oesophagus squamous cell cancer cDNA library. Tissue
CC localisation studies revealed it to be expressed at high levels
CC in normal ovary and testis but not in normal colon, kidney, liver,
CC brain, oesophagus and skin. It was expressed in certain tumours and
CC tumour cell lines with some degree of frequency - these included
CC melanoma specimens and cell lines, and breast and bladder cancer
CC specimens, with expression in other tumour types being sporadic.
CC These NY-ESO-1-derived peptides may be used in methods and
CC compositions used for the treatment, diagnosis and prevention of
CC cancers (such as melanoma, breast cancer, prostate cancer, lung
CC cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer,
CC or lymphoma) and to stimulate the proliferation of T cells.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 88; DB 21; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQQL 18
Db 1 aadhrqlqlsissclqql 18

RESULT 2
AAE07770
ID AAE07770 standard; peptide; 18 AA.
XX
AC AAE07770;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human NY ESO-1 HLA DR restricted T cell cancer peptide #2.
XX
KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.
XX
OS Homo sapiens.
XX
PN WO200155393-A2.
XX
PD 02-AUG-2001.
XX
PF 26-JAN-2001; 2001WO-US02765.
XX
PR 28-JAN-2000; 2000US-0179004.
PR 29-SEP-2000; 2000US-0237107.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang R, Rosenberg SA, Zeng G;
XX
DR WPI; 2001-496851/54.
XX
PT New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -
XX
PS Claim 84; Page 84; 134pp; English.

XX The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or haptan and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is human
CC NY ESO-1 HLA DR restricted T cell cancer peptide.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 88; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQQL 18
Db 1 aadhrqlqlsissclqql 18

RESULT 3
AAU01539
ID AAU01539 standard; Peptide; 18 AA.
XX
AC AAU01539;
XX
DT 18-JUL-2001 (first entry)
XX
DE HLA-DR53 recognising NY-ESO-1 peptide #1.
XX
KW NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
KW human leukocyte antigen-determining region; disease progression;
KW disease regression; disease onset; body tissue; body fluid; enzyme label;
KW radioactive label; monoclonal antibody.
XX
OS Homo sapiens.
XX
PN WO200123560-A2.
XX
PD 05-APR-2001.
XX
PF 26-SEP-2000; 2000WO-US26411.
XX
PR 29-SEP-1999; 99US-0408036.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Tureci O, Sahin U, Pfreundschuh M;
XX
DR WPI; 2001-266156/27.
XX
PT Polypeptides binding to major histocompatibility complex class II human
PT leukocyte antigen-determining region molecule having amino acid
PT sequence found in tumour rejection antigen precursor used for
PT stimulating proliferation of helper T cells -
XX
PS Example 13; Page 19; 62pp; English.
XX
CC The sequence represents a human NY-ESO-1 tumour rejection antigen
CC precursor fragment which recognises and binds to HLA-DR53. NY-ESO-1 and
CC SSX-2 polypeptides, or fragments of, bind to major histocompatibility

CC complex (MHC) Class II molecules such as human leukocyte
CC antigen-determining region (HLA-DR) molecules and stimulate proliferation
CC of helper T cells. The peptides can be administered to an HLA-DR positive
CC subject in order to stimulate the helper T cells. An MHC Class II
CC HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell or
CC present in free form is useful for this stimulation. The nucleic acid is
CC useful for screening for a cancerous condition, which involves contacting
CC a subject sample to a cell line transfected with the immunoreactive cell
CC (helper T cell), where interaction is indicative of cancer. In addition,
CC a sample from a patient (for example, a body fluid or tissue) can be
CC monitored for the amount of the complex present in the bloodstream. This
CC is useful for determining regression, progression or onset of a cancerous
CC condition. The method involves contacting the sample with a radioactive
CC labelled or enzyme labelled monoclonal antibody which specifically binds
CC with the complex.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 88; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQQL 18
| | | | | | | | | | | | | | | |
Db 1 aadhrqlqlsissclqql 18

RESULT 4
AAB69939
ID AAB69939 standard; Peptide; 18 AA.

XX AAB69939;

DT 27-APR-2001 (first entry)

XX Human NY-ESO-1 HLA-DR53 binding motif #1.

KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW non-small cell lung carcinoma; tumour status determination.

XX Homo sapiens.

XX WO200107917-A1.

PN 01-FEB-2001.

PD 14-JUL-2000; 2000WO-US19220.

XX 23-JUL-1999; 99US-0359503.

XX (LUDW-) LUDWIG INST CANCER RES.

PA (SLOK) SLOAN KETTERING INST CANCER RES.

PA (CORR) CORNELL RES FOUND INC.

XX Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;

PI WPI; 2001-182822/18.

XX Method useful for determining the status (e.g. progression, regression
PT or stability of the disease) of a cancerous condition, involves
PT determining the levels of NY-ESO-1 specific antibodies in a sample
PT taken from a patient .

XX Example 16; Page 27; 50pp; English.

XX The present sequence is given in a specification relating to a method
CC for determining the status of a cancerous condition in a patient
CC with a tumour that expresses NY-ESO-1. The method comprises assaying a
CC sample taken from the patient for antibodies that specifically bind to
CC the NY-ESO-1 and comparing the value obtained to a prior value obtained
CC from assay of a prior sample taken from the patient. Any difference

CC between the values is indicative of a change in status of the cancerous
CC condition. The method is useful for determining whether a cancerous
CC condition is progressing, regressing or remaining stable, in particular
CC in patients receiving treatment for a melanoma, adenocarcinoma,
CC non-small cell lung carcinoma or bladder carcinoma.

XX Sequence 18 AA;

Query Match 100.0%; Score 88; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQQL 18
| | | | | | | | | | | | | | | |
Db 1 aadhrqlqlsissclqql 18

RESULT 5

AAE07735

ID AAE07735 standard; peptide; 17 AA.

XX AAE07735;

XX 06-NOV-2001 (first entry)

XX Human NY ESO-1 MHC class II restricted T cell epitope #19.

KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.

XX Homo sapiens.

XX WO200155393-A2.

XX 02-AUG-2001.

XX 26-JAN-2001; 2001WO-US02765.

XX 28-JAN-2000; 2000US-0179004.

XX 29-SEP-2000; 2000US-0237107.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang R, Rosenberg SA, Zeng G;

XX WPI; 2001-496851/54.

XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -

PS Claim 4; Page 17; 134pp; English.

XX The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or hapten and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is MHC

CC class II restricted T cell epitope of human NY ESO-1 protein.
XX
SQ Sequence 17 AA;

Query Match 90.9%; Score 80; DB 22; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DHRQLQLSISSCLQQL 18
| | | | | | | | | | | | | | | | | |
Db 1 dhrqlqlsissclql 16

RESULT 6
AAE07736
ID AAE07736 standard; peptide; 14 AA.

XX
AC AAE07736;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human NY ESO-1 MHC class II restricted T cell epitope #20.

XX
KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
immunotherapy.

XX Homo sapiens.
OS
XX
PN WO200155393-A2.
XX
PD 02-AUG-2001.
XX
PF 26-JAN-2001; 2001WO-US02765.
XX
PR 28-JAN-2000; 2000US-0179004.
PR 29-SEP-2000; 2000US-0237107.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang R, Rosenberg SA, Zeng G;
XX WPI; 2001-496851/54.

PT New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -

XX Claim 4; Page 17; 134pp; English.

XX The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or haptens and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is MHC
CC class II restricted T cell epitope of human NY ESO-1 protein.

XX Sequence 14 AA;

Query Match 80.7%; Score 71; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DHRQLQLSISSCLQ 16
| | | | | | | | | | | | | | | | | |
Db 1 dhrqlqlsissclq 14

RESULT 7
AAE07737
ID AAE07737 standard; peptide; 13 AA.

XX
AC AAE07737;
XX
DT 06-NOV-2001 (first entry)

XX Human NY ESO-1 MHC class II restricted T cell epitope #21.

XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
immunotherapy.

XX Homo sapiens.
OS
XX WO200155393-A2.
PN
XX
PD 02-AUG-2001.
XX
PF 26-JAN-2001; 2001WO-US02765.
XX
PR 28-JAN-2000; 2000US-0179004.
PR 29-SEP-2000; 2000US-0237107.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang R, Rosenberg SA, Zeng G;
XX WPI; 2001-496851/54.

PT New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -

XX Claim 4; Page 17; 134pp; English.

XX The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or haptens and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is MHC
CC class II restricted T cell epitope of human NY ESO-1 protein.

XX Sequence 13 AA;

Query Match 69.3%; Score 61; DB 22; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QLQLSISSC LQOL 18
Db 1 qlqlsissclql 13

RESULT 8
AAY06011
ID AAY06011 standard; Peptide; 10 AA.
XX
AC AAY06011;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; human leukocyte antigen; HLA.
XX
OS Homo sapiens.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US19609.
XX
PR 08-OCT-1997; 97US-0061428.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rosenberg SA, Wang RF;
XX
DR WPI; 1999-277270/23.
XX
PT Cancer antigen NY ESOL/CAG-3
XX
PS Example 10; Page 42; 88pp; English.
XX
CC This peptide was identified as an HLA peptide motif following a
CC screen for epitopes from the coding region of human ESO-1/CAG-3
CC ORF1 (see AAX58599). 30 Epitopes (see AAY05988-Y06017) were identified.
CC The present peptide (ranked 24) corresponds to amino acid residues
CC 143-152 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent
CC tumour antigen capable of eliciting an antigen specific immune
CC response by T cells. Cancer peptides (see AAY05967-87) derived from
CC CAG-3, portions of CAG-3 and their variants, are useful as cancer
CC vaccines. A claimed method of preventing or inhibiting cancer
CC involves administering a cancer peptide, with or without an HLA
CC molecule. The cancer peptides form part of, or are derived
CC from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer and
CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
CC thyroid cancers.
XX
SQ Sequence 10 AA;

Query Match 54.5%; Score 48; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQLQLSISSC 14
Db 1 rqlqlsissc 10

RESULT 9
AAY06016
ID AAY06016 standard; Peptide; 10 AA.
XX
AC AAY06016;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; human leukocyte antigen; HLA.
XX
OS Homo sapiens.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US19609.
XX
PR 08-OCT-1997; 97US-0061428.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rosenberg SA, Wang RF;
XX
DR WPI; 1999-277270/23.
XX
PT Cancer antigen NY ESOL/CAG-3
XX
PS Example 10; Page 42; 88pp; English.
XX
CC This peptide was identified as an HLA peptide motif following a
CC screen for epitopes from the coding region of human ESO-1/CAG-3
CC ORF1 (see AAX58599). 30 Epitopes (see AAY05988-Y06017) were identified.
CC The present peptide (ranked 29) corresponds to amino acid residues
CC 144-153 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent
CC tumour antigen capable of eliciting an antigen specific immune
CC response by T cells. Cancer peptides (see AAY05967-87) derived from
CC CAG-3, portions of CAG-3 and their variants, are useful as cancer
CC vaccines. A claimed method of preventing or inhibiting cancer
CC involves administering a cancer peptide, with or without an HLA
CC molecule. The cancer peptides form part of, or are derived
CC from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer and
CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
CC thyroid cancers.
XX
SQ Sequence 10 AA;

Query Match 53.4%; Score 47; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QLQLSISSC L 15
Db 1 qlqlsisscl 10

RESULT 10
AAG67179
ID AAG67179 standard; peptide; 9 AA.
XX
AC AAG67179;
XX

DT 13-NOV-2001 (first entry)
XX
DE Cancer testis tumour antigen NY-ESO-1 derived peptide.
XX
KW Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;
KW HLA; HLA binding peptide; major histocompatibility complex; MHC;
KW tumour; cancer; testis tumour.
XX
OS Homo sapiens.
XX
PN WO200162917-A1.
XX
PD 30-AUG-2001.
XX
PF 22-JAN-2001; 2001WO-US02126.
XX
PR 22-FEB-2000; 2000US-0510635.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Lethe B, Boon-Falleur T;
XX
DR WPI; 2001-550091/61.
XX
PT Genomic sequences of tumour associated antigen EY-ESO-1 (LAGE-2) useful
PT for diagnosing testicular tumours -
XX
PS Example 13; Page 26; 50pp; English.
XX
CC AAG67169-AAG67206 represent peptides which are derived from cancer
CC testis tumour antigen NY-ESO-1 (also called LAGE-2). The peptides
CC bind to human leukocyte antigens (HLAs). NY-ESO-1 is a molecule that
CC is processed to at least one human leukocyte antigen (HLA) binding
CC peptide, which binds to Class I and Class II major histocompatibility
CC complex (MHC). NY-ESO-1 is expressed in tumour mRNA and in testis,
CC but not normal colon, kidney, liver or brain tissue. The presence or
CC level of expression of NY-ESO-1 may be assayed for the diagnosis of
CC cancer, especially testis tumours.
XX
SQ Sequence 9 AA;

Query Match 51.1%; Score 45; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQL 9
Db 1 aadhrqlql 9

RESULT 11
AAB69911
ID AAB69911 standard; Peptide; 9 AA.
XX
AC AAB69911;
XX
DT 27-APR-2001 (first entry)
XX
DE Human NY-ESO-1 HLA binding motif #11.
XX
KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW non-small cell lung carcinoma; tumour status determination.
XX
OS Homo sapiens.
XX
PN WO200107917-A1.
XX
PD 01-FEB-2001.
XX
PF 14-JUL-2000; 2000WO-US19220.
XX

PR 23-JUL-1999; 99US-0359503.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.
XX
PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
XX
DR WPI; 2001-182822/18.
XX
PT Method useful for determining the status (e.g. progression, regression
PT or stability of the disease) of a cancerous condition, involves
PT determining the levels of NY-ESO-1 specific antibodies in a sample
PT taken from a patient -
XX
PS Example 14; Page 25; 50pp; English.
XX
CC The present sequence is given in a specification relating to a method
CC for determining the status of a cancerous condition in a patient
CC with a tumour that expresses NY-ESO-1. The method comprises assaying a
CC sample taken from the patient for antibodies that specifically bind to
CC the NY-ESO-1 and comparing the value obtained to a prior value obtained
CC from assay of a prior sample taken from the patient. Any difference
CC between the values is indicative of a change in status of the cancerous
CC condition. The method is useful for determining whether a cancerous
CC condition is progressing, regressing or remaining stable, in particular
CC in patients receiving treatment for a melanoma, adenocarcinoma,
CC non-small cell lung carcinoma or bladder carcinoma.
XX
SQ Sequence 9 AA;

Query Match 51.1%; Score 45; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQL 9
Db 1 aadhrqlql 9

RESULT 12
AAG67202
ID AAG67202 standard; peptide; 10 AA.
XX
AC AAG67202;
XX
DT 13-NOV-2001 (first entry)
XX
DE Cancer testis tumour antigen NY-ESO-1 derived peptide.
XX
KW Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;
KW HLA; HLA binding peptide; major histocompatibility complex; MHC;
KW tumour; cancer; testis tumour.
XX
OS Homo sapiens.
XX
PN WO200162917-A1.
XX
PD 30-AUG-2001.
XX
PF 22-JAN-2001; 2001WO-US02126.
XX
PR 22-FEB-2000; 2000US-0510635.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Lethe B, Boon-Falleur T;
XX
DR WPI; 2001-550091/61.
XX
PT Genomic sequences of tumour associated antigen EY-ESO-1 (LAGE-2) useful
PT for diagnosing testicular tumours -

XX
PS Example 13; Page 26; 50pp; English.
XX
CC AAG67169-AAG67206 represent peptides which are derived from cancer
CC testis tumour antigen NY-ESO-1 (also called LAGE-2). The peptides
CC bind to human leukocyte antigens (HLAs). NY-ESO-1 is a molecule that
CC is processed to at least one human leukocyte antigen (HLA) binding
CC peptide, which binds to Class I and Class II major histocompatibility
CC complex (MHC). NY-ESO-1 is expressed in tumour mRNA and in testis,
CC but not normal colon, kidney, liver or brain tissue. The presence or
CC level of expression of NY-ESO-1 may be assayed for the diagnosis of
CC cancer, especially testis tumours.
XX
SQ Sequence 10 AA;

Query Match 51.1%; Score 45; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQL 9
Db 2 aadhrqlql 10

RESULT 13
AAB69934
ID AAB69934 standard; Peptide; 10 AA.
XX
AC AAB69934;
XX
DT 27-APR-2001 (first entry)
XX
DE Human NY-ESO-1 HLA binding motif #34.
XX
KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW non-small cell lung carcinoma; tumour status determination.
XX
OS Homo sapiens.
XX
PN WO200107917-A1.
XX
PD 01-FEB-2001.
XX
PF 14-JUL-2000; 2000WO-US19220.
XX
PR 23-JUL-1999; 99US-0359503.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.
XX
PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
XX
DR WPI; 2001-182822/18.
XX
PT Method useful for determining the status (e.g. progression, regression
PT or stability of the disease) of a cancerous condition, involves
PT determining the levels of NY-ESO-1 specific antibodies in a sample
PT taken from a patient .
XX
PS Example 14; Page 25; 50pp; English.
XX
CC The present sequence is given in a specification relating to a method
CC for determining the status of a cancerous condition in a patient
CC with a tumour that expresses NY-ESO-1. The method comprises assaying a
CC sample taken from the patient for antibodies that specifically bind to
CC the NY-ESO-1 and comparing the value obtained to a prior value obtained
CC from assay of a prior sample taken from the patient. Any difference
CC between the values is indicative of a change in status of the cancerous
CC condition. The method is useful for determining whether a cancerous
CC condition is progressing, regressing or remaining stable, in particular

CC in patients receiving treatment for a melanoma, adenocarcinoma,
CC non-small cell lung carcinoma or bladder carcinoma.
XX
SQ Sequence 10 AA;

Query Match 51.1%; Score 45; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQL 9
Db 2 aadhrqlql 10

RESULT 14
AAY06035
ID AAY06035 standard; Peptide; 9 AA.
XX
AC AAY06035;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; human leukocyte antigen; HLA.
XX
OS Homo sapiens.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US19609.
XX
PR 08-OCT-1997; 97US-0061428.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rosenberg SA, Wang RF;
XX
DR WPI; 1999-277270/23.
XX
PT Cancer antigen NY ESO1/CAG-3
XX
PS Example 10; Page 43; 88pp; English.
XX
CC This peptide was identified as an HLA peptide motif following a
CC screen for epitopes from the coding region of human ESO-1/CAG-3
CC ORF1 (see AAX58599). 30 Epitopes (see AAY06018-47) were identified.
CC The present peptide (ranked 18) corresponds to amino acid residues
CC 148-156 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent
CC tumour antigen capable of eliciting an antigen specific immune
CC response by T cells. Cancer peptides (see AAY05967-87) derived from
CC CAG-3, portions of CAG-3 and their variants, are useful as cancer
CC vaccines. A claimed method of preventing or inhibiting cancer
CC involves administering a cancer peptide, with or without an HLA
CC molecule. The cancer peptides form part of, or are derived
CC from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer and
CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
CC thyroid cancers.
XX
SQ Sequence 9 AA;

Query Match 48.9%; Score 43; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 SISSCLQQL 18
|
Db 1 sissclqql 9

RESULT 15
AAAY79748
ID AAY79748 standard; Peptide; 9 AA.
XX
AC AAY79748;
XX

DT 10-MAY-2000 (first entry)
XX

DE NY-ESO-1 derived peptide #4.
XX

KW Cancer; SSX family; SSX-1; SSX-2; SSX-3; SSX-4; SSX-5; NY-ESO-1;
KW HLA binding; human leukocyte antigen; cytolytic T cell; CTL;
KW cytostatic; melanoma; synovial sarcoma.
XX

OS Homo sapiens.
XX

PN WO200000824-A1.
XX

PD 06-JAN-2000.
XX

PF 25-JUN-1999; 99WO-US14493.
XX

PR 26-JUN-1998; 98US-0105839.
XX

PA (LUDW-) LUDWIG INST CANCER RES.
XX

PI Tureci O, Sahin U, Pfreundschuh M, Rammensee G, Stevanovic S;
PI Chen Y, Gure A, Old LJ;
XX

DR WPI; 2000-170933/15.
XX

PT Determining the possible presence of breast, endometrial, colorectal,
PT lung, bladder or head-neck cancer -
XX

PS Example 13; Page 26; 40pp; English.
XX

CC A method has been developed for determining the possible presence of a
CC cancer, which is not melanoma or synovial sarcoma. The method comprises
CC assaying a sample taken from the subject to determine the expression of
CC an SSX gene, and determining the expression as a determination of the
CC possible presence of cancer. Expression of SSX1 gene indicates possible
CC presence of breast, endometrial, colorectal, lung, bladder or head-neck
CC cancer. These cancers are also detected by SSX2 and SSX4 gene
CC expression. SSX2 gene expression additionally indicates possible presence
CC of lymphoma, renal cell cancer, glioma and prostate cancer. Expression
CC of SSX4 gene also indicates possible presence of ovarian or stomach
CC cancer. SSX5 gene expression indicates the same cancers as SSX1, except
CC breast cancer. Determining expression of SSX gene can be used to monitor
CC progress of melanoma or synovial sarcoma, which is not cancer. The
CC SSX-derived peptide complex stimulates proliferation of cytolytic T
CC cells. This is useful for treating cancer, especially melanoma. AAY78464
CC to AAY78468 represent specifically claimed HLA binding peptides for use
CC in the method of the invention. AAZ88452 to AAZ88465 represent PCR
CC primers used in the isolation of SSX genes in the exemplification of the
CC present invention. AAY78469 to AAY78500, and AAY79684 to AAY79762
CC represent peptides derived from SSX proteins or NY-ESO-1, which are used
CC in the exemplification of the present invention.
XX

SQ Sequence 9 AA;

Query Match 48.9%; Score 43; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 SISSCLQQL 18
|
Db 1 sissclqql 9

Search completed: July 3, 2002, 11:26:57
Job time: 954 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 11:24:14 ; Search time 560.51 Seconds
(without alignments)
11.303 Million cell updates/sec

Title: US-09-165-546A-8
Perfect score: 88
Sequence: 1 AADHRQLQLSISSCLQQL 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 451056

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_AA_Main:
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2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
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26: /cgn2_6/ptodata/2/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	88	100.0	18	15 US-09-165-546A-8	Sequence 8, Appli
2	88	100.0	18	18 US-09-408-036B-7	Sequence 7, Appli
3	48	54.5	10	19 US-09-529-206-99	Sequence 99, Appli
4	48	54.5	10	19 US-09-529-206A-99	Sequence 99, Appli
5	48	54.5	10	19 US-09-529-206B-99	Sequence 99, Appli
6	47	53.4	10	19 US-09-529-206-103	Sequence 103, App
7	47	53.4	10	19 US-09-529-206A-103	Sequence 103, App

8	47	53.4	10	19	US-09-529-206B-103	Sequence 103, App
9	43	48.9	9	18	US-09-409-455A-115	Sequence 115, App
10	43	48.9	9	19	US-09-529-206-74	Sequence 74, Appl
11	43	48.9	9	19	US-09-529-206A-74	Sequence 74, Appl
12	43	48.9	9	19	US-09-529-206B-74	Sequence 74, Appl
13	43	48.9	9	22	US-09-833-039-115	Sequence 115, App
14	42	47.7	9	19	US-09-529-206-75	Sequence 75, Appl
15	42	47.7	9	19	US-09-529-206A-75	Sequence 75, Appl
16	42	47.7	9	19	US-09-529-206B-75	Sequence 75, Appl
17	39	44.3	9	19	US-09-529-206-79	Sequence 79, Appl
18	39	44.3	9	19	US-09-529-206A-79	Sequence 79, Appl
19	39	44.3	9	19	US-09-529-206B-79	Sequence 79, Appl
20	36	40.9	9	18	US-09-409-455A-121	Sequence 121, App
21	36	40.9	9	22	US-09-833-039-121	Sequence 121, App
22	32	36.4	16	3	US-07-949-472-8	Sequence 8, Appli
23	32	36.4	18	15	US-09-165-546A-13	Sequence 13, Appl
24	32	36.4	18	18	US-09-408-036B-12	Sequence 12, Appl
25	30	34.1	16	1	PCT-US01-23046-341	Sequence 341, App
26	30	34.1	16	20	US-09-620-091-341	Sequence 341, App
27	29	33.0	18	14	US-09-079-030-201	Sequence 201, App
28	29	33.0	18	14	US-09-079-030-202	Sequence 202, App
29	28	31.8	9	1	PCT-US01-28124A-97	Sequence 97, Appl
30	28	31.8	10	19	US-09-572-404B-396	Sequence 396, App
31	28	31.8	10	19	US-09-572-404B-398	Sequence 398, App
32	28	31.8	10	19	US-09-572-404B-736	Sequence 736, App
33	28	31.8	15	19	US-09-593-793A-805	Sequence 805, App
34	28	31.8	15	20	US-09-605-783A-805	Sequence 805, App
35	28	31.8	15	20	US-09-605-785-805	Sequence 805, App
36	28	31.8	15	20	US-09-636-215-805	Sequence 805, App
37	28	31.8	15	20	US-09-651-236-805	Sequence 805, App
38	28	31.8	15	20	US-09-657-279-805	Sequence 805, App
39	28	31.8	15	20	US-09-679-426-805	Sequence 805, App
40	28	31.8	15	20	US-09-685-166-805	Sequence 805, App
41	28	31.8	15	20	US-09-685-166A-805	Sequence 805, App
42	28	31.8	15	21	US-09-759-143-805	Sequence 805, App
43	28	31.8	15	21	US-09-780-669-805	Sequence 805, App
44	28	31.8	15	22	US-09-822-827-805	Sequence 805, App
45	28	31.8	15	22	US-09-852-911-805	Sequence 805, App

ALIGNMENTS

RESULT 1
US-09-165-546A-8
; Sequence 8, Application US/09165546A
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao,
; Canlan, Matt; Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO
; AMINO ACID SEQUENCES OF NY-ESO-1, WHICH BIND TO
; MHC CLASS I AND MHC CLASS II MOLECULES, AND
; USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,546A
; FILING DATE: 02-Oct-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998

; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-165-546A-8

Query Match 100.0%; Score 88; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQQL 18
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Db 1 AADHRQLQLSISSCLQQL 18

RESULT 2
US-09-408-036B-7
; Sequence 7, Application US/09408036B
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Isolated Peptides Which Bind to MHC Class II Molecules and Uses T
; FILE REFERENCE: LUD 5624
; CURRENT APPLICATION NUMBER: US/09/408,036B
; CURRENT FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/165,546
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 7
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-408-036B-7

Query Match 100.0%; Score 88; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQQL 18
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Db 1 AADHRQLQLSISSCLQQL 18

RESULT 3
US-09-529-206-99
; Sequence 99, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08

; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 99
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-99

Query Match 54.5%; Score 48; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RQLQLSISSC 14
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Db 1 RQLQLSISSC 10

RESULT 4
US-09-529-206A-99
; Sequence 99, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206A-99

Query Match 54.5%; Score 48; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RQLQLSISSC 14
| | | | | | | | | |
Db 1 RQLQLSISSC 10

RESULT 5
US-09-529-206B-99
; Sequence 99, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-99

Query Match 54.5%; Score 48; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RQLQLSISSC 14
Db 1 RQLQLSISSC 10

RESULT 6
US-09-529-206-103
; Sequence 103, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 103
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-103

Query Match 53.4%; Score 47; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QLQLSISSCL 15
Db 1 QLQLSISSCL 10

RESULT 7
US-09-529-206A-103
; Sequence 103, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 103
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206A-103

Query Match 53.4%; Score 47; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QLQLSISSCL 15
Db 1 QLQLSISSCL 10

RESULT 8
US-09-529-206B-103
; Sequence 103, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 103
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-103

Query Match 53.4%; Score 47; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QLQLSISSCL 15
Db 1 QLQLSISSCL 10

RESULT 9
US-09-409-455A-115
; Sequence 115, Application US/09409455A
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622
; CURRENT APPLICATION NUMBER: US/09/409,455A
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 115
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-409-455A-115

Query Match 48.9%; Score 43; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 SISSCLOQL 18
Db 1 SISSCLOQL 9

RESULT 10
US-09-529-206-74
; Sequence 74, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as


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; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-529-206-74

Query Match      48.9%; Score 43; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 SISSCLQQL 18
Db 1 SISSCLQQL 9

RESULT 11
US-09-529-206A-74
; Sequence 74, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-529-206A-74

Query Match      48.9%; Score 43; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 SISSCLQQL 18
Db 1 SISSCLQQL 9

RESULT 12
US-09-529-206B-74
; Sequence 74, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
```

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; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-529-206B-74

Query Match      48.9%; Score 43; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 SISSCLQQL 18
Db 1 SISSCLQQL 9

RESULT 13
US-09-833-039-115
; Sequence 115, Application US/098333039
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 115
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-833-039-115

Query Match      48.9%; Score 43; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 SISSCLQQL 18
Db 1 SISSCLQQL 9

RESULT 14
US-09-529-206-75
; Sequence 75, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-529-206-75
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Query Match 47.7%; Score 42; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LQLSISSCL 15
| | | | | | | |
Db 1 LQLSISSCL 9

RESULT 15
US-09-529-206A-75
; Sequence 75, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206A-75

Query Match 47.7%; Score 42; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LQLSISSCL 15
| | | | | | | |
Db 1 LQLSISSCL 9

Search completed: July 3, 2002, 11:38:24
Job time: 850 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:24:49 ; Search time 61.64 Seconds
(without alignments)
29.545 Million cell updates/sec

Title: US-09-165-546A-8
Perfect score: 88
Sequence: 1 AADHRQLQLSISSCLQQL 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 308740 seqs, 101176262 residues

Total number of hits satisfying chosen parameters: 45157

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
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4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
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7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	53.4	10	6 US-10-117-937-194	Sequence 194, App
2	45	51.1	9	6 US-10-117-937-192	Sequence 192, App
3	45	51.1	10	6 US-10-117-937-195	Sequence 195, App
4	43	48.9	9	5 US-09-344-040C-115	Sequence 115, App
5	43	48.9	9	6 US-10-117-937-193	Sequence 193, App
6	36	40.9	9	5 US-09-344-040C-121	Sequence 121, App
7	35	39.8	9	6 US-10-117-937-198	Sequence 198, App
8	35	39.8	10	6 US-10-117-937-201	Sequence 201, App
9	31	35.2	9	6 US-10-117-937-200	Sequence 200, App
10	26	29.5	17	6 US-10-062-831-186	Sequence 186, App
11	25	28.4	9	6 US-10-001-469-48	Sequence 48, App1
12	25	28.4	10	6 US-10-001-469-155	Sequence 155, App
13	25	28.4	10	6 US-10-001-469-571	Sequence 571, App
14	25	28.4	10	6 US-10-001-469-2426	Sequence 2426, Ap
15	25	28.4	13	6 US-10-120-604-60	Sequence 60, App1
16	25	28.4	13	6 US-10-120-604-79	Sequence 79, App1
17	25	28.4	14	6 US-10-012-456A-42	Sequence 42, App1
18	25	28.4	15	6 US-10-001-469-2646	Sequence 2646, Ap
19	25	28.4	15	6 US-10-001-469-2755	Sequence 2755, Ap
20	25	28.4	15	6 US-10-001-469-2791	Sequence 2791, Ap
21	25	28.4	15	6 US-10-001-469-2861	Sequence 2861, Ap
22	24	27.3	13	6 US-10-105-299-5965	Sequence 5965, Ap
23	24	27.3	13	6 US-10-105-299-5966	Sequence 5966, Ap
24	24	27.3	16	5 US-09-661-992-106	Sequence 106, App
25	24	27.3	17	5 US-09-855-604-59	Sequence 59, App1
26	24	27.3	17	5 US-09-855-604-540	Sequence 540, App

27	24	27.3	17	6 US-10-115-123-414	Sequence 414, App
28	24	27.3	18	6 US-10-145-206-147	Sequence 147, App
29	23	26.1	11	5 US-09-050-359B-40	Sequence 40, Appl
30	23	26.1	11	5 US-09-069-827A-40	Sequence 40, Appl
31	23	26.1	11	6 US-10-012-034A-122	Sequence 122, App
32	23	26.1	17	5 US-09-721-506-83	Sequence 83, Appl
33	23	26.1	17	6 US-10-044-539-83	Sequence 83, Appl
34	23	26.1	18	6 US-10-012-034A-43	Sequence 43, Appl
35	22	25.0	9	5 US-09-722-250-307	Sequence 307, App
36	22	25.0	9	5 US-09-722-250-307	Sequence 307, App
37	22	25.0	10	5 US-09-554-467A-20	Sequence 20, Appl
38	22	25.0	10	6 US-10-128-711-47	Sequence 47, Appl
39	22	25.0	10	6 US-10-128-711-54	Sequence 54, Appl
40	22	25.0	10	6 US-10-128-711-126	Sequence 126, App
41	22	25.0	10	6 US-10-128-711-133	Sequence 133, App
42	22	25.0	11	5 US-09-423-037A-47	Sequence 47, Appl
43	22	25.0	11	6 US-10-137-867-454	Sequence 454, App
44	22	25.0	13	5 US-09-999-220B-20	Sequence 20, Appl
45	22	25.0	13	5 US-09-999-220B-72	Sequence 72, Appl

ALIGNMENTS

RESULT 1
US-10-117-937-194
; Sequence 194, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 194
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-194

Query Match 53.4%; Score 47; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LSISSCLQQL 18
| | | | | | | | | |
Db 1 LSISSCLQQL 10

RESULT 2
US-10-117-937-192
; Sequence 192, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937

; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 192
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-192

Query Match 51.1%; Score 45; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQL 9
| | | | | | | | |
Db 1 AADHRQLQL 9

RESULT 3
US-10-117-937-195
; Sequence 195, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 195
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-195

Query Match 51.1%; Score 45; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQL 9
| | | | | | | | | |
Db 2 AADHRQLQL 10

RESULT 4
US-09-344-040C-115
; Sequence 115, Application US/09344040C
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determining Presence of an SSX Gene, Peptides Derived From Said SSX Gene a

; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 115
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-115

Query Match 48.9%; Score 43; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 SSSCLQQL 18
| | | | | | | | | |
Db 1 SSSCLQQL 9

RESULT 5
US-10-117-937-193
; Sequence 193, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 193
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-193

Query Match 48.9%; Score 43; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 SSSCLQQL 18
| | | | | | | | | |
Db 1 SSSCLQQL 9

RESULT 6
US-09-344-040C-121
; Sequence 121, Application US/09344040C
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determining Presence of an SSX Gene, Peptides Derived From Said SSX Gen

```
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 121
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-121
```

```
Query Match      40.9%; Score 36; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AADHRQL 7
    |||
Db 3 AADHRQL 9
```

```
RESULT 7
US-10-117-937-198
; Sequence 198, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-198
```

```
Query Match      39.8%; Score 35; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 12 SSCLQQL 18
    |||
Db 1 SSCLQQL 7
```

```
RESULT 8
US-10-117-937-201
; Sequence 201, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
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; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 201
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-201
```

```
Query Match      39.8%; Score 35; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 12 SSCLQQL 18
    |||
Db 1 SSCLQQL 7
```

```
RESULT 9
US-10-117-937-200
; Sequence 200, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 200
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-200
```

```
Query Match      35.2%; Score 31; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 13 SCLQQL 18
    |||
Db 1 SCLQQL 6
```

```
RESULT 10
US-10-062-831-186
; Sequence 186, Application US/10062831
; GENERAL INFORMATION:
; APPLICANT: Steven M. Ruben, et al.
; TITLE OF INVENTION: 32 Human Secreted Proteins
; FILE REFERENCE: PZ006P1
; CURRENT APPLICATION NUMBER: US/10/062,831
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/690,454
```

; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: PCT/US98/10868
; PRIOR FILING DATE: May 28, 1998
; PRIOR APPLICATION NUMBER: 60/044,039
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,093
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,190
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/050,935
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,101
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,356
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/056,250
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,296
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,293
; PRIOR FILING DATE: August 29, 1997
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 186
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-831-186

Query Match 29.5%; Score 26; DB 6; Length 17;
Best Local Similarity 62.5%; Pred. No. 4.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 LSISSCLQ 16
:|:| |
Db 9 VSIDRCLQ 16

RESULT 11
US-10-001-469-48
; Sequence 48, Application US/10001469
; GENERAL INFORMATION:
; APPLICANT: JAKOBOVITS, AYA
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: HUBERT, RENE
; APPLICANT: FARIS, MARY
; APPLICANT: CHALLITA-EID, PIA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; FILE OF INVENTION: 101P3A11 USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20024.20
; CURRENT APPLICATION NUMBER: US/10/001,469
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/157,902
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/291,118
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/680,728
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 2888
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-001-469-48

Query Match 28.4%; Score 25; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 9 LSISSCLQ 17
|:|:| |
Db 1 LSHSYCLHQ 9

RESULT 12
US-10-001-469-155
; Sequence 155, Application US/10001469
; GENERAL INFORMATION:
; APPLICANT: JAKOBOVITS, AYA
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: HUBERT, RENE
; APPLICANT: FARIS, MARY
; APPLICANT: CHALLITA-EID, PIA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; FILE OF INVENTION: 101P3A11 USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20024.20
; CURRENT APPLICATION NUMBER: US/10/001,469
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/157,902
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/291,118
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/680,728
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 2888
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 155
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-001-469-155

Query Match 28.4%; Score 25; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.9e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 9 LSISSCLQ 17
|:|:| |
Db 2 LSHSYCLHQ 10

RESULT 13
US-10-001-469-571
; Sequence 571, Application US/10001469
; GENERAL INFORMATION:
; APPLICANT: JAKOBOVITS, AYA
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: HUBERT, RENE
; APPLICANT: FARIS, MARY
; APPLICANT: CHALLITA-EID, PIA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; FILE OF INVENTION: 101P3A11 USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20024.20
; CURRENT APPLICATION NUMBER: US/10/001,469
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/157,902
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/291,118
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/680,728
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 2888
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 571
; LENGTH: 10
; TYPE: PRT


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; ORGANISM: Homo sapiens
; US-10-001-469-571

Query Match      28.4%; Score 25; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.9e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 LSISSCLQQ 17
Db 2 LSHSYCLHQ 10

RESULT 14
US-10-001-469-2426
; Sequence 2426, Application US/10001469
; GENERAL INFORMATION:
; APPLICANT: JAKOBOVITS, AYA
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: HUBERT, RENE
; APPLICANT: FARIS, MARY
; APPLICANT: CHALLITA-EID, PIA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 101P3A11 USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20024.20
; CURRENT APPLICATION NUMBER: US/10/001,469
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/157,902
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/291,118
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/680,728
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 2888
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2426
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-001-469-2426

Query Match      28.4%; Score 25; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.9e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 LSISSCLQQ 17
Db 2 LSHSYCLHQ 10

RESULT 15
US-10-120-604-60
; Sequence 60, Application US/10120604
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING TWO NOVEL HUMAN G-PROTEIN COUPLED RECEPT
; TITLE OF INVENTION: HGPRBM28 AND HGPRBM29, AND SPLICE VARIANTS THEREOF
; FILE REFERENCE: D0143NP
; CURRENT APPLICATION NUMBER: US/10/120,604
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US 60/283,145
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/283,161
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/288,468
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 60/300,619
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn version 3.0
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; SEQ ID NO 60
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-120-604-60

Query Match      28.4%; Score 25; DB 6; Length 13;
Best Local Similarity 62.5%; Pred. No. 5.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 DHRQLQLS 10
Db 2 DHRQSRRS 9

Search completed: July 3, 2002, 11:39:32
Job time: 883 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:28:56 ; Search time 57.51 Seconds
(without alignments)
30.075 Million cell updates/sec

Title: US-09-165-546A-9
Perfect score: 84
Sequence: 1 VLLKEFTVSGNILTIRLT 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 3210

Minimum DB seq'length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	29	34.5	12	2 PN0170	alcohol dehydrogen
2	26	31.0	17	4 I76673	hypothetical COII/
3	25	29.8	11	2 I65231	CCK-B gastrin rece
4	24.5	29.2	15	2 I46909	voltage-dependent
5	23	27.4	10	2 PN0165	triose-phosphate i
6	23	27.4	16	2 S36876	aquacobalamine redu
7	23	27.4	16	2 S69361	carbamoyle-phosphat
8	23	27.4	17	2 S58129	hypothetical prote
9	22	26.2	12	2 S17540	agglutinin-III lec
10	22	26.2	15	2 PA0097	starch phosphoryla
11	21.5	25.6	12	2 PC4377	telomeric and tetr
12	21	25.0	10	2 A27617	triose-phosphate i
13	21	25.0	14	2 B44854	L-2,4-diaminobutyr
14	21	25.0	14	2 B39111	Ig heavy chain V r
15	21	25.0	15	2 PA0063	ubiquitin - fungus
16	21	25.0	16	2 I46275	hemoglobin beta-x
17	21	25.0	16	2 A61530	triose-phosphate i
18	21	25.0	18	2 PN0175	glutathione transf
19	20	23.8	9	2 PH0902	T-cell receptor be
20	20	23.8	11	2 S33519	probable secreted
21	20	23.8	11	2 A34243	H-hyosophorin - Ja
22	20	23.8	12	2 A61309	glycoprotein hormo
23	20	23.8	16	2 A42291	tail fiber protein
24	20	23.8	17	2 E28587	T-cell receptor be
25	20	23.8	17	2 H53284	T-cell receptor be
26	19	22.6	10	2 G60787	sperm-activating p
27	19	22.6	10	2 E60787	sperm-activating p
28	19	22.6	11	2 S41747	chaperonin 10 homo
29	19	22.6	11	2 PH0906	T-cell receptor be

30	19	22.6	12	2 A37933	Ig lambda chain J
31	19	22.6	14	2 S19803	ubiquitin - potato
32	19	22.6	15	2 PA0090	protein QF100022 -
33	19	22.6	15	2 G41299	T-cell receptor al
34	19	22.6	15	2 S10741	phosphoglucomutase
35	19	22.6	15	2 A35141	T-cell receptor de
36	19	22.6	16	2 F41299	T-cell receptor al
37	19	22.6	16	2 S59901	pyruvate dehydroge
38	19	22.6	18	2 S29491	GTP-binding protei
39	19	22.6	18	2 B57789	kidney stone matri
40	18	21.4	10	2 E39572	sperm-activating p
41	18	21.4	10	2 D60589	sperm-activating p
42	18	21.4	10	2 A60588	ecdysteroid UDPglu
43	18	21.4	10	2 A61617	nuclease Bhl (EC 3
44	18	21.4	10	2 A59173	27K bile and gallb
45	18	21.4	11	2 D58502	

ALIGNMENTS

RESULT 1
PN0170
alcohol dehydrogenase (EC 1.1.1.1) - fungus (Fusarium sporotrichioides) (fragment)
C;Species: Fusarium sporotrichioides
C;Date: 05-Aug-1994 #sequence_revision 06-Jan-1995 #text_change 31-Jan-1997
C;Accession: PN0170
R;Fukaya, N.; Chow, L.P.; Sugiyura, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.
submitted to JIPID, May 1994
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotr
A;Reference number: PN0160
A;Accession: PN0170
A;Molecule type: protein
A;Residues: 1-12 <FUK>
A;Experimental source: strain M-1-1
C;Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 34.5%; Score 29; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LLKEFTVSG 10
| | | : | | |
Db 2 LLKGYTVDG 10

RESULT 2
I76673
hypothetical COII/ND5 mutant fusion protein - mouse mitochondrion (fragment)
N;Alternate names: COII/ND5 protein
C;Species: mitochondrion Mus musculus (house mouse)
C;Date: 12-Aug-1996 #sequence_revision 16-Jul-1998 #text_change 20-Apr-2000
C;Accession: I76673; I76674
R;Nelson, I.; Gerasimov, S.; Marsac, C.; Lestienne, P.; Boursot, P.
Mamm. Genome 4, 680-683, 1993
A;Title: Sequence analysis of a deleted mitochondrial DNA molecule in heteroplasmic m
A;Reference number: I57011; MUID:94108239
A;Accession: I76673
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-17 <NEL1>
A;Cross-references: GB:S68119; NID:g544777
A;Accession: I76674
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 8-17 <NEL2>
A;Cross-references: GB:S68119; NID:g544777
C;Comment: This is the hypothetical translation of a sequence believed to result from
C;Genetics:
A;Gene: COII/ND5
A;Genome: mitochondrion
A;Genetic code: SGCl

C;Keywords: fusion protein; mitochondrion
F;1-7/Region: cytochrome-c oxidase chain II
F;8-17/Region: NADH dehydrogenase (ubiquinone) chain 5

Query Match 31.0%; Score 26; DB 4; Length 17;
Best Local Similarity 45.5%; Pred. No. 4.9e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 LKEFTVSGNIL 13
|| | : ||:
Db 5 LKPLTFNNNII 15

RESULT 3
I65231
CCK-B gastrin receptor isoform - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: I65231
R;Miyake, A.
Biochem. Biophys. Res. Commun. 208, 230-237, 1995
A;Title: A truncated isoform of human CCK-B/gastrin receptor generated by alternative us
A;Reference number: I52307; MUID:95194412
A;Accession: I65231
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-11 <RES>
A;Cross-references: GB:S76072; NID:g913752; PIDN:AAB33740.1; PID:g913753
C;Genetics:
A;Gene: CCK-B

Query Match 29.8%; Score 25; DB 2; Length 11;
Best Local Similarity 55.6%; Pred. No. 4.5e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 TVSGNILTI 15
: |||: | |
Db 2 SVGGNMLII 10

RESULT 4
I46909
voltage-dependent dihydropyridine-sensitive calcium channel alpha 1 subunit 155 kda isof
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 05-Nov-1999
C;Accession: I46909
R;Malouf, N.N.; McMahon, D.K.; Hainsworth, C.N.; Kay, B.K.
Neuron 8, 899-906, 1992
A;Title: A two-motif isoform of the major calcium channel subunit in skeletal muscle.
A;Reference number: I46909; MUID:92265303
A;Accession: I46909
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-15 <MAL>
A;Cross-references: GB:S36895; NID:g249481; PIDN:AAB22180.1; PID:g249482

Query Match 29.2%; Score 24.5; DB 2; Length 15;
Best Local Similarity 41.2%; Pred. No. 7.7e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 3; Gaps 1;

QY 1 VLLKEFTVSGNILTIRL 17
||| ||: | | :
Db 2 VLLSLFTI---IFTLEM 15

RESULT 5
PN0165
triose-phosphate isomerase (EC 5.3.1.1) - fungus (Fusarium sporotrichioides) (fragment)
C;Species: Fusarium sporotrichioides
C;Date: 05-Aug-1994 #sequence_revision 06-Jan-1995 #text_change 23-Mar-1995

C;Accession: PN0165
R;Fukaya, N.; Chow, L.P.; Sugiyura, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.
submitted to JIPID, May 1994
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotr
A;Reference number: PN0160
A;Accession: PN0165
A;Molecule type: protein
A;Residues: 1-10 <FUK>
A;Experimental source: strain M-1-1
C;Keywords: intramolecular oxidoreductase; isomerase

Query Match 27.4%; Score 23; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 9e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 KEFTVSGN 11
: : | | |
Db 2 RKFFVGGN 9

RESULT 6
S36876
aquacobalamin reductase (NADPH) (EC 1.6.99.11) - Euglena gracilis (fragment)
C;Species: Euglena gracilis
C;Date: 10-Dec-1993 #sequence_revision 09-May-1997 #text_change 07-May-1999
C;Accession: S36876
R;Watanabe, F.; Yamaji, R.; Isegawa, Y.; Yamamoto, T.; Tamura, Y.; Nakano, Y.
Arch. Biochem. Biophys. 305, 421-427, 1993
A;Title: Characterization of aquacobalamin reductase (NADPH) from Euglena gracilis.
A;Reference number: S36876; MUID:93384296
A;Accession: S36876
A;Molecule type: protein
A;Residues: 1-16 <WAT>
C;Keywords: flavoprotein; NADP; oxidoreductase

Query Match 27.4%; Score 23; DB 2; Length 16;
Best Local Similarity 71.4%; Pred. No. 1.5e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 SGNILTI 15
||| : ||
Db 5 SGNHVTI 11

RESULT 7
S69361
carbamoyl-phosphate synthetase I - rat (fragments)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998
C;Accession: S69361
R;Alonso, E.; Rubio, V.
Eur. J. Biochem. 229, 377-384, 1995
A;Title: Affinity cleavage of carbamoyl-phosphate synthetase I localizes regions of t
A;Reference number: S69361; MUID:95262701
A;Accession: S69361
A;Molecule type: protein
A;Residues: 1-8;9-16 <ALO>

Query Match 27.4%; Score 23; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 1.5e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 EFTVSGN 11
: | | | |
Db 10 QFLVKGN 16

RESULT 8
S58129
hypothetical protein - moss (Ceratodon purpureus)

C;Species: Ceratodon purpureus
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 31-Oct-1997
C;Accession: S58129
R;Hughes, J.; Mittmann, F.
submitted to the EMBL Data Library, July 1995
A;Description: The moss Ceratodon purpureus contains and expresses a second, conventional
A;Reference number: S58129
A;Accession: S58129
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-17 <HUG>
A;Cross-references: GB:U56698; EMBL:X89725; NID:q1314836; PID:q1322246

```

Query Match          27.4%; Score 23; DB 2; Length 17;
Best Local Similarity 38.5%; Pred. NO. 1.6e+03;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

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Qy	3	LKEFTVSGNIIITI	15
		: :	
Db	1	MKEFSSTSRSLMI	13

RESULT 9
S17540
agglutinin-III lectin - European elder (fragment)
C:Species: Sambucus nigra (European elder)
C:Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
C:Accession: S17540
R:Mach, L.; Scherf, W.; Ammann, M.; Poetsch, J.; Maerz, W.; Maerz, J.; Gloessl, J.
Biochem. J. 278, 667-671, 1991
A:Title: Purification and partial characterization of a novel lectin from elder (Sambucus nigra)
A:Reference number: S17540; MUID:91378923
A:Accession: S17540
A:Molecule type: protein
A:Residues: 1-12 <NAC>
A:Experimental source: fruit
C:Keywords: glycoprotein; lectin

```
Query Match      26.2%; Score 22; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. NO. 1.6e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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Qy 8 VSGNIL 13
::|||:
Db 5 ITGNII 10

RESULT 10
PA0097
starch phosphorylase (EC 2.4.1.1) - fungus (Fusarium sporotrichioides) (fragment)
N:Alternate names: maltodextrin phosphorylase
C:Species: Fusarium sporotrichioides
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C:Accession: PA0097
R:Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides
A:Reference number: PA0051
A:Accession: PA0097
A:Molecule type: protein
A:Residues: 1-15 <CHO>
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match	26.2%;	Score 22;	DB 2;	Length 15;
Best Local Similarity	37.5%;	Pred. No. 2.1e+03;		
Matches	3;	Conservative	3;	Mismatches 2;
				Indels 0;
				Gaps 0;

Qy 6 FTVSGNIL 13
 ||::| :
 Db 6 FTITGOAI 13

RESULT 11
PC4377
telomeric and tetraplex DNA binding protein qTBP42 VIII - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 07-May-1999
C:Accession: PC4377
R:Sarig, G.; Weisman-Shomer, P.; Fry, M.
Biochem. Biophys. Res. Commun. 237, 617-623, 1997
A:Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the
A:Reference number: PC4371: MUID:97445086

Query Match	25.6%	Score 21.5;	DB 2;	Length 12;
Best Local Similarity	66.7%	Pred. No. 2e+03;		
Matches	6: Conservative	2: Mismatches	0: Indels	1: Gaps

Qy 4 KEF-TVSGN 11
|:| |||:
Db 2 KKEHTVSGS 10

RESULT 12
A27617
triose-phosphate isomerase (EC 5.3.1.1) - curled-leaved tobacco (fragment)
C:Species: Nicotiana glauca (curled-leaved tobacco)
C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 28-Apr-1993
C:Accession: A27617
R:Baauw, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.
Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987
A:Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid sequencing
A:Reference number: A94167
A:Accession: A27617
A:Molecule type: protein
A:Residues: 1-10 <BAU>
C:Keywords: gluconeogenesis; glycolysis; intramolecular oxidoreductase; isomerase; pe

Query Match	25.0%;	Score 21;	DB 2;	Length 10;
Best Local Similarity	50.0%;	Pred. No. 2e+03;		
Matches	4: Conservative	1: Mismatches	3: Indels	0: Gaps

Qy 4 KEFTVSGN 11
: | | | |
Db 2 RTFVVGNN 9

```

RESULT 13
B44854
L-2,4-diaminobutyrate decarboxylase (EC 4.1.1.-) - Vibrio alginolyticus (fragment)
C:Species: Vibrio alginolyticus
C:Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 10-Nov-1995
C:Accession: B44854; B41817
R:Yamamoto, S.; Tsuzaki, Y.; Tougou, K.; Shinoda, S.
J. Gen. Microbiol. 138, 1461-1465, 1992
A:Title: Purification and characterization of L-2,4-diaminobutyrate decarboxylase from
A:Reference number: A44854; MUID:92381494
A:Accession: B44854
A:Molecule type: protein
A:Residues: 1-14 <YAM>
A:Note: sequence extracted from NCBI backbone (NCBIP:112332)
C:Keywords: carbon-carbon lyase; carboxy-lyase

```

```
Query Match      25.0%; Score 21; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.8e+03;
Matches 5: Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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Qy 6 FTVSGNLTIT 15
| | | | |
Db 4 FEVDSNIWNI 13

RESULT 14

B39111
Ig heavy chain V region - Pacific hagfish (fragment)
C:Species: Eptatretus stouti (Pacific hagfish)
C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-1996
C:Accession: B39111
R:Varner, J.; Neame, P.; Litman, G.W.
Proc. Natl. Acad. Sci. U.S.A. 88, 1746-1750, 1991
A:Title: A serum heterodimer from hagfish (Eptatretus stoutii) exhibits structural simil
A:Reference number: A39111; MUID:91156684
A:Accession: B39111
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <VAR>
C:Keywords: heterotetramer; immunoglobulin

Query Match 25.0%; Score 21; DB 2; Length 14;
Best Local Similarity 40.0%; Pred. No. 2.8e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 7 TVSGNLTIR 16
| | | | |
Db 2 TAYGNLAAIQ 11

RESULT 15

PA0063
ubiquitin - fungus (Fusarium sporotrichioides) (fragment)
C:Species: Fusarium sporotrichioides
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C:Accession: PA0063
R:Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
A:Reference number: PA0051
A:Accession: PA0063
A:Molecule type: protein
A:Residues: 1-15 <ACC>

Query Match 25.0%; Score 21; DB 2; Length 15;
Best Local Similarity 33.3%; Pred. No. 3e+03;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 7 TVSGNLTIT 15
| : | : |
Db 7 TLTGKTIITL 15

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:41:54 ; Search time 27.94 Seconds
(without alignments)
24.945 Million cell updates/sec

Title: US-09-165-546A-9
Perfect score: 84
Sequence: 1 VLLKEFTVSGNILTIRLT 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 923

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	25.0	10	1 TPIS_NICPL	P19118 nicotiana p
2	21	25.0	12	1 OPS3_DROVI	P17645 drosophila
3	21	25.0	13	1 BP37_LEUMA	P81754 leucophaea
4	21	25.0	15	1 CDN3_LITGI	P56248 litoria gil
5	21	25.0	15	1 CDN4_LITCE	P82076 litoria cae
6	20	23.8	15	1 CDN2_LITGI	P56247 litoria gil
7	20	23.8	15	1 THL_CLOPA	P81347 clostridium
8	20	23.8	16	1 ODPB_SOLTU	P81419 solanum tub
9	20	23.8	17	1 TPIS_PINPS	P81666 pinus pinas
10	19	22.6	13	1 TEMC_RANTE	P56918 rana tempor
11	19	22.6	13	1 TEMD_RANTE	P56919 rana tempor
12	19	22.6	13	1 TEME_RANTE	P56920 rana tempor
13	19	22.6	17	1 NU4M_TRIRU	Q36834 trichophyto
14	18	21.4	12	1 DCML_PSECA	P19919 pseudomonas
15	18	21.4	15	1 FRE2_LITIN	P82022 litoria inf
16	18	21.4	16	1 RIPK_TRIKI	P16093 trichosanth
17	18	21.4	17	1 BOL4_MEGPE	P07495 megabombus
18	18	21.4	17	1 ITHB_HIRME	P28502 hirudo medi
19	17	20.2	10	1 LABA_JATMU	P13270 jatropa mu
20	17	20.2	13	1 FIBA_CAVPO	P14445 cavia porce
21	17	20.2	13	1 GER1_HORVU	P28525 hordeum vul
22	17	20.2	14	1 ATP6_SPIOL	P80086 spinacia ol
23	17	20.2	15	1 ACT_PINPS	P81085 pinus pinas
24	17	20.2	15	1 RKGG_CARCR	P21586 caretta car
25	17	20.2	15	1 SODP_PINPS	P81082 pinus pinas
26	17	20.2	16	1 FIBA_MELME	P14456 meles meles
27	17	20.2	16	1 PGTL_PELAC	P80563 pelobacter
28	17	20.2	17	1 AU33_LITRA	P82396 litoria ran
29	17	20.2	17	1 RM35_YEAST	P36530 saccharomyc
30	17	20.2	18	1 MU21_LITGE	P82068 litoria gen
31	16	19.0	12	1 V25K_WSSV	P82004 white spot
32	16	19.0	13	1 GER2_HORVU	P28526 hordeum vul
33	16	19.0	13	1 PHGR_EUBOX	P57793 eubacterium

34	16	19.0	13	1 SA2A_ONCMY	P82238 oncorhynchu
35	16	19.0	13	1 SA2B_ONCMY	P82239 oncorhynchu
36	16	19.0	15	1 FIBA_SYNCA	P14463 syncerus ca
37	16	19.0	15	1 KLOM_LUMTE	P11918 lumbricus t
38	16	19.0	15	1 TRPA_LEUMA	P81753 leucophaea
39	16	19.0	15	1 UC13_MAIZE	P80619 zea mays (m
40	16	19.0	16	1 CT11_LITCI	P81835 litoria cit
41	16	19.0	16	1 FIBA_FELCA	P14450 felis silve
42	16	19.0	16	1 FIBA_HYLLA	P14453 hylobates l
43	16	19.0	16	1 FIBA_MANLE	P14455 mandrillus
44	16	19.0	16	1 FIBA_MUSVI	P14458 mustela vis
45	16	19.0	16	1 FIBA_ODOHE	P14459 odocoileus

ALIGNMENTS

RESULT 1
TPIS_NICPL
ID TPIS_NICPL STANDARD; PRT; 10 AA.
AC P19118;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Triosephosphate isomerase, cytosolic (EC 5.3.1.1) (TIM) (Fragment).
OS Nicotiana plumbaginifolia (leadwort-leaved tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4092;
RN [1]
RP SEQUENCE.
RA Bauw G., de Loose M., Inze D., van Montagu M., Vandekerckhove J.;
RT "Alterations in the phenotype of plant cells studied by NH2-terminal
RT amino acid-sequence analysis of proteins electroblooded from two-
RT dimensional gel-separated total extracts.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4806-4810(1987).
CC -!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate -> glycerone
CC phosphate.
CC -!- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- MISCELLANEOUS: IN PLANTS, THERE ARE TWO TYPES OF TPIS, CYTOSOLIC
CC AND PLASTID.
CC -!- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
DR PIR; A27617; A27617.
DR InterPro; IPR000652; Trioseph_isomerase.
DR Pfam; PF00121; TIM; 1.
DR PROSITE; PS00171; TIM; PARTIAL.
KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
KW Pentose shunt.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1140 MW; 80B9D37862C9C9D1 CRC64;

Query Match 25.0%; Score 21; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 6.8e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 4 KEFTVSGN 11
: | | | |
Db 2 RTFFVGGN 9

RESULT 2
OPS3_DROVI
ID OPS3_DROVI STANDARD; PRT; 12 AA.
AC P17645;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Opsin Rh3 (Inner R7 photoreceptor cells opsin) (Fragment).
GN RH3.

OS Drosophila virilis (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7244;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90249748; PubMed=2140105;
RA Fortini M.E., Rubin G.M.;
RT "Analysis of cis-acting requirements of the Rh3 and Rh4 genes reveals
RT a bipartite organization to rhodopsin promoters in Drosophila
RT melanogaster.";
RL Genes Dev. 4:444-463(1990).
CC -!- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT
CC LINKED TO CIS-RETINAL.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- MISCELLANEOUS: EACH DROSOPHILA EYE IS COMPOSED OF 800 FACETS OR
CC OMATIDIA. EACH OMATIDIUM CONTAINS 8 PHOTORECEPTOR CELLS (R1-R8),
CC THE R1 TO R6 CELLS ARE OUTER CELLS, WHILE R7 AND R8 ARE INNER
CC CELLS.
CC -!- MISCELLANEOUS: OPSIN RH3 IS SENSITIVE TO UV LIGHT.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC OPSIN SUBFAMILY.
CC -----
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CC -----
CC EMBL; X51350; CAA35742.1; -.
DR GCRDb; GCR 0779; -.
DR FlyBase; FBgn0013091; Dvir\Rh3.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR001760; Opsin.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; PARTIAL.
DR PROSITE; PS00238; OPSIN; PARTIAL.
KW Photoreceptor; Retinal protein; Transmembrane; Phosphorylation;
KW Glycoprotein; G-protein coupled receptor; Vision.
FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (PROBABLE).
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1253 MW; 04024E43495865B0 CRC64;

Query Match 25.0%; Score 21; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. No. 8.3e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 EFTVSG 10
: | : | |
Db 2 DFNISG 7

RESULT 3
BP37_LEUMA
ID BP37_LEUMA STANDARD; PRT; 13 AA.
AC P81754;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Brain protein 37F3.
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Brain;
RX MEDLINE=97269266; PubMed=9114447;

RA Muren J.E., Naessel D.R.;
RT "Seven tachykinin-related peptides isolated from the brain of the
RT madeira cockroach; evidence for tissue-specific expression of
RT isoforms.";
RL Peptides 18:7-15(1997).
CC -!- TISSUE SPECIFICITY: BRAIN.
CC -!- MASS SPECTROMETRY: MW=1435.7; METHOD=MALDI.
SQ SEQUENCE 13 AA; 1436 MW; 8E532C9DE9A7D1B5 CRC64;

Query Match 25.0%; Score 21; DB 1; Length 13;
Best Local Similarity 62.5%; Pred. No. 9.1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LLKEFTVS 9
: | : | | | |
Db 2 LFEESTVS 9

RESULT 4
CDN3_LITGI
ID CDN3_LITGI STANDARD; PRT; 15 AA.
AC P56248;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Caeridin 3.
OS Litoria gilleni (Centralian tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=39405;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Parotoid gland;
RA Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structures of the caerins and
RT caeridins from Litoria gilleni.";
RL J. Chem. Res. 139:937-961(1993).
CC -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC ANTIBIOTIC ACTIVITY.
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
CC GLANDS.
CC -!- MASS SPECTROMETRY: MW=1428; METHOD=FAB.
KW Amphibian skin; Amidation.
FT MOD_RES 15 15 AMIDATION.
SQ SEQUENCE 15 AA; 1430 MW; 06E90A797AF70CBF CRC64;

Query Match 25.0%; Score 21; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 FTVSGNIL 13
: | : | : |
Db 3 FDAIGNLL 10

RESULT 5
CDN4_LITCE
ID CDN4_LITCE STANDARD; PRT; 15 AA.
AC P82076;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Caeridin 4.
OS Litoria caerulea (Green tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=30344;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.

```
RC TISSUE=Parotoid gland;
RA Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. Structures of the caeridins from
RT Litoria caerulea.";
RL J. Chem. Soc. Perkin Trans. 1:573-576(1993).
CC -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC ANTIBIOTIC ACTIVITY.
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
CC GLANDS.
CC -!- MASS SPECTROMETRY: MW=1504; METHOD=FAB.
KW Amphibian skin; Amidation.
FT MOD_RES 15 15 AMIDATION.
SQ SEQUENCE 15 AA; 1506 MW; 06F1BBFBBC5195F CRC64;

Query Match 25.0%; Score 21; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 VSGNIL 13
| ||:|
Db 5 VVG NVL 10

RESULT 6
CDN2_LITGI STANDARD; PRT; 15 AA.
AC P56247;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Caeridin 2.
OS Litoria gilleni (Centralian tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=39405;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Parotoid gland;
RA Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structures of the caerins and
RT caeridins from Litoria gilleni.";
RL J. Chem. Res. 139:937-961(1993).
CC -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC ANTIBIOTIC ACTIVITY.
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
CC GLANDS.
CC -!- MASS SPECTROMETRY: MW=1408; METHOD=FAB.
KW Amphibian skin; Amidation.
FT MOD_RES 15 15 AMIDATION.
SQ SEQUENCE 15 AA; 1410 MW; 06F1BBF272550CBF CRC64;

Query Match 23.8%; Score 20; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.6e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 VSGNIL 13
| ||:|
Db 5 VVG NVL 10

RESULT 7
THL_CLOPA STANDARD; PRT; 15 AA.
AC P81347;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Acetyl-CoA acetyltransferase (EC 2.3.1.9) (Acetoacetyl-CoA thiolase)
DE (CP 13) (Fragment).
GN THL.
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OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -!- CATALYTIC ACTIVITY: 2 acetyl-CoA = CoA + acetoacetyl-CoA.
CC -!- PATHWAY: JUNCTION IN THE PATHWAY LEADING TO THE PRODUCTION OF
CC EITHER ACIDS (ACETATE OR BUTYRATE) OR SOLVENTS (ACETONE, BUTANOL
CC OR ETHANOL).
CC -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE THIOLASE FAMILY.
DR InterPro; IPR002155; Thiolase.
DR PROSITE; PS00098; THIOLASE_1; PARTIAL.
DR PROSITE; PS00737; THIOLASE_2; PARTIAL.
DR PROSITE; PS00099; THIOLASE_3; PARTIAL.
KW Transferase; Acyltransferase.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1496 MW; 9735820D61BB35FC CRC64;

Query Match 23.8%; Score 20; DB 1; Length 15;
Best Local Similarity 25.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 3 LKEFTVSGNILT 14
:| | : : |
Db 1 MKEVVVIASAVXT 12

RESULT 8
ODPB_SOLTU STANDARD; PRT; 16 AA.
AC P81419;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Pyruvate dehydrogenase E1 component beta subunit, mitochondrial
DE (EC 1.2.4.1) (PDHE1-B) (Fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE.
RC STRAIN=CV. ROMANO; TISSUE=Tuber;
RX MEDLINE=98399821; PubMed=9729464;
RA Millar A.H., Knorpp C., Leaver C.J., Hill S.A.;
RT "plant mitochondrial pyruvate dehydrogenase complex: purification and
RT identification of catalytic components in potato.";
RL Biochem. J. 334:571-576(1998).
CC -!- FUNCTION: THE PYRUVATE DEHYDROGENASE COMPLEX CATALYZES THE OVERALL
CC CONVERSION OF PYRUVATE TO ACETYL-COA & CO(2). IT CONTAINS MULTIPLE
CC COPIES OF THREE ENZYMOLOGIC COMPONENTS: PYRUVATE DEHYDROGENASE (E1),
CC DIHYDROLIPOAMIDE ACETYLTRANSFERASE (E2) & LIPOAMIDE DEHYDROGENASE
CC (E3).
CC -!- CATALYTIC ACTIVITY: Pyruvate + lipoamide - S-
CC acetyldihydrolipoamide + CO(2).
CC -!- COFACTOR: THIAMINE PYROPHOSPHATE.
CC -!- SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA SUBUNITS (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
KW Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate;
KW Phosphorylation; Mitochondrion.
FT NON_TER 16 16
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SQ SEQUENCE 16 AA; 1705 MW; FF6ED80EC804F797 CRC64;

Query Match      23.8%; Score 20; DB 1; Length 16;
Best Local Similarity 66.7%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LKEFTV 8
   :|| ||
Db 4 VKEMTV 9

RESULT 9
TPIS_PINPS
ID TPIS_PINPS STANDARD; PRT; 17 AA.
AC P81666;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Triosephosphate isomerase, cytosolic (EC 5.3.1.1) (TIM) (Fragments).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate -> glycerone
CC phosphate.
CC -!- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- INDUCTION: BY WATER STRESS.
CC -!- MISCELLANEOUS: IN PLANTS, THERE ARE TWO TYPES OF TPIS, CYTOSOLIC
CC AND PLASTID.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN
CC (SPOT N139) IS: 5.9, ITS MW IS: 24 kDa.
CC -!- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
DR InterPro; IPR000652; Trioseph_isomerase.
DR PROSITE; PS00171; TIM; PARTIAL.
KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
FT NON_TER 1 1
FT NON_CONS 9 10
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 2053 MW; 183DB41757AF13CB CRC64;

Query Match      23.8%; Score 20; DB 1; Length 17;
Best Local Similarity 66.7%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 FTVSGN 11
   | | | |
Db 10 FFVCGN 15

RESULT 10
TEMC_RANTE
ID TEMC_RANTE STANDARD; PRT; 13 AA.
AC P56918;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Temporin C.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
RT temporaria.";
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE
CC BACTERIA.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC FAMILY.
KW Amphibian skin; Antibiotic; Amidation; Multigene family.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1363 MW; 2201403A655B2448 CRC64;

Query Match      22.6%; Score 19; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 VSGNIL 13
   : ||:|
Db 4 ILGNLL 9

RESULT 11
TEMD_RANTE
ID TEMD_RANTE STANDARD; PRT; 13 AA.
AC P56919;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Temporin D.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Skin;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
RT temporaria.";
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: HAS NO ANTIBACTERIAL ACTIVITY.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC FAMILY.
KW Amphibian skin; Amidation; Multigene family.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1379 MW; 3EF35DFA655B2448 CRC64;

Query Match      22.6%; Score 19; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 VSGNIL 13
   : ||:|
Db 4 IVGNLL 9

RESULT 12
TEME_RANTE
ID TEME_RANTE STANDARD; PRT; 13 AA.
AC P56920;
```


DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Temporin E.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
RT temporaria.";
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE
CC BACTERIA.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC FAMILY.
KW Amphibian skin; Antibiotic; Amidation; Multigene family.
FT MOD_RES 13
FT SEQUENCE 13 AA; 1379 MW; 26505DFA79A92448 CRC64;

Query Match 22.6%; Score 19; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 VSGNIL 13
Db :||:|
4 IIGNLL 9

RESULT 13
NU4M_TRIRU
ID NU4M_TRIRU STANDARD; PRT; 17 AA.
AC Q36834;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE NADH-ubiquinone oxidoreductase chain 4 (EC 1.6.5.3) (Fragment).
GN ND4.
OS Trichophyton rubrum.
OG Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Onygenales; Arthrodermataceae; mitosporic Arthrodermataceae;
OC Trichophyton.
OX NCBI_TaxID=5551;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IP.1817.89;
RX MEDLINE=96132111; PubMed=8593686;
RA de Bievre C., Dujon B.;
RT "Organisation of the mitochondrial genome of Trichophyton rubrum. DNA
RT sequence analysis of the ND4 gene, the ATPase subunit-6 gene, the
RT ribosomal RNA small-subunit gene, the ND6 gene, the COXIII gene, the
RT ATPase subunit-8 gene and six tRNA genes that correspond respectively
RT to the tyrosine, lysine, glutamine, asparagine, isoleucine and
RT tryptophan isoacceptors.";
RL Curr. Genet. 28:553-559(1995).
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; X88896; CAA61354.1; .
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 17 AA; 1834 MW; 225A167CE76F84BA CRC64;

Query Match 22.6%; Score 19; DB 1; Length 17;
Best Local Similarity 57.1%; Pred. No. 2.7e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 FTVSGNI 12
Db :|||:|
9 YSVSGLI 15

RESULT 14
DCML_PSECA
ID DCML_PSECA STANDARD; PRT; 12 AA.
AC P19919;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Carbon monoxide oxygenase [cytochrome B-561] large chain (EC 1.2.2.4)
DE (Fragment).
OS Pseudomonas carboxydovorans.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Bradyrhizobium group; Oligotropha.
OX NCBI_TaxID=40137;
RN [1]
RP SEQUENCE.
RC STRAIN=OM5;
RX MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
RT carboxydotrophic bacteria.";
RL Arch. Microbiol. 152:335-341(1989).
CC -!- CATALYTIC ACTIVITY: CO + H(2)O + ferrocytochrome b-561 = CO(2) + 2
CC H(+) + ferricytochrome b-561.
CC -!- COFACTOR: MOLYBDENUM.
CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
CC SMALL.
DR PIR; P10138; P10138.
KW Oxidoreductase; Molybdenum.
FT VARIANT 11 12 GE -> EK.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1289 MW; 9B170C688E6B02D1 CRC64;

Query Match 21.4%; Score 18; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.8e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 NILTIRLT 18
Db |||:|
2 NIQTVEPT 9

RESULT 15
FRE2_LITIN
ID FRE2_LITIN STANDARD; PRT; 15 AA.
AC P82022;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Frenatin 2.
OS Litoria infrafrenata (Giant tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=61195;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;

RX MEDLINE=97368637; PubMed=9225251;
RA Raftery M.J., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "The structures of the frenatin peptides from the skin secretion of
RT the giant tree frog Litoria infrarenata.";
RL J. Pept. Sci. 2:117-124(1996).
CC -!- FUNCTION: WIDE SPECTRUM ANTIMICROBIAL PEPTIDE.
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
CC GLANDS.
CC -!- MASS SPECTROMETRY: MW=1423; METHOD=FAB.
KW Antibiotic; Amphibian skin; Amidation.
FT MOD_RES 15 15 AMIDATION.
SQ SEQUENCE 15 AA; 1425 MW; 06ED4B7BB1650CBF CRC64;

Query Match 21.4%; Score 18; DB 1; Length 15;
Best Local Similarity 75.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY -10 GNIL 13
||:|
Db 7 GNLL 10

Search completed: July 3, 2002, 11:41:54
Job time: 835 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:41:20 ; Search time 100.54 Seconds
(without alignments)
30.972 Million cell updates/sec

Title: US-09-165-546A-9
Perfect score: 84
Sequence: 1 VLLKEFTVSGNILTIRLT 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 4250

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archheap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	27	32.1	15	1	Q9UWH9	Q9uwh9 thermococcu
2	25	29.8	16	2	Q47605	Q47605 escherichia
3	24.5	29.2	15	6	Q28822	Q28822 oryctolagus
4	23	27.4	11	11	Q9QYF6	Q9qyf6 mus musculu
5	23	27.4	16	2	Q52901	Q52901 rhizobium m
6	23	27.4	16	13	Q9PRQ0	Q9prq0 oncorhynchu
7	23	27.4	17	7	Q31213	Q31213 mus musculu
8	23	27.4	17	10	O24445	O24445 ceratodon p
9	23	27.4	17	12	Q9IHJ0	Q9ihj0 human polio
10	23	27.4	17	12	Q9IHI9	Q9ih9 human polio
11	23	27.4	17	12	Q9IHI8	Q9ih8 human polio
12	23	27.4	17	12	Q9IHI7	Q9ih7 human polio
13	23	27.4	17	12	Q9IHI6	Q9ih6 human polio
14	23	27.4	17	12	Q9IHI5	Q9ih5 human polio
15	23	27.4	17	12	Q9IHI4	Q9ih4 human polio
16	23	27.4	17	12	Q9IHI3	Q9ih3 human polio

17	23	27.4	17	12	Q9IHI2	Q9ih2 human polio
18	23	27.4	17	12	Q9IHI1	Q9ih1 human polio
19	23	27.4	17	12	Q9IHI0	Q9ih0 human polio
20	23	27.4	17	12	Q9IHH9	Q9ih9 human polio
21	23	27.4	17	12	Q9IHH8	Q9ih8 human polio
22	23	27.4	17	12	Q9IHH7	Q9ih7 human polio
23	23	27.4	17	12	Q9IHH6	Q9ih6 human polio
24	23	27.4	17	12	Q9IHH5	Q9ih5 human polio
25	23	27.4	17	12	Q9IHH4	Q9ih4 human polio
26	23	27.4	17	12	Q9IHH3	Q9ih3 human polio
27	23	27.4	17	12	Q9IHH2	Q9ih2 human polio
28	23	27.4	17	12	Q9IHH1	Q9ih1 human polio
29	23	27.4	17	12	Q9IHH0	Q9ih0 human polio
30	23	27.4	17	12	Q9IHG9	Q9ihg9 human polio
31	23	27.4	17	12	Q9IHG8	Q9ihg8 human polio
32	23	27.4	17	12	Q9IHG7	Q9ihg7 human polio
33	23	27.4	17	12	Q9IHG6	Q9ihg6 human polio
34	23	27.4	17	12	Q9IHG5	Q9ihg5 human polio
35	23	27.4	17	12	Q9IHG4	Q9ihg4 human polio
36	23	27.4	17	12	Q9IHG3	Q9ihg3 human polio
37	23	27.4	17	12	Q9IHG2	Q9ihg2 human polio
38	23	27.4	18	3	Q01672	Q01672 pneumocysti
39	22	26.2	10	2	Q9X529	Q9x529 citrobacter
40	22	26.2	10	2	Q9X531	Q9x531 escherichia
41	22	26.2	10	2	Q9X532	Q9x532 comamonas t
42	22	26.2	10	2	Q51812	Q51812 escherichia
43	22	26.2	12	10	Q9S931	Q9s931 sambucus ni
44	22	26.2	16	11	Q9R0J9	Q9r0j9 rattus norv
45	22	26.2	17	5	Q9TWF6	Q9twf6 artemia (br

ALIGNMENTS

RESULT 1
Q9UWH9
ID Q9UWH9 PRELIMINARY; PRT; 15 AA.
AC Q9UWH9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ALDEHYDE FERREDOXIN OXIDOREDUCTASE (FRAGMENT).
OS Thermococcus sp. (strain KI).
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Thermococcus.
OX NCBI_TaxID=35749;
RN [1]
RP SEQUENCE.
RC STRAIN=ES-1;
RX MEDLINE=95370155; Pubmed=7642503;
RA Heider J., Ma K., Adams M.W.;
RT "Purification, characterization, and metabolic function of tungsten-
containing aldehyde ferredoxin oxidoreductase from the
hyperthermophilic and proteolytic archaeon Thermococcus strain ES-1.";
RL J. Bacteriol. 177:4757-4764(1995).
SQ SEQUENCE 15 AA; 1750 MW; 0441670278198619 CRC64;

Query Match 32.1%; Score 27; DB 1; Length 15;
Best Local Similarity 46.2%; Pred. No. 5.8e+02;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 6 FTVSGNILTIRLT 18
| | | | |
Db 2 FGYHGKILRVNLT 14

RESULT 2
Q47605
ID Q47605 PRELIMINARY; PRT; 16 AA.
AC Q47605;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)

DE C (FRAGMENT).

GN C.

OS Escherichia coli.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.

OX NCBI_TaxID=562;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91139577; PubMed=1995588;

RA Tao T., Bourne J.C., Blumenthal R.M.;

RT "A family of regulatory genes associated with type II restriction-

RT modification systems.";

RL J. Bacteriol. 173:1367-1375(1991).

DR EMBL; M63622; AAA24561.1; -.

FT NON_TER 1

SQ SEQUENCE 16 AA; 1853 MW; E46774511496607C CRC64;

Query Match 29.8%; Score 25; DB 2; Length 16;

Best Local Similarity 55.6%; Pred. No. 1.4e+03;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 LKEFTVSGN 11

Db 3 LLDFTTGN 11

RESULT 3

Q28822

ID Q28822 PRELIMINARY; PRT; 15 AA.

AC Q28822;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)

DE VOLTAGE-DEPENDENT DIHYDROPYRIDINE-SENSITIVE CALCIUM CHANNEL ALPHA 1

DE SUBUNIT 155 KDA ISOFORM (FRAGMENT).

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92265303; PubMed=1316766;

RA Malouf N.N., McMahon D.K., Hainsworth C.N., Kay B.K.;

RT "A two-motif isoform of the major calcium channel subunit in skeletal

RT muscle.";

RL Neuron 8:899-906(1992).

DR EMBL; S36895; AAB22180.1; -.

FT NON_TER 1

SQ SEQUENCE 15 AA; 1796 MW; 841B2DB08BFE99DB CRC64;

Query Match 29.2%; Score 24.5; DB 6; Length 15;

Best Local Similarity 41.2%; Pred. No. 1.6e+03;

Matches 7; Conservative 3; Mismatches 4; Indels 3; Gaps 1;

QY 1 VLLKEFTVSGNLTIRL 17

Db 2 VLLSLFTI---IFTLEM 15

RESULT 4

Q9QYF6

ID Q9QYF6 PRELIMINARY; PRT; 11 AA.

AC Q9QYF6;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

DE PANCREAS TRANSCRIPTION FACTOR1 P48 SUBUNIT (FRAGMENT).

GN P4F1P48.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=129SV;

RA Obata J., Mimura H., Goto T., Nakayama R., Kondo M., Oka C.,

RA Kawaichi M.;

RT "p48 subunit of mouse PTF1 binds to RBP-Jkappa/CBF-1, the

RT intracellular mediator of Notch signaling, and is expressed in the

RT neural tube of the early stage embryos.";

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB035674; BAA88247.1; -.

FT NON_TER 11

SQ SEQUENCE 11 AA; 1327 MW; CA4662F8E3372732 CRC64;

Query Match 27.4%; Score 23; DB 11; Length 11;

Best Local Similarity 83.3%; Pred. No. 2.1e+03;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLLKEF 6

Db 4 VLLKHF 9

RESULT 5

Q52901

ID Q52901 PRELIMINARY; PRT; 16 AA.

AC Q52901;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)

DE NOSY PROTEIN (FRAGMENT).

GN NOSY.

OS Rhizobium meliloti (Sinorhizobium meliloti).

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Rhizobiaceae; Sinorhizobium.

OX NCBI_TaxID=382;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=JJ1C10;

RX MEDLINE=96198150; PubMed=8626275;

RA Holloway P., McCormick W., Watson R.J., Chan Y.K.;

RT "Identification and analysis of the dissimilatory nitrous oxide

RT reduction genes, nosRZDFY, of Rhizobium meliloti.";

RL J. Bacteriol. 178:1505-1514(1996).

DR EMBL; U47133; AAC44026.1; -.

FT NON_TER 16

SQ SEQUENCE 16 AA; 1735 MW; 0CF7165CF62AA3B8 CRC64;

Query Match 27.4%; Score 23; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 3.2e+03;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 NILTI 15

Db 3 NILTI 7

RESULT 6

Q9PRQ0

ID Q9PRQ0 PRELIMINARY; PRT; 16 AA.

AC Q9PRQ0;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE SULFIDE LINKED SERUM AMYLOID p-COMPONENT (FRAGMENT).

OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

OX NCBI_TaxID=8022;

RN [1]

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=129SV;

RA Obata J., Mimura H., Goto T., Nakayama R., Kondo M., Oka C.,

RA Kawaichi M.;

RT "p48 subunit of mouse PTF1 binds to RBP-Jkappa/CBF-1, the

RT intracellular mediator of Notch signaling, and is expressed in the

RT neural tube of the early stage embryos.";

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB035674; BAA88247.1; -.

FT NON_TER 11

SQ SEQUENCE 11 AA; 1327 MW; CA4662F8E3372732 CRC64;

Query Match 27.4%; Score 23; DB 11; Length 11;

Best Local Similarity 83.3%; Pred. No. 2.1e+03;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLLKEF 6

Db 4 VLLKHF 9

RESULT 5

Q52901

ID Q52901 PRELIMINARY; PRT; 16 AA.

AC Q52901;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)

DE NOSY PROTEIN (FRAGMENT).

GN NOSY.

OS Rhizobium meliloti (Sinorhizobium meliloti).

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Rhizobiaceae; Sinorhizobium.

OX NCBI_TaxID=382;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=JJ1C10;

RX MEDLINE=96198150; PubMed=8626275;

RA Holloway P., McCormick W., Watson R.J., Chan Y.K.;

RT "Identification and analysis of the dissimilatory nitrous oxide

RT reduction genes, nosRZDFY, of Rhizobium meliloti.";

RL J. Bacteriol. 178:1505-1514(1996).

DR EMBL; U47133; AAC44026.1; -.

FT NON_TER 16

SQ SEQUENCE 16 AA; 1735 MW; 0CF7165CF62AA3B8 CRC64;

Query Match 27.4%; Score 23; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 3.2e+03;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 NILTI 15

Db 3 NILTI 7

RESULT 6

Q9PRQ0

ID Q9PRQ0 PRELIMINARY; PRT; 16 AA.

AC Q9PRQ0;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE SULFIDE LINKED SERUM AMYLOID p-COMPONENT (FRAGMENT).

OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

OX NCBI_TaxID=8022;

RN [1]

RP SEQUENCE.
RX MEDLINE=96192413; PubMed=8617401;
RA Jensen L.E., Petersen T.E., Thiel S., Jensenius J.C.;
RT "Isolation of a pentraxin-like protein from rainbow trout serum."
RL Dev. Comp. Immunol. 19:305-314(1995).
SQ SEQUENCE 16 AA; 1764 MW; B6817B064852C2FA CRC64;

Query Match 27.4%; Score 23; DB 13; Length 16;
Best Local Similarity 36.4%; Pred. No. 3.2e+03;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 8 VSGNLTIRLT 18
:|:|:|:|:
Db 5 LSGKVFVIPMT 15

RESULT 7
Q31213 PRELIMINARY; PRT; 17 AA.
AC Q31213;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE INTEGRAL MEMBRANE PROTEIN (FRAGMENT).
GN J-ALPHA TA61.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPH-NODE;
RX MEDLINE=92165347; PubMed=1371499;
RA Nakajima P.B., Di Vincenzo J.P., Jameson S.C., Gascoigne N.R.J.;
RT "Chromosome 14 in B10.A (18R) mice is recombinant and includes Tcra-V alleles."
RL Immunogenetics 35:190-198(1992).
DR EMBL; M55634; AAA39702.1; -.
FT NON_TER 1
SQ SEQUENCE 17 AA; 1748 MW; 427C4F4FFD162173 CRC64;

Query Match 27.4%; Score 23; DB 7; Length 17;
Best Local Similarity 42.9%; Pred. No. 3.4e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 10 GNILTIR 16
|:|:|:
Db 10 GTVLTVK 16

RESULT 8
O24445 PRELIMINARY; PRT; 17 AA.
ID O24445;
AC O24445;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE ORF (PHYTOCHROME PHOTORECEPTOR CERPU;PHY0;2) (PHY0;2).
GN CPHY2.
OS Ceratodon purpureus (Moss).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Dicranidae; Dicranales; Ditrichaceae; Ceratodon.
OX NCBI_TaxID=3225;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WT3;
RA Hughes J.E., Lamparter T., Mittmann F.;
RT "CpPHY2 (PHYCER2), a normal phytochrome in Ceratodon (Accession No. U56698) (PGR96-067).";
RL Plant Physiol. 112:446-446(1996).
RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN=WT3;
RX MEDLINE=98345942; PubMed=9680964;
RA Pasentsis K., Paulo N., Algarrá P., Ditttrich P., Thummel F.;
RT "Characterization and expression of the phytochrome gene family in the moss Ceratodon purpureus."
RL Plant J. 13:51-61(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Lamparter T., Podlowski S., Mittmann F., Schneider-Poetsch H.-J., Hartmann E., Hughes J.E.;
RT "Phytochrome from protonemal tissue of the moss Ceratodon purpureus."
RL J. Plant Physiol. 147:426-434(1995).
DR EMBL; U72993; AAB19059.1; -.
DR EMBL; U56698; AAB67862.1; -.
SQ SEQUENCE 17 AA; 1949 MW; 072DF72059DF1C7C CRC64;

Query Match 27.4%; Score 23; DB 10; Length 17;
Best Local Similarity 38.5%; Pred. No. 3.4e+03;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 LKEFTVSGNLT 15
:|:|:|:|:
Db 1 MKEFSSTSRSLMI 13

RESULT 9
Q9IHJ0 PRELIMINARY; PRT; 17 AA.
ID Q9IHJ0;
AC Q9IHJ0;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE CORE PROTEIN 2C (FRAGMENT).
OS Human poliovirus 1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=12080;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2677USA81D23;
RX MEDLINE=20366294; PubMed=10906191;
RA Gavrilin G.V., Cherkasova E.A., Lipskaya G.Y., Kew O.M., Agol V.I.;
RT "Evolution of circulating wild poliovirus and of vaccine-derived poliovirus in an immunodeficient patient: a unifying model."
RL J. Virol. 74:7381-7390(2000).
DR EMBL; AF233165; AAF35069.1; -.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1826 MW; 6B3DEB222D713050 CRC64;

Query Match 27.4%; Score 23; DB 12; Length 17;
Best Local Similarity 55.6%; Pred. No. 3.4e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 LKEFTVSGN 11
|:|:|:|:
Db 5 LKKFTEACN 13

RESULT 10
Q9IH19 PRELIMINARY; PRT; 17 AA.
ID Q9IH19;
AC Q9IH19;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE CORE PROTEIN 2C (FRAGMENT).
OS Human poliovirus 1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.

```
OX NCBI_TaxID=12080;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2677USA81D48;
RX MEDLINE=20366294; PubMed=10906191;
RA Gavrilin G.V., Cherkasova E.A., Lipskaya G.Y., Kew O.M., Agol V.I.;
RT "Evolution of circulating wild poliovirus and of vaccine-derived
RL J. Virol. 74:7381-7390(2000).
DR EMBL; AF233166; AAF35070.1; -.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1826 MW; 6B3DEB222D713050 CRC64;

Query Match 27.4%; Score 23; DB 12; Length 17;
Best Local Similarity 55.6%; Pred. No. 3.4e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 LKEFTVSGN 11
Db 5 LKKFTEACN 13

RESULT 11
Q9IHI8
ID Q9IHI8 PRELIMINARY; PRT; 17 AA.
AC Q9IHI8;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TremBLrel. 15, Last annotation update)
DE CORE PROTEIN 2C (FRAGMENT).
OS Human poliovirus 1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OC NCBI_TaxID=12080;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3038USA81D126;
RX MEDLINE=20366294; PubMed=10906191;
RA Gavrilin G.V., Cherkasova E.A., Lipskaya G.Y., Kew O.M., Agol V.I.;
RT "Evolution of circulating wild poliovirus and of vaccine-derived
RL J. Virol. 74:7381-7390(2000).
DR EMBL; AF233167; AAF35071.1; -.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1826 MW; 6B3DEB222D713050 CRC64;

Query Match 27.4%; Score 23; DB 12; Length 17;
Best Local Similarity 55.6%; Pred. No. 3.4e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 LKEFTVSGN 11
Db 5 LKKFTEACN 13

RESULT 12
Q9IHI7
ID Q9IHI7 PRELIMINARY; PRT; 17 AA.
AC Q9IHI7;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TremBLrel. 15, Last annotation update)
DE CORE PROTEIN 2C (FRAGMENT).
OS Human poliovirus 1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OC NCBI_TaxID=12080;
RN [1]
RP SEQUENCE*FROM N.A.
```

```
RC STRAIN=3038USA82D158;
RX MEDLINE=20366294; PubMed=10906191;
RA Gavrilin G.V., Cherkasova E.A., Lipskaya G.Y., Kew O.M., Agol V.I.;
RT "Evolution of circulating wild poliovirus and of vaccine-derived
RL J. Virol. 74:7381-7390(2000).
DR EMBL; AF233168; AAF35072.1; -.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1826 MW; 6B3DEB222D713050 CRC64;

Query Match 27.4%; Score 23; DB 12; Length 17;
Best Local Similarity 55.6%; Pred. No. 3.4e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 LKEFTVSGN 11
Db 5 LKKFTEACN 13

RESULT 13
Q9IHI6
ID Q9IHI6 PRELIMINARY; PRT; 17 AA.
AC Q9IHI6;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TremBLrel. 15, Last annotation update)
DE CORE PROTEIN 2C (FRAGMENT).
OS Human poliovirus 1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OC NCBI_TaxID=12080;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3038USA82D200;
RX MEDLINE=20366294; PubMed=10906191;
RA Gavrilin G.V., Cherkasova E.A., Lipskaya G.Y., Kew O.M., Agol V.I.;
RT "Evolution of circulating wild poliovirus and of vaccine-derived
RL J. Virol. 74:7381-7390(2000).
DR EMBL; AF233169; AAF35073.1; -.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1826 MW; 6B3DEB222D713050 CRC64;

Query Match 27.4%; Score 23; DB 12; Length 17;
Best Local Similarity 55.6%; Pred. No. 3.4e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 LKEFTVSGN 11
Db 5 LKKFTEACN 13

RESULT 14
Q9IHI5
ID Q9IHI5 PRELIMINARY; PRT; 17 AA.
AC Q9IHI5;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TremBLrel. 15, Last annotation update)
DE CORE PROTEIN 2C (FRAGMENT).
OS Human poliovirus 1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OC NCBI_TaxID=12080;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=169AZB59;
RX MEDLINE=20366294; PubMed=10906191;
RA Gavrilin G.V., Cherkasova E.A., Lipskaya G.Y., Kew O.M., Agol V.I.;
```



```
RT "Evolution of circulating wild poliovirus and of vaccine-derived
RT poliovirus in an immunodeficient patient: a unifying model.";
RL J. Virol. 74:7381-7390(2000).
DR EMBL; AF233170; AAF35074.1; -.
FT NON_TER 1 17
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1826 MW; 6B3DEB222D713050 CRC64;

Query Match 27.4%; Score 23; DB 12; Length 17;
Best Local Similarity 55.6%; Pred. No. 3.4e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 LKEFTVSGN 11
Db 5 LKKFTEACN 13

RESULT 15
Q9IHI4 PRELIMINARY; PRT; 17 AA.
AC Q9IHI4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE CORE PROTEIN 2C (FRAGMENT).
OS Human poliovirus 1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=12080;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=422RUS91;
RX MEDLINE=20366294; PubMed=10906191;
RA Gavrilin G.V., Cherkasova E.A., Lipskaya G.Y., Kew O.M., Agol V.I.;
RT "Evolution of circulating wild poliovirus and of vaccine-derived
RT poliovirus in an immunodeficient patient: a unifying model.";
RL J. Virol. 74:7381-7390(2000).
DR EMBL; AF233171; AAF35075.1; -.
FT NON_TER 1 17
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1826 MW; 6B3DEB222D713050 CRC64;

Query Match 27.4%; Score 23; DB 12; Length 17;
Best Local Similarity 55.6%; Pred. No. 3.4e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 LKEFTVSGN 11
Db 5 LKKFTEACN 13

Search completed: July 3, 2002, 11:41:20
Job time: 856 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 11:26:57 ; Search time 128.9 Seconds
(without alignments)
15.511 Million cell updates/sec

Title: US-09-165-546A-9

Perfect score: 84

Sequence: 1 VLLKEFTVSGNILTIRLT 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 214377

Minimum DB seq length: 0

Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802.*

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- 2: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT.*
- 3: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT.*
- 4: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT.*
- 5: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT.*
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- 8: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1987.DAT.*
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- 11: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT.*
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- 13: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1992.DAT.*
- 14: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT.*
- 15: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1994.DAT.*
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- 18: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT.*
- 19: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT.*
- 20: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT.*
- 21: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT.*
- 22: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84	100.0	18	AAE07769	Human NY ESO-1 HLA
2	84	100.0	18	AAU01540	HLA-DR53 recognisi
3	84	100.0	18	AAE07769	Human NY-ESO-1 HLA
4	71	84.5	15	AAE07726	Human NY ESO-1 MHC
5	71	84.5	15	AAE07727	Human NY ESO-1 MHC
6	71	84.5	15	AAE07786	Human NY ESO-1 pep
7	71	84.5	15	AAE07787	Human NY ESO-1 pep
8	68.5	81.5	17	AAE07728	Human tumour antig
9	67	79.8	14	AAE07728	Human NY ESO-1 MHC
10	67	79.8	14	AAE07788	Human NY ESO-1 pep
11	57	67.9	18	AAU01541	HLA-DR53 recognisi

12	57	67.9	18	22	AAE07769	Human NY-ESO-1 HLA
13	56	66.7	18	21	AAE07769	Human tumour antig
14	56	66.7	18	22	AAU01544	HLA-DR53 recognisi
15	56	66.7	18	22	AAE07769	Human NY-ESO-1 HLA
16	48	57.1	10	20	AAE07769	Human cancer antig
17	47	56.0	10	20	AAE07769	Human cancer antig
18	47	56.0	10	20	AAE07769	Human cancer antig
19	47	56.0	10	22	AAE07769	Human NY ESO-1 MHC
20	47	56.0	10	22	AAE07769	Human NY ESO-1 pep
21	47	56.0	11	22	AAE07769	Human NY ESO-1 MHC
22	47	56.0	11	22	AAE07769	Human NY ESO-1 pep
23	47	56.0	12	22	AAE07769	Human NY ESO-1 MHC
24	47	56.0	12	22	AAE07769	Human NY ESO-1 MHC
25	47	56.0	12	22	AAE07769	Human NY ESO-1 pep
26	47	56.0	13	22	AAE07769	Human NY ESO-1 MHC
27	47	56.0	13	22	AAE07769	Human NY ESO-1 pep
28	47	56.0	14	22	AAE07769	Human NY ESO-1 MHC
29	47	56.0	14	22	AAE07769	Human NY ESO-1 pep
30	47	56.0	15	22	AAE07769	Human NY ESO-1 MHC
31	47	56.0	15	22	AAE07769	Human NY ESO-1 pep
32	47	56.0	16	22	AAE07769	Human NY ESO-1 rel
33	47	56.0	16	22	AAE07769	Human NY ESO-1 pep
34	47	56.0	17	22	AAE07769	Human NY ESO-1 pep
35	44	52.4	9	21	AAE07769	NY-ESO-1 derived p
36	42	50.0	9	20	AAE07769	Human cancer antig
37	42	50.0	9	20	AAE07769	Human cancer antig
38	42	50.0	9	20	AAE07769	Human cancer antig
39	42	50.0	9	21	AAE07769	NY-ESO-1 derived p
40	41	48.8	17	22	AAE07769	Human NY ESO-1 MHC
41	40	47.6	10	22	AAE07769	Cancer testis tumo
42	40	47.6	10	22	AAE07769	Human NY-ESO-1 HLA
43	37	44.0	9	20	AAE07769	Human cancer antig
44	37	44.0	9	20	AAE07769	Human cancer antig
45	37	44.0	10	20	AAE07769	Human cancer antig

ALIGNMENTS

RESULT	1
AAE07769	
ID	AAE07769 standard; peptide; 18 AA.
XX	
AC	AAE07769;
XX	
DT	06-NOV-2001 (first entry)
XX	
DE	Human NY ESO-1 HLA DR restricted T cell cancer peptide #1.
XX	
KW	Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW	class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW	NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW	tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW	immunotherapy.
XX	
OS	Homo sapiens.
XX	
PN	WO200155393-A2.
XX	
PD	02-AUG-2001.
XX	
PF	26-JAN-2001; 2001WO-US02765.
XX	
PR	28-JAN-2000; 2000US-0179004.
PR	29-SEP-2000; 2000US-0237107.
XX	
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.
XX	
PI	Wang R, Rosenberg SA, Zeng G;
XX	
DR	WPI; 2001-496851/54.
XX	
PT	New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,

PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -
PS Claim 84; Page 84; 134pp; English.
XX
CC The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or haptent and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is human
CC NY ESO-1 HLA DR restricted T cell cancer peptide.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 84; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNILTIRLT 18
Db |||||||||||||||
1 vllkeftvsgniltirtl 18

RESULT 2
AAU01540
ID AAU01540 standard; Peptide; 18 AA.
XX
AC AAU01540;
XX
DT 18-JUL-2001 (first entry)
XX
DE HLA-DR53 recognising NY-ESO-1 peptide #2.
XX
KW NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
KW major.histocompatibility complex; helper T cell; HLA-DR; cancer;
KW human leukocyte antigen-determining region; disease progression;
KW disease regression; disease onset; body tissue; body fluid; enzyme label;
KW radioactive label; monoclonal antibody.
XX
OS Homo sapiens.
XX
PN WO200123560-A2.
XX
PD 05-APR-2001.
XX
PF 26-SEP-2000; 2000WO-US26411.
XX
XX 29-SEP-1999; 99US-0408036.
PR (LUDW-) LUDWIG INST CANCER RES.
PA
XX Tureci O, Sahin U, Pfreundschuh M;
PI WPI; 2001-266156/27.
XX
DR Polypeptides binding to major histocompatibility complex class II human
PT leukocyte antigen-determining region molecule having amino acid
PT sequence found in tumour rejection antigen precursor used for
PT stimulating proliferation of helper T cells -
XX
PS Example 13; Page 19; 62pp; English.

XX The sequence represents a human NY-ESO-1 tumour rejection antigen
CC precursor fragment which recognises and binds to HLA-DR53. NY-ESO-1 and
CC SSX-2 polypeptides, or fragments of, bind to major histocompatibility
CC complex (MHC) Class II molecules such as human leukocyte
CC antigen-determining region (HLA-DR) molecules and stimulate proliferation
CC of helper T cells. The peptides can be administered to an HLA-DR positive
CC subject in order to stimulate the helper T cells. An MHC Class II
CC HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell or
CC present in free form is useful for this stimulation. The nucleic acid is
CC useful for screening for a cancerous condition, which involves contacting
CC a subject sample to a cell line transfected with the immunoreactive cell
CC (helper T cell), where interaction is indicative of cancer. In addition,
CC a sample from a patient (for example, a body fluid or tissue) can be
CC monitored for the amount of the complex present in the bloodstream. This
CC is useful for determining regression, progression or onset of a cancerous
CC condition. The method involves contacting the sample with a radioactive
CC labelled or enzyme labelled monoclonal antibody which specifically binds
CC with the complex.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 84; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNILTIRLT 18
Db |||||||||||||||
1 vllkeftvsgniltirtl 18

RESULT 3
AAB69940
ID AAB69940 standard; Peptide; 18 AA.
XX
AC AAB69940;
XX
DT 27-APR-2001 (first entry)
XX
DE Human NY-ESO-1 HLA-DR53 binding motif #2.
XX
KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW non-small cell lung carcinoma; tumour status determination.
XX
OS Homo sapiens.
XX
PN WO200107917-A1.
XX
PD 01-FEB-2001.
XX
PF 14-JUL-2000; 2000WO-US19220.
XX
PR 23-JUL-1999; 99US-0359503.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.
XX
PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
XX WPI; 2001-182822/18.
DR
XX Method useful for determining the status (e.g. progression, regression
PT or stability of the disease) of a cancerous condition, involves
PT determining the levels of NY-ESO-1 specific antibodies in a sample
PT taken from a patient -
XX
PS Example 16; Page 27; 50pp; English.
XX
CC The present sequence is given in a specification relating to a method
CC for determining the status of a cancerous condition in a patient

CC with a tumour that expresses NY-ESO-1. The method comprises assaying a
CC sample taken from the patient for antibodies that specifically bind to
CC the NY-ESO-1 and comparing the value obtained to a prior value obtained
CC from assay of a prior sample taken from the patient. Any difference
CC between the values is indicative of a change in status of the cancerous
CC condition. The method is useful for determining whether a cancerous
CC condition is progressing, regressing or remaining stable, in particular
CC in patients receiving treatment for a melanoma, adenocarcinoma,
CC non-small cell lung carcinoma or bladder carcinoma.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 84; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNLTIRLT 18
Db 1 vlleftvsgniltirtl 18

RESULT 4
AAE07726
ID AAE07726 standard; peptide; 15 AA.
XX

AC AAE07726;

XX 06-NOV-2001 (first entry)

DT Human NY ESO-1 MHC class II restricted T cell epitope #12.

XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.

XX Homo sapiens.

XX WO200155393-A2.

XX 02-AUG-2001.

XX 26-JAN-2001; 2001WO-US02765.

XX 28-JAN-2000; 2000US-0179004.

XX 29-SEP-2000; 2000US-0237107.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang R, Rosenberg SA, Zeng G;

XX WPI; 2001-496851/54.

XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -

XX Claim 4; Page 16; 134pp; English.

XX The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also

CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or hapten and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is MHC
CC class II restricted T cell epitope of human NY ESO-1 protein.
XX
SQ Sequence 15 AA;

Query Match 84.5%; Score 71; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLKEFTVSGNLTIR 16
Db 1 llkeftvsgniltir 15

RESULT 5
AAE07727
ID AAE07727 standard; peptide; 15 AA.
XX

AC AAE07727;

XX 06-NOV-2001 (first entry)

XX Human NY ESO-1 MHC class II restricted T cell epitope #13.

XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.

XX Homo sapiens.

XX WO200155393-A2.

XX 02-AUG-2001.

XX 26-JAN-2001; 2001WO-US02765.

XX 28-JAN-2000; 2000US-0179004.

XX 29-SEP-2000; 2000US-0237107.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang R, Rosenberg SA, Zeng G;

XX WPI; 2001-496851/54.

XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -

XX Claim 4; Page 16; 134pp; English.

XX The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or hapten and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is MHC

CC class II restricted T cell epitope of human NY ESO-1 protein.

XX Sequence 15 AA;

Query Match 84.5%; Score 71; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LKEFTVSGNILTIRL 17
| | | | | | | | | | | | | | |
Db 1 lkeftvsgniltirl 15

RESULT 6
AAE07786
ID AAE07786 standard; peptide; 15 AA.

XX AC AAE07786;

XX DT 06-NOV-2001 (first entry)

XX DE Human NY ESO-1 peptide #20 to characterise epitope recognised by TE4-1.

XX KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.

XX OS Homo sapiens.

XX PN WO200155393-A2.

XX PD 02-AUG-2001.

XX PF 26-JAN-2001; 2001WO-US02765.

XX PR 28-JAN-2000; 2000US-0179004.

XX PR 29-SEP-2000; 2000US-0237107.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Wang R, Rosenberg SA, Zeng G;

XX DR WPI; 2001-496851/54.

XX PT New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -

XX PS Example 6; Fig 6A; 134pp; English.

XX CC The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or haptens and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is human
CC NY ESO-1 peptide used in the characterisation of the NY ESO-1 epitope
XX recognised by TE4-1.

XX Sequence 15 AA;

Query Match 84.5%; Score 71; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLKEFTVSGNILTIR 16
| | | | | | | | | | | | | | |
Db 1 llkeftvsgniltir 15

RESULT 7
AAE07787
ID AAE07787 standard; peptide; 15 AA.

XX AC AAE07787;

XX DT 06-NOV-2001 (first entry)

XX DE Human NY ESO-1 peptide #21 to characterise epitope recognised by TE4-1.

XX KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.

XX OS Homo sapiens.

XX PN WO200155393-A2.

XX PD 02-AUG-2001.

XX PF 26-JAN-2001; 2001WO-US02765.

XX PR 28-JAN-2000; 2000US-0179004.

XX PR 29-SEP-2000; 2000US-0237107.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Wang R, Rosenberg SA, Zeng G;

XX DR WPI; 2001-496851/54.

XX PT New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -

XX PS Example 6; Fig 6A; 134pp; English.

XX CC The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or haptens and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is human
CC NY ESO-1 peptide used in the characterisation of the NY ESO-1 epitope
XX recognised by TE4-1.

XX Sequence 15 AA;

Query Match 84.5%; Score 71; DB 22; Length 15;


```

RESULT 10
AAE07788
ID AAE07788 standard; peptide; 14 AA.
XX
AC AAE07788;
XX
XX 06-NOV-2001 (first entry)
XX
DE Human NY ESO-1 peptide #22 to characterise epitope recognised by TE4-1.
XX
KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.
XX
OS Homo sapiens.
XX
PN WO200155393-A2.
XX
PD 02-AUG-2001.
XX
PF 26-JAN-2001; 2001WO-US02765.
XX
PR 28-JAN-2000; 2000US-0179004.
PR 29-SEP-2000; 2000US-0237107.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang R, Rosenberg SA, Zeng G;
XX
DR WPI; 2001-496851/54.
XX
PT New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -
XX
PS Example 6; Fig 6A; 134pp; English.
XX
CC The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-Dp
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or hapten and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is human
CC NY ESO-1 peptide used in the characterisation of the NY ESO-1 epitope
CC recognised by TE4-1.
XX
SQ Sequence 14 AA;

Query Match 79.8%; Score 67; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KEFTVSGNLTIRL 17
Db 1 keftvsgniltirl 14

RESULT 11
AAU01541
ID AAU01541 standard; Peptide; 18 AA.
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XX AAU01541;
AC
XX
DT 18-JUL-2001 (first entry)
XX
DE HLA-DR53 recognising NY-ESO-1 peptide #3.
XX
KW NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
KW human leukocyte antigen-determining region; disease progression;
KW disease regression; disease onset; body tissue; body fluid; enzyme label;
KW radioactive label; monoclonal antibody.
XX
OS Homo sapiens.
XX
PN WO200123560-A2.
XX
PD 05-APR-2001.
XX
PF 26-SEP-2000; 2000WO-US26411.
XX
PR 29-SEP-1999; 99US-0408036.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Tureci O, Sahin U, Pfreundschuh M;
XX
DR WPI; 2001-266156/27.
XX
PT Polypeptides binding to major histocompatibility complex class II human
PT leukocyte antigen-determining region molecule having amino acid
PT sequence found in tumour rejection antigen precursor used for
PT stimulating proliferation of helper T cells -
XX
PS Example 13; Page 19; 62pp; English.
XX
CC The sequence represents a human NY-ESO-1 tumour rejection antigen
CC precursor fragment which recognises and binds to HLA-DR53. NY-ESO-1 and
CC SSX-2 polypeptides, or fragments of, bind to major histocompatibility
CC complex (MHC) Class II molecules such as human leukocyte
CC antigen-determining region (HLA-DR) molecules and stimulate proliferation
CC of helper T cells. The peptides can be administered to an HLA-DR positive
CC subject in order to stimulate the helper T cells. An MHC Class II
CC HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell or
CC present in free form is useful for this stimulation. The nucleic acid is
CC useful for screening for a cancerous condition, which involves contacting
CC a subject sample to a cell line transfected with the immunoreactive cell
CC (helper T cell), where interaction is indicative of cancer. In addition,
CC a sample from a patient (for example, a body fluid or tissue) can be
CC monitored for the amount of the complex present in the bloodstream. This
CC is useful for determining regression, progression or onset of a cancerous
CC condition. The method involves contacting the sample with a radioactive
CC labelled or enzyme labelled monoclonal antibody which specifically binds
CC with the complex.
XX
SQ Sequence 18 AA;

Query Match 67.9%; Score 57; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.00081;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNI 12
Db 7 vllkeftvsgni 18

RESULT 12
AAB69941
ID AAB69941 standard; Peptide; 18 AA.
XX
AC AAB69941;
XX
```

DT 27-APR-2001 (first entry)
XX Human NY-ESO-1 HLA-DR53 binding motif #3.
DE
XX Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW non-small cell lung carcinoma; tumour status determination.
XX Homo sapiens.
OS WO200107917-A1.
XX 01-FEB-2001.
PD 14-JUL-2000; 2000WO-US19220.
XX 23-JUL-1999; 99US-0359503.
PR (LUDW-) LUDWIG INST CANCER RES.
XX (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.
XX Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
PI WPI; 2001-182822/18.
DR Method useful for determining the status (e.g. progression, regression
XX or stability of the disease) of a cancerous condition, involves
PT determining the levels of NY-ESO-1 specific antibodies in a sample
PT taken from a patient -
XX Example 16; Page 27; 50pp; English.
PS The present sequence is given in a specification relating to a method
XX for determining the status of a cancerous condition in a patient
CC with a tumour that expresses NY-ESO-1. The method comprises assaying a
CC sample taken from the patient for antibodies that specifically bind to
CC the NY-ESO-1 and comparing the value obtained to a prior value obtained
CC from assay of a prior sample taken from the patient. Any difference
CC between the values is indicative of a change in status of the cancerous
CC condition. The method is useful for determining whether a cancerous
CC condition is progressing, regressing or remaining stable, in particular
CC in patients receiving treatment for a melanoma, adenocarcinoma,
CC non-small cell lung carcinoma or bladder carcinoma.
XX Sequence 18 AA;
SQ

Query Match 67.9%; Score 57; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.00081;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNI 12
Db 7 vllkeftvsgni 18

RESULT 13
AAAY52440
ID AAY52440 standard; Protein; 18 AA.
XX AAY52440;
AC
XX 15-FEB-2000 (first entry)
DT Human tumour antigen NY-ESO-1 peptide #13.
DE Cancer; tumour; antigen; MHC; major histocompatibility complex; Class II;
XX T-cell; helper; stimulation; proliferation; treatment;
KW diagnosis; prevention; melanoma; breast cancer; ovarian cancer;
KW prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer;
KW lymphoma.

QY 27-APR-2001 (first entry)
XX Homo sapiens.
DE WO9953938-A1.
XX 28-OCT-1999.
PD 24-MAR-1999; 99WO-US06875.
XX 17-APR-1998; 98US-0062422.
PR 02-OCT-1998; 98US-0165546.
XX (LUDW-) LUDWIG INST CANCER RES.
PA Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
PI Gure A, Ritter G;
XX WPI; 2000-038483/03.
DR Novel peptides which bind to MHC class I and MHC class II molecules,
XX useful for therapeutic and diagnostic purposes -
PT Claim 4; Page 22; 49pp; English.
PS Peptides #8-#13 (AAY52435-Y52440) are peptides derived from the human
XX tumour antigen, NY-ESO-1 (AAY52430) which can bind to MHC(major
CC histocompatibility Class II HLA-DR53 molecules, thereby stimulating
CC proliferation of helper T-cells. cDNA encoding NY-ESO-1 was initially
CC isolated from an oesophagus squamous cell cancer cDNA library. Tissue
CC localisation studies revealed it to be expressed at high levels
CC in normal ovary and testis but not in normal colon, kidney, liver,
CC brain, oesophagus and skin. It was expressed in certain tumours and
CC tumour cell lines with some degree of frequency - these included
CC melanoma specimens and cell lines, and breast and bladder cancer
CC specimens, with expression in other tumour types being sporadic.
CC These NY-ESO-1-derived peptides may be used in methods and
CC compositions used for the treatment, diagnosis and prevention of
CC cancers (such as melanoma, breast cancer, prostate cancer, lung
CC cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer,
CC or lymphoma) and to stimulate the proliferation of T cells.
XX Sequence 18 AA;
SQ

Query Match 66.7%; Score 56; DB 21; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TVSGNLTIRLT 18
Db 1 tvsgnltirlt 12

RESULT 14
AAU01544
ID AAU01544 standard; Peptide; 18 AA.
XX AAU01544;
AC
XX 18-JUL-2001 (first entry)
DT HLA-DR53 recognising NY-ESO-1 peptide #6.
DE NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
XX major histocompatibility complex; helper T cell; HLA-DR; cancer;
KW human leukocyte antigen-determining region; disease progression;
KW disease regression; disease onset; body tissue; body fluid; enzyme label;
KW radioactive label; monoclonal antibody.
XX Homo sapiens.
OS WO200123560-A2.
XX

PD 05-APR-2001.
XX
PF 26-SEP-2000; 2000WO-US26411.
XX
PR 29-SEP-1999; 99US-0408036.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Tureci O, Sahin U, Pfreundschuh M;
XX WPI; 2001-266156/27.
XX Polypeptides binding to major histocompatibility complex class II human
PT leukocyte antigen-determining region molecule having amino acid
PT sequence found in tumour rejection antigen precursor used for
PT stimulating proliferation of helper T cells -
XX
PS Example 13; Page 19; 62pp; English.
XX
CC The sequence represents a human NY-ESO-1 tumour rejection antigen
CC precursor fragment which recognises and binds to HLA-DR53. NY-ESO-1 and
CC SSX-2 polypeptides, or fragments of, bind to major histocompatibility
CC complex (MHC) Class II molecules such as human leukocyte
CC antigen-determining region (HLA-DR) molecules and stimulate proliferation
CC of helper T cells. The peptides can be administered to an HLA-DR positive
CC subject in order to stimulate the helper T cells. An MHC Class II
CC HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell or
CC present in free form is useful for this stimulation. The nucleic acid is
CC useful for screening for a cancerous condition. The nucleic acid is
CC a subject sample to a cell line transfected with the immunoreactive cell
CC (helper T cell), where interaction is indicative of cancer. In addition,
CC a sample from a patient (for example, a body fluid or tissue) can be
CC monitored for the amount of the complex present in the bloodstream. This
CC is useful for determining regression, progression or onset of a cancerous
CC condition. The method involves contacting the sample with a radioactive
CC labelled or enzyme labelled monoclonal antibody which specifically binds
CC with the complex.
XX
SQ Sequence 18 AA;

Query Match 66.7%; Score 56; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TVSGNILTIRLT 18
Db ||||||
1 tvsgniltirt 12

RESULT 15
AAB69944
ID AAB69944 standard; Peptide; 18 AA.
XX
AC AAB69944;
XX
DT 27-APR-2001 (first entry)
XX
DE Human NY-ESO-1 HLA-DR53 binding motif #6.
XX
KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW non-small cell lung carcinoma; tumour status determination.
XX
OS Homo sapiens.
XX
PN WO200107917-A1.
XX
PD 01-FEB-2001.
XX
PF 14-JUL-2000; 2000WO-US19220.
XX
PR 23-JUL-1999; 99US-0359503.

XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.
XX
PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
XX WPI; 2001-182822/18.
XX
PT Method useful for determining the status (e.g. progression, regression
PT or stability of the disease) of a cancerous condition, involves
PT determining the levels of NY-ESO-1 specific antibodies in a sample
PT taken from a patient -
XX
PS Example 16; Page 28; 50pp; English.
XX
CC The present sequence is given in a specification relating to a method
CC for determining the status of a cancerous condition in a patient
CC with a tumour that expresses NY-ESO-1. The method comprises assaying a
CC sample taken from the patient for antibodies that specifically bind to
CC the NY-ESO-1 and comparing the value obtained to a prior value obtained
CC from assay of a prior sample taken from the patient. Any difference
CC between the values is indicative of a change in status of the cancerous
CC condition. The method is useful for determining whether a cancerous
CC condition is progressing, regressing or remaining stable, in particular
CC in patients receiving treatment for a melanoma, adenocarcinoma,
CC non-small cell lung carcinoma or bladder carcinoma.
XX
SQ Sequence 18 AA;

Query Match 66.7%; Score 56; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TVSGNILTIRLT 18
Db ||||||
1 tvsgniltirt 12

Search completed: July 3, 2002, 11:26:58
Job time: 955 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:38:24 ; Search time 560.51 Seconds
(without alignments)
11.303 Million cell updates/sec

Title: US-09-165-546A-9
Perfect score: 84
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 451056

Minimum DB seq length: 0
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Listing first 45 summaries

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26:	/cgn2_6/ptodata/2/paa/US60_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	84	100.0	18	18 US-09-408-036B-8	Sequence 8, Appli
3	57	67.9	18	15 US-09-165-546A-10	Sequence 10, Appl
4	57	67.9	18	18 US-09-408-036B-9	Sequence 9, Appli
5	56	66.7	18	15 US-09-165-546A-13	Sequence 13, Appl
6	56	66.7	18	18 US-09-408-036B-12	Sequence 12, Appl
7	48	57.1	10	19 US-09-529-206-91	Sequence 91, Appl

8	48	57.1	10	19	US-09-529-206A-91	Sequence 91, Appl
9	48	57.1	10	19	US-09-529-206B-91	Sequence 91, Appl
10	47	56.0	10	19	US-09-529-206-15	Sequence 15, Appl
11	47	56.0	10	19	US-09-529-206-84	Sequence 84, Appl
12	47	56.0	10	19	US-09-529-206A-15	Sequence 15, Appl
13	47	56.0	10	19	US-09-529-206A-84	Sequence 84, Appl
14	47	56.0	10	19	US-09-529-206B-15	Sequence 15, Appl
15	47	56.0	10	19	US-09-529-206B-84	Sequence 84, Appl
16	44	52.4	9	18	US-09-409-455A-120	Sequence 120, App
17	44	52.4	9	22	US-09-833-039-120	Sequence 120, App
18	42	50.0	9	18	US-09-409-455A-125	Sequence 125, App
19	42	50.0	9	19	US-09-529-206-12	Sequence 12, Appl
20	42	50.0	9	19	US-09-529-206-69	Sequence 69, Appl
21	42	50.0	9	19	US-09-529-206A-12	Sequence 12, Appl
22	42	50.0	9	19	US-09-529-206A-69	Sequence 69, Appl
23	42	50.0	9	19	US-09-529-206A-113	Sequence 113, App
24	42	50.0	9	19	US-09-529-206B-12	Sequence 12, Appl
25	42	50.0	9	19	US-09-529-206B-69	Sequence 69, Appl
26	42	50.0	9	19	US-09-529-206B-113	Sequence 113, App
27	42	50.0	9	22	US-09-833-039-125	Sequence 125, App
28	37	44.0	9	19	US-09-529-206-66	Sequence 66, Appl
29	37	44.0	9	19	US-09-529-206-67	Sequence 67, Appl
30	37	44.0	9	19	US-09-529-206A-66	Sequence 66, Appl
31	37	44.0	9	19	US-09-529-206A-67	Sequence 67, Appl
32	37	44.0	9	19	US-09-529-206B-66	Sequence 66, Appl
33	37	44.0	9	19	US-09-529-206B-67	Sequence 67, Appl
34	37	44.0	10	19	US-09-529-206-90	Sequence 90, Appl
35	37	44.0	10	19	US-09-529-206A-90	Sequence 90, Appl
36	37	44.0	10	19	US-09-529-206B-90	Sequence 90, Appl
37	33	39.3	18	1	PCT-US99-09676-285	Sequence 285, App
38	33	39.3	18	14	US-09-071-838-285	Sequence 285, App
39	33	39.3	18	15	US-09-177-206-285	Sequence 285, App
40	33	39.3	18	22	US-09-812-283-285	Sequence 285, App
41	31	36.9	9	19	US-09-529-206-73	Sequence 73, Appl
42	31	36.9	9	19	US-09-529-206A-73	Sequence 73, Appl
43	31	36.9	9	19	US-09-529-206B-73	Sequence 73, Appl
44	31	36.9	11	23	US-09-966-871-6	Sequence 6, Appli
45	30	35.7	14	1	PCT-US01-03653-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-165-546A-9
; Sequence 9, Application US/09165546A
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao,
; Canlan, Matt; Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO
; AMINO ACID SEQUENCES OF NY-ESO-1, WHICH BIND TO
; MHC CLASS I AND MHC CLASS II MOLECULES, AND
; USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,546A
; FILING DATE: 02-Oct-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998

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; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-165-546A-9

Query Match          100.0%; Score 84; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNLTIRLT 18
   |||||
Db 1 VLLKEFTVSGNLTIRLT 18

RESULT 2
US-09-408-036B-8
; Sequence 8, Application US/09408036B
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Isolated Peptides Which Bind to MHC Class II Molecules and Uses T
; FILE REFERENCE: LUD 5624
; CURRENT APPLICATION NUMBER: US/09/408,036B
; CURRENT FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/165,546
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-408-036B-8

Query Match          100.0%; Score 84; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNLTIRLT 18
   |||||
Db 1 VLLKEFTVSGNLTIRLT 18

RESULT 3
US-09-165-546A-10
; Sequence 10, Application US/09165546A
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao,
; Canlan, Matt; Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO
; AMINO ACID SEQUENCES OF NY-ESO-1, WHICH BIND TO
; MHC CLASS I AND MHC CLASS II MOLECULES, AND
; USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:

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; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,546A
; FILING DATE: 02-Oct-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-165-546A-10

Query Match          67.9%; Score 57; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTVSGNI 12
   |||||
Db 7 VLLKEFTVSGNI 18

RESULT 4
US-09-408-036B-9
; Sequence 9, Application US/09408036B
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Isolated Peptides Which Bind to MHC Class II Molecules and Use
; FILE REFERENCE: LUD 5624
; CURRENT APPLICATION NUMBER: US/09/408,036B
; CURRENT FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/165,546
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 9
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-408-036B-9

Query Match          67.9%; Score 57; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 VLLKFTVSGNI 12
| | | | | | | | | |
Db 7 VLLKFTVSGNI 18

RESULT 5

US-09-165-546A-13
; Sequence 13, Application US/09165546A
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao,
; Canlan, Matt; Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO
; AMINO ACID SEQUENCES OF NY-ESO-1, WHICH BIND TO
; MHC CLASS I AND MHC CLASS II MOLECULES, AND
; USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,546A
; FILING DATE: 02-Oct-1998
; CLASSIFICATION: 530

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996

ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 13:
; US-09-165-546A-13

Query Match 66.7%; Score 56; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TVSGNLTIRLT 18
| | | | | | | | | |
Db 1 TVSGNLTIRLT 12

RESULT 6

US-09-408-036B-12
; Sequence 12, Application US/09408036B
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; TITLE OF INVENTION: Isolated Peptides Which Bind to MHC Class II Molecules and Uses T

; FILE REFERENCE: LUD 5624
; CURRENT APPLICATION NUMBER: US/09/408,036B
; CURRENT FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/165,546
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 12
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-408-036B-12

Query Match 66.7%; Score 56; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TVSGNLTIRLT 18
| | | | | | | | | |
Db 1 TVSGNLTIRLT 12

RESULT 7

US-09-529-206-91
; Sequence 91, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 91
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-91

Query Match 57.1%; Score 48; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FTVSGNLT 15
| | | | | | | | | |
Db 1 FTVSGNLT 10

RESULT 8

US-09-529-206A-91
; Sequence 91, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 10

;
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206A-91

Query Match 57.1%; Score 48; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FTVSGNLTIT 15
|||||
Db 1 FTVSGNLTIT 10

RESULT 9

US-09-529-206B-91
; Sequence 91, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-91

Query Match 57.1%; Score 48; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FTVSGNLTIT 15
|||||
Db 1 FTVSGNLTIT 10

RESULT 10

US-09-529-206-15
; Sequence 15, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-15

Query Match 56.0%; Score 47; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TVSGNLTIR 16

Db 1 TVSGNLTIR 10
|||||

RESULT 11

US-09-529-206-84
; Sequence 84, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-84

Query Match 56.0%; Score 47; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TVSGNLTIR 16
|||||
Db 1 TVSGNLTIR 10

RESULT 12

US-09-529-206A-15
; Sequence 15, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206A-15

Query Match 56.0%; Score 47; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TVSGNLTIR 16
|||||
Db 1 TVSGNLTIR 10

RESULT 13

US-09-529-206A-84
; Sequence 84, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven

```
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206A-84

Query Match          56.0%; Score 47; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 TVSGNILTIR 16
      |||||
Db      1 TVSGNILTIR 10

RESULT 14
US-09-529-206B-15
; Sequence 15, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-15

Query Match          56.0%; Score 47; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 TVSGNILTIR 16
      |||||
Db      1 TVSGNILTIR 10

RESULT 15
US-09-529-206B-84
; Sequence 84, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
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; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-84

Query Match          56.0%; Score 47; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 TVSGNILTIR 16
      |||||
Db      1 TVSGNILTIR 10

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Job time: 850 sec
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:39:32 ; Search time 61.64 Seconds
(without alignments)
29.545 Million cell updates/sec

Title: US-09-165-546A-9
Perfect score: 84
Sequence: 1 VLLKEFTVSGNLTIRLT 18

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Searched: 308740 seqs, 101176262 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	57.1	10	6 US-10-117-937-186	Sequence 186, App
2	47	56.0	10	6 US-10-117-937-188	Sequence 188, App
3	44	52.4	9	5 US-09-344-040C-120	Sequence 120, App
4	43	51.2	9	6 US-10-117-937-189	Sequence 189, App
5	42	50.0	9	5 US-09-344-040C-125	Sequence 125, App
6	42	50.0	9	6 US-10-117-937-185	Sequence 185, App
7	37	44.0	9	6 US-10-117-937-187	Sequence 187, App
8	31	36.9	11	6 US-10-039-645-6	Sequence 6, Appli
9	28	33.3	9	6 US-10-117-937-182	Sequence 182, App
10	28	33.3	9	6 US-10-117-937-190	Sequence 190, App
11	28	33.3	10	6 US-10-117-937-183	Sequence 183, App
12	28	33.3	10	6 US-10-117-937-191	Sequence 191, App
13	27.5	32.7	13	1 PCT-US02-04329-17	Sequence 17, Appl
14	27.5	32.7	13	1 PCT-US02-04329-31	Sequence 31, Appl
15	25	29.8	9	5 US-09-722-250-253	Sequence 253, App
16	25	29.8	9	5 US-09-722-250-253	Sequence 253, App
17	25	29.8	11	5 US-09-924-889-4	Sequence 4, Appli
18	25	29.8	16	6 US-10-014-436-5	Sequence 5, Appli
19	24	28.6	12	6 US-10-014-340-473	Sequence 473, App
20	24	28.6	13	5 US-09-988-493-46	Sequence 46, Appl
21	24	28.6	14	6 US-10-014-340-520	Sequence 520, App
22	24	28.6	15	5 US-09-988-493-103	Sequence 103, App
23	24	28.6	16	6 US-10-115-123-441	Sequence 441, App
24	24	28.6	16	7 US-60-368-671-63	Sequence 63, Appl
25	24	28.6	16	7 US-60-368-671-99	Sequence 99, Appl
26	24	28.6	16	7 US-60-371-420-63	Sequence 63, Appl

27	24	28.6	16	7 US-60-371-420-99	Sequence 99, Appl
28	24	28.6	18	1 PCT-US02-10293-53	Sequence 53, Appl
29	24	28.6	18	6 US-10-116-252-33	Sequence 33, Appl
30	23.5	28.0	18	6 US-10-012-034A-20	Sequence 20, Appl
31	23	27.4	10	6 US-10-089-783-32	Sequence 32, Appl
32	23	27.4	13	6 US-10-043-487-559	Sequence 559, App
33	23	27.4	14	5 US-09-563-286B-52	Sequence 52, Appl
34	23	27.4	14	5 US-09-563-286B-55	Sequence 55, Appl
35	23	27.4	14	6 US-10-115-123-299	Sequence 299, App
36	23	27.4	18	6 US-10-014-340-666	Sequence 666, App
37	22	26.2	8	6 US-10-044-844-52	Sequence 52, Appl
38	22	26.2	9	1 PCT-US02-10133-3	Sequence 3, Appli
39	22	26.2	9	5 US-09-580-339B-74	Sequence 74, Appl
40	22	26.2	9	6 US-10-114-091-3	Sequence 3, Appli
41	22	26.2	10	5 US-09-910-180-11	Sequence 11, Appl
42	22	26.2	10	5 US-09-755-630B-38	Sequence 38, Appl
43	22	26.2	10	6 US-10-044-844-214	Sequence 214, App
44	22	26.2	12	1 PCT-US02-11167-2	Sequence 2, Appli
45	22	26.2	12	5 US-09-563-286B-1079	Sequence 1079, Ap

ALIGNMENTS

RESULT 1
US-10-117-937-186
; Sequence 186, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 186
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-186

Query Match 57.1%; Score 48; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FTVSGNLT 15
Db 1 FTVSGNLT 10
|||||

RESULT 2
US-10-117-937-188
; Sequence 188, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937

; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 188
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-188

Query Match 56.0%; Score 47; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLLKEFTVSG 10
|||||
Db 1 VLLKEFTVSG 10

RESULT 3
US-09-344-040C-120
; Sequence 120, Application US/09344040C
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determin
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LJD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 120
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-120

Query Match 52.4%; Score 44; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FTVSGNILT 14
|||||
Db 1 FTVSGNILT 9

RESULT 4
US-10-117-937-189
; Sequence 189, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937

; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 189
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-189

Query Match 51.2%; Score 43; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LLKEFTVSG 10
|||||
Db 1 LLKEFTVSG 9

RESULT 5
US-09-344-040C-125
; Sequence 125, Application US/09344040C
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Deter
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gen
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LJD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 125
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-125

Query Match 50.0%; Score 42; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TVSGNILT 15
|||||
Db 1 TVSGNILT 9

RESULT 6
US-10-117-937-185
; Sequence 185, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937

; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 185
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-185

Query Match 50.0%; Score 42; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TVSGNILTI 15
| | | | | | | |
Db 1 TVSGNILTI 9

RESULT 7
US-10-117-937-187
; Sequence 187, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPI TOPE SEQUENCES
; FILE REFERENCE: CTLMIM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 187
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-187

Query Match 44.0%; Score 37; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEFTV 8
| | | | | | | |
Db 2 VLLKEFTV 9

RESULT 8
US-10-039-645-6
; Sequence 6, Application US/10039645
; GENERAL INFORMATION:
; APPLICANT: Kopin, Alan S.
; APPLICANT: Beinborn, Martin
; TITLE OF INVENTION: Constitutively Active, Hypersensitive,
; TITLE OF INVENTION: and Nonfunctional Receptors as Novel Therapeutic Agents
; FILE REFERENCE: 00398/510002
; CURRENT APPLICATION NUMBER: US/10/039,645
; CURRENT FILING DATE: 2001-10-25

; PRIOR APPLICATION NUMBER: US 60/243,550
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-645-6

Query Match 36.9%; Score 31; DB 6; Length 11;
Best Local Similarity 60.0%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 FTVSGNILTI 15
| : | | | | |
Db 1 FAIVGNILVI 10

RESULT 9
US-10-117-937-182
; Sequence 182, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPI TOPE SEQUENCES
; FILE REFERENCE: CTLMIM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 182
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-182

Query Match 33.3%; Score 28; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEF 6
| | | | | |
Db 4 VLLKEF 9

RESULT 10
US-10-117-937-190
; Sequence 190, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPI TOPE SEQUENCES
; FILE REFERENCE: CTLMIM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017

; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 190
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-190

Query Match 33.3%; Score 28; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEF 6
|||||
Db 4 VLLKEF 9

RESULT 11
US-10-117-937-183
; Sequence 183, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 183
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-183

Query Match 33.3%; Score 28; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEF 6
|||||
Db 5 VLLKEF 10

RESULT 12
US-10-117-937-191
; Sequence 191, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06

; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 191
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-191

Query Match 33.3%; Score 28; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLKEF 6
|||||
Db 5 VLLKEF 10

RESULT 13
PCT-US02-04329-17
; Sequence 17, Application PC/TUS0204329
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL GLYCINE RECEPTOR ALPHA SUBUNIT
; TITLE OF INVENTION: IN THE GASTROINTESTINAL TRACT, HGRA4, and SPLICE VARIANT THEREOF
; FILE REFERENCE: D0079 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/04329
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: US 60/269,535
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 13
; TYPE: PRT
; ORGANISM: homo sapiens
PCT-US02-04329-17

Query Match 32.7%; Score 27.5; DB 1; Length 13;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 10 GNIL-TIRLT 18
||:|:||||
Db 1 GNVLYSIRLT 10

RESULT 14
PCT-US02-04329-31
; Sequence 31, Application PC/TUS0204329
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL GLYCINE RECEPTOR ALPHA SUBUNIT
; TITLE OF INVENTION: IN THE GASTROINTESTINAL TRACT, HGRA4, and SPLICE VARIANT THEREOF
; FILE REFERENCE: D0079 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/04329
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: US 60/269,535
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 13
; TYPE: PRT
; ORGANISM: homo sapiens
PCT-US02-04329-31

Query Match 32.7%; Score 27.5; DB 1; Length 13;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 10 GNIL-TIRLT 18
||:| :|||
Db 1 GNVLSIRLT 10

RESULT 15
US-09-722-250-253
; Sequence 253, Application US/09722250
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 4514
; CURRENT APPLICATION NUMBER: US/09/722,250
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 253
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-722-250-253

Query Match 29.8%; Score 25; DB 5; Length 9;
Best Local Similarity 71.4%; Pred. No. 2.8e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 GNILTIR 16
||:| |
Db 2 GNLLTRR 8

Search completed: July 3, 2002, 11:39:32
Job time: 883 sec

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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:28:57 ; Search time 57.51 Seconds
(without alignments)
30.075 Million cell updates/sec

Title: US-09-165-546A-10
Perfect score: ~ 92
Sequence: 1 PLPVGVLKKEFTVSGNI 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 3210

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	36	39.1	18	2	S13974	chlorophyll a/b-bi
2	29	31.5	12	2	PN0170	alcohol dehydrogen
3	26	28.3	17	2	S59481	hydroxyproline-ric
4	24	26.1	13	2	A60856	inhibin alpha chai
5	24	26.1	15	2	B35389	urease (EC 3.5.1.5
6	24	26.1	15	2	A36315	recycling receptor
7	24	26.1	17	4	I76673	hypothetical COII/
8	23	25.0	10	2	PN0165	triose-phosphate.i
9	23	25.0	12	2	PN0663	dystrophin-associa
10	23	25.0	15	2	I46909	voltage-dependent
11	23	25.0	15	2	A56963	acid phosphatase (
12	23	25.0	16	2	S69361	carbamoyl-phosphat
13	23	25.0	18	2	PC2280	prolylendopeptidas
14	23	25.0	18	2	A32917	protein phosphatas
15	22	23.9	13	2	S09395	hypothetical prote
16	21.5	23.4	12	2	PC4377	telomeric and tetr
17	21	22.8	10	2	A27617	triose-phosphate i
18	21	22.8	11	2	C61497	seed protein ws-18
19	21	22.8	12	2	B46662	collagen alpha 2(V
20	21	22.8	12	2	E45691	probable minor cap
21	21	22.8	13	2	A33208	calreticulin, hepa
22	21	22.8	15	2	B39109	hypothetical 1.5K
23	21	22.8	15	2	PA0097	starch phosphoryla
24	21	22.8	15	2	G60977	protein 425 - Cali
25	21	22.8	16	2	S11760	flgL protein - Cau
26	21	22.8	16	2	A61530	triose-phosphate i
27	21	22.8	18	2	A49857	megakaryocyte pote
28	20	21.7	9	2	PH0902	T-cell receptor be
29	20	21.7	11	2	S33519	probable secreted

30	20	21.7	11	2	A34243	H-hyosophorin - Ja
31	20	21.7	12	2	A61309	glycoprotein hormo
32	20	21.7	12	2	E58502	43.2K bile stone p
33	20	21.7	12	2	S17540	agglutinin-III lec
34	20	21.7	15	2	B33208	calreticulin, uter
35	20	21.7	15	2	PA0034	protein QA300024 -
36	20	21.7	15	2	B41436	ovostatin - green
37	20	21.7	17	2	A49237	45/47K antigen - M
38	20	21.7	17	2	PC1318	large granule L6 c
39	19	20.7	6	2	A61049	halo-toxin - Pseud
40	19	20.7	9	2	S26508	collagen alpha 2(V
41	19	20.7	10	2	G60787	sperm-activating p
42	19	20.7	10	2	E60787	sperm-activating p
43	19	20.7	10	2	A61218	alpha-gliadin 4Ha
44	19	20.7	10	2	B61218	alpha-gliadin 6Ha
45	19	20.7	11	2	S41747	chaperonin 10 homo

ALIGNMENTS

RESULT 1
S13974
Chlorophyll a/b-binding protein type I - garden pea (fragment)
C:Species: Pisum sativum (garden pea)
C>Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
C:Accession: S13974
R;Jahns, P.; Junge, W.
Eur. J. Biochem. 193, 731-736, 1990
A;Title: Dicyclohexylcarbodiimide-binding proteins related to the short circuit of th
A;Reference number: S13973; MUID:91065379
A;Accession: S13974
A;Molecule type: protein
A;Residues: 1-18 <JAH>
C;Genetics:
A;Genome: nuclear
C;Keywords: chlorophyll; chloroplast; light-harvesting complex; photosystem I; thylak

Query Match 39.1%; Score 36; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy	2	LPVPGVLLKKEFTVSGN 17
		:
Db	1	LAVPGILVPEALGLGN 16

RESULT 2
PN0170
alcohol dehydrogenase (EC 1.1.1.1) - fungus (Fusarium sporotrichioides) (fragment)
C:Species: Fusarium sporotrichioides
C>Date: 05-Aug-1994 #sequence_revision 06-Jan-1995 #text_change 31-Jan-1997
C:Accession: PN0170
R;Fukaya, N.; Chow, L.P.; Sugiyura, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.
submitted to JIPID, May 1994
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotr
A;Reference number: PN0160
A;Accession: PN0170
A;Molecule type: protein
A;Residues: 1-12 <FUK>
A;Experimental source: strain M-1-1
C;Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 31.5%; Score 29; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy	8	LLKEFTVSG 16
		:
Db	2	LLKGYTVDG 10

RESULT 3
S59481
hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)
C;Species: Phaseolus vulgaris (kidney bean)
C;Date: 27-Apr-1996 #sequence_revision 19-Jul-1996 #text_change 05-Dec-1998
C;Accession: S59481
R;Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.
Plant Mol. Biol. 28, 1075-1087, 1995
A;Title: Specificity in the immobilisation of cell wall proteins in response to differer
A;Reference number: S59481; MUID:96011753
A;Accession: S59481
A;Molecule type: protein
A;Residues: 1-17 <WOJ>
C;Keywords: glycoprotein; hydroxyproline
F;6,8,9,10,11/Modified site: hydroxyproline (Pro) #status experimental

Query Match 28.3%; Score 26; DB 2; Length 17;
Best Local Similarity 41.7%; Pred. No. 5.8e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEF 12
|:| | |:
Db 6 PVPPPPVVPYPTF 17

RESULT 4
A60856
inhibin alpha chain - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: A60856
R;Leversha, L.J.; Robertson, D.M.; de Vos, F.L.; Morgan, F.J.; Hearn, M.T.W.; Wettenhall
J. Endocrinol. 113, 213-221, 1987
A;Title: Isolation of inhibin from ovine follicular fluid.
A;Reference number: A60856; MUID:87224684
A;Accession: A60856
A;Molecule type: protein
A;Residues: 1-13 <LEV>
C;Comment: Inhibin suppresses follicle-stimulating hormone secretion.
C;Superfamily: inhibin
C;Keywords: disulfide bond; glycoprotein; gonad; heterodimer; hormone

Query Match 26.1%; Score 24; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 9.6e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLPVP 5
| | |
Db 4 PLXP 8

RESULT 5
B35389
urease (EC 3.5.1.5) 15K chain - Morganella morganii (fragment)
C;Species: Morganella morganii
C;Date: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 23-Jun-1993
C;Accession: B35389
R;Hu, L.T.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.
J. Bacteriol. 172, 3073-3080, 1990
A;Title: Morganella morganii urease: purification, characterization, and isolation of ge
A;Reference number: A35389; MUID:90264298
A;Accession: B35389
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <HUA>
C;Keywords: hydrolase

Query Match 26.1%; Score 24; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLPVPGVL 8
| | |:
Db 6 PTPLGGVI 13

RESULT 6
A36315
recycling receptor p180 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 25-Jan-1991 #sequence_revision 25-Jan-1991 #text_change 30-Sep-1993
C;Accession: A36315
R;Isacke, C.M.; van der Geer, P.; Hunter, T.; Trowbridge, I.S.
Mol. Cell. Biol. 10, 2606-2618, 1990
A;Title: p180, a novel recycling transmembrane glycoprotein with restricted cell type
A;Reference number: A36315; MUID:90258846
A;Accession: A36315
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <ISA>

Query Match 26.1%; Score 24; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 LPVPGVLL 9
| | | | |
Db 7 LPEPNVFL 14

RESULT 7
I76673
hypothetical COII/ND5 mutant fusion protein - mouse mitochondrion (fragment)
N;Alternate names: COII/ND5 protein
C;Species: mitochondrion Mus musculus (house mouse)
C;Date: 12-Aug-1996 #sequence_revision 16-Jul-1998 #text_change 20-Apr-2000
C;Accession: I76673; I76674
R;Nelson, I.; Gerasimov, S.; Marsac, C.; Lestienne, P.; Boursot, P.
Mamm. Genome 4, 680-683, 1993
A;Title: Sequence analysis of a deleted mitochondrial DNA molecule in heteroplasmic m
A;Reference number: I57011; MUID:94108239
A;Accession: I76673
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-17 <NEL1>
A;Cross-references: GB:S68119; NID:g544777
A;Accession: I76674
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 8-17 <NEL2>
A;Cross-references: GB:S68119; NID:g544777
C;Comment: This is the hypothetical translation of a sequence believed to result from
C;Genetics:
A;Gene: COII/ND5
A;Genome: mitochondrion
A;Genetic code: SGC1
C;Keywords: fusion protein; mitochondrion
F;1-7/Region: cytochrome-c oxidase chain II
F;8-17/Region: NADH dehydrogenase (ubiquinone) chain 5

Query Match 26.1%; Score 24; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 9 LKEFTVSGNI 18
| | | | |
Db 5 LKPLTTNNNI 14

RESULT 8

PN0165
triose-phosphate isomerase (EC 5.3.1.1) - fungus (Fusarium sporotrichioides) (fragment)
C;Species: Fusarium sporotrichioides
C;Date: 05-Aug-1994 #sequence_revision 06-Jan-1995 #text_change 23-Mar-1995
C;Accession: PN0165
R;Fukaya, N.; Chow, L.P.; Suglura, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.
submitted to JIPID, May 1994
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides
A;Reference number: PN0160
A;Accession: PN0165
A;Molecule type: protein
A;Residues: 1-10 <FUK>
A;Experimental source: strain M-1-1
C;Keywords: intramolecular oxidoreductase; isomerase

Query Match 25.0%; Score 23; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 10 KEFTVSGN 17
:| | | |
Db 2 RKFFVGGN 9

RESULT 9
PN0663
dystrophin-associated glycoprotein A3a-II - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999
C;Accession: PN0663
R;Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.
J. Biochem. 114, 634-639, 1993
A;Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained
A;Reference number: PN0662; MUID:94156881
A;Accession: PN0663
A;Molecule type: protein
A;Residues: 1-12 <YOS>
C;Comment: This protein is retained in Duchenne type muscular dystrophy muscle.
C;Keywords: glycoprotein; skeletal muscle

Query Match 25.0%; Score 23; DB 2; Length 12;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLPVP 5
| | | |
Db 3 PLPPP 7

RESULT 10
I46909
voltage-dependent dihydropyridine-sensitive calcium channel alpha 1 subunit 155 kda isoform
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 05-Nov-1999
C;Accession: I46909
R;Malouf, N.N.; McMahon, D.K.; Hainsworth, C.N.; Kay, B.K.
Neuron 8, 899-906, 1992
A;Title: A two-motif isoform of the major calcium channel subunit in skeletal muscle.
A;Reference number: I46909; MUID:92265303
A;Accession: I46909
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: mRNA
A;Residues: 1-15 <MAL>
A;Cross-references: GB:S36895; NID:g249481; PIDN:AAB22180.1; PID:g249482

Query Match 25.0%; Score 23; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 VLLKEFTV 14

Db 2 VLLSLFTI 9
| | | | | |
RESULT 11
A56963
acid phosphatase (EC 3.1.3.2) - mushroom (Pholiota nameko) (fragment)
C;Species: Pholiota nameko
C;Date: 18-Aug-1995 #sequence_revision 27-Oct-1995 #text_change 27-Oct-1995
C;Accession: A56963
R;Malick, D.H.
submitted to the Protein Sequence Database, August 1995
A;Reference number: A56963
A;Accession: A56963
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <MAL>
C;Keywords: phosphoric monoester hydrolase

Query Match 25.0%; Score 23; DB 2; Length 15;
Best Local Similarity 44.4%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 VPGVLLKEF 12
| | | : |
Db 5 VPGAVFDRF 13

RESULT 12
S69361
carbamoyl-phosphate synthetase I - rat (fragments)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998
C;Accession: S69361
R;Alonso, E.; Rubio, V.
Eur. J. Biochem. 229, 377-384, 1995
A;Title: Affinity cleavage of carbamoyl-phosphate synthetase I localizes regions of t
A;Reference number: S69361; MUID:95262701
A;Accession: S69361
A;Molecule type: protein
A;Residues: 1-8;9-16 <ALO>

Query Match 25.0%; Score 23; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 11 EFTVSGN 17
: | | | | |
Db 10 QFLVKGN 16

RESULT 13
PC2280
prolylendopeptidase-inhibiting peptide - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 28-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-May-1997
C;Accession: PC2280
R;Ohmori, T.; Nakagami, T.; Tanaka, H.; Maruyama, S.
Biochem. Biophys. Res. Commun. 202, 809-815, 1994
A;Title: Isolation of prolylendopeptidase-inhibiting peptides from bovine brain.
A;Reference number: PC2280; MUID:94324971
A;Accession: PC2280
A;Molecule type: protein
A;Residues: 1-18 <OHM>
A;Experimental source: brain
C;Superfamily: cytoskeletal keratin

Query Match 25.0%; Score 23; DB 2; Length 18;
Best Local Similarity 31.2%; Pred. No. 2e+03;
Matches 5; Conservative 6; Mismatches 3; Indels 2; Gaps 1;

QY 1 PLPVPGVLLKEFTVSG 16
| | | : | : |
Db 2 PPPLPARV--DFSLAG 15

RESULT 14
A32917
protein phosphatase - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 08-Dec-1989 #sequence_revision 08-Dec-1989 #text_change 30-Sep-1993
C;Accession: A32917
R;Tamura, S.; Yasui, A.; Tsuiki, S.
Biochem. Biophys. Res. Commun. 163, 131-136, 1989
A;Title: Expression Of rat protein phosphatase 2C (IA) in Escherichia coli.
A;Reference number: A32917; MUID:89374212
A;Accession: A32917
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-18 <TAM>

Query Match 25.0%; Score 23; DB 2; Length 18;
Best Local Similarity 38.5%; Pred. No. 2e+03;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 4 VPGVLLKEFTVSG 16
| | | | : |
Db 6 VPGDPLEDQVIMG 18

RESULT 15
S09395
hypothetical protein - fruit fly (Drosophila melanogaster) (fragment)
C;Species: Drosophila melanogaster
C;Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 24-Jul-1997
C;Accession: S09395
R;Gisselmann, G.; Sewing, S.; Madsen, B.W.; Mallart, A.; Angaut-Petit, D.; Mueller-Holtk
EMBO J. 8, 2359-2364, 1989
A;Title: The interference of truncated with normal potassium channel subunits leads to a
A;Reference number: S09395; MUID:90005442
A;Accession: S09395
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <GIS>

Query Match 23.9%; Score 22; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPVP 5
| | | |
Db 5 LPVP 8

RX MEDLINE=90264298; PubMed=2345135;
RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;
RT "Morganella morganii urease: purification, characterization, and
RT isolation of gene sequences.";
RL J. Bacteriol. 172:3073-3080(1990).
CC -!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
CC -!- SUBUNIT: (ALPHA, BETA, GAMMA)(3) (BY SIMILARITY).
CC -!- SIMILARITY: TO OTHER UREASES BETA SUBUNITS.
DR PIR; B35389; B35389.
KW Hydrolase.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1530 MW; 2D98944F2F20C7E8 CRC64;

Query Match 26.1%; Score 24; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLPVPGVLL 8
| | | | |
Db 6 PTPLGGVI 13

RESULT 3
CRBL_VESMA
ID CRBL_VESMA STANDARD; PRT; 13 AA.
AC P17232;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Vespid chemotactic peptide M (VESCP-M).
OS Vespa mandarinia (Hornet).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Vespoidea; Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7446;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Yasuhara T., Nakajima T., Fukuda K., Tsukamoto Y., Mori M., Kitada C.,
RA Fujino M.;
RL (In) Munekata E. (eds.);
RL Peptide chemistry 1983, pp.185-190, Protein Research Foundation,
RL Osaka (1984).
CC -!- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. INDUCES THE CHEMOTAXIS
CC OF NEUTROPHILS.
KW Mast cell degranulation; Chemotaxis; Venom; Amidation.
FT MOD_RES 13 13
SQ SEQUENCE 13 AA; 1384 MW; 2650402B9DF92338 CRC64;

Query Match 25.0%; Score 23; DB 1; Length 13;
Best Local Similarity 62.5%; Pred. No. 5.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LPVPGVLL 9
| | | | |
Db 2 LPIIGKLL 9

RESULT 4
TEM_D_RANTE
ID TEMD_RANTE STANDARD; PRT; 13 AA.
AC P56919;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Temporin D.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX NCBI_TaxID=8407;
RN [1]

RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Skin;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
RT temporaria.";
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: HAS NO ANTIBACTERIAL ACTIVITY.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC FAMILY.
KW Amphibian skin; Amidation; Multigene family.
FT MOD_RES 13 13
SQ SEQUENCE 13 AA; 1379 MW; 3EF35DFA655B2448 CRC64;

Query Match 25.0%; Score 23; DB 1; Length 13;
Best Local Similarity 62.5%; Pred. No. 5.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LPVPGVLL 9
| | | | |
Db 2 LPIVGNLL 9

RESULT 5
TEM_C_RANTE
ID TEMC_RANTE STANDARD; PRT; 13 AA.
AC P56918;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Temporin C.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
RT temporaria.";
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE
CC BACTERIA.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC FAMILY.
KW Amphibian skin; Antibiotic; Amidation; Multigene family.
FT MOD_RES 13 13
SQ SEQUENCE 13 AA; 1363 MW; 2201403A655B2448 CRC64;

Query Match 23.9%; Score 22; DB 1; Length 13;
Best Local Similarity 62.5%; Pred. No. 8.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LPVPGVLL 9
| | | | |
Db 2 LPILGNLL 9

RESULT 6
TEME_RANTE
ID TEME_RANTE STANDARD; PRT; 13 AA.
AC P56920;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
RT temporaria.";
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE
CC BACTERIA.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC FAMILY.
KW Amphibian skin; Antibiotic; Amidation; Multigene family.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1379 MW; 26505DFA79A92448 CRC64;

Query Match 23.9%; Score 22; DB 1; Length 13;
Best Local Similarity 62.5%; Pred. No. 8.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LPVPGVLL 9
II: | | |
Db 2 LPIIGNLL 9

RESULT 7
TPIS_NICPL
ID TPIS_NICPL STANDARD; PRT; 10 AA.
AC P19118;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Triosephosphate isomerase, cytosolic (EC 5.3.1.1) (TIM) (Fragment).
OS Nicotiana plumbaginifolia (Leadwort-leaved tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4092;
RN [1]
RP SEQUENCE.
RA Bauw G., de Loose M., Inze D., van Montagu M., Vandekerckhove J.;
RT "Alterations in the phenotype of plant cells studied by NH2-terminal
RT amino acid-sequence analysis of proteins electroblotted from two-
RT dimensional gel-separated total extracts.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4806-4810(1987).
CC -!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycerone
CC phosphate.
CC -!- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- MISCELLANEOUS: IN PLANTS, THERE ARE TWO TYPES OF TPIS, CYTOSOLIC
CC AND PLASTID.
CC -!- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
DR PIR; A27617; A27617.
DR InterPro; IPR000652; Trioseph_isomerase.
DR Pfam; PF00121; TIM; 1.
DR PROSITE; PS00171; TIM; PARTIAL.
KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
KW Pentose shunt.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1140 MW; 80B9D37862C9C9D1 CRC64;

Query Match 22.8%; Score 21; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 9.2e+02;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 KEFTVSGN 17
: | | | |
Db 2 RTFFVGGN 9

RESULT 8
TIN4_HOPTI
ID TIN4_HOPTI STANDARD; PRT; 11 AA.
AC P82654;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tigerin-4.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RC TISSUE=Skin;
RX PubMed=11031261;
RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaram N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST B.SUBTILIS, E.COLI,
CC S.AUREUS, M.LUTEUS, P.PUTIDA AND S.CEREVISIAE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: SKIN.
CC -!- MASS SPECTROMETRY: MW=1247; METHOD=MALDI.
KW Amphibian skin; Antibiotic.
FT DISULFID 3 11
SQ SEQUENCE 11 AA; 1248 MW; 117D8EFD37605DCB CRC64;

Query Match 22.8%; Score 21; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPV 4
| | |
Db 7 PLPI 10

RESULT 9
OPS3_DROVI
ID OPS3_DROVI STANDARD; PRT; 12 AA.
AC P17645;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Opsin Rh3 (Inner R7 photoreceptor cells opsin) (Fragment).
GN RH3.
OS Drosophila virilis (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7244;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90249748; PubMed=2140105;
RA Fortini M.E., Rubin G.M.;
RT "Analysis of cis-acting requirements of the Rh3 and Rh4 genes reveals
RT a bipartite organization to rhodopsin promoters in Drosophila
RT melanogaster.";
RL Genes Dev. 4:444-463(1990).
CC -!- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT
CC MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
CC LINKED TO CIS-RETINAL.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- MISCELLANEOUS: EACH DROSOPHILA EYE IS COMPOSED OF 800 FACETS OR
CC OMMATIDIA. EACH OMMATIDIUM CONTAINS 8 PHOTORECEPTOR CELLS (R1-R8),
CC THE R1 TO R6 CELLS ARE OUTER CELLS, WHILE R7 AND R8 ARE INNER
CC CELLS.
CC -!- MISCELLANEOUS: OPSIN RH3 IS SENSITIVE TO UV LIGHT.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC OPSIN SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----

DR EMBL; X51350; CAA35742.1; -.
DR GCRDb; GCR_0779; -.
DR FlyBase; FBgn0013091; Dvir\Rh3.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR001760; Opsin.
DR PROSITE; PS00237; G.PROTEIN_RECEP_F1_1; PARTIAL.
DR PROSITE; PS00238; OPSIN; PARTIAL.
KW Photoreceptor; Retinal protein; Transmembrane; Phosphorylation;
KW Glycoprotein; G-protein coupled receptor; Vision.
FT CARBOHYD 10 10 N-LINKED (GLCNAC. .) (PROBABLE).
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1253 MW; 04024E43495865B0 CRC64;

Query Match 22.8%; Score 21; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 EFTVSG 16
:|:|:
Db 2 DFNISG 7

RESULT 10
TIN2_HOPTI STANDARD; PRT; 12 AA.
ID BP37_LEUMA
AC P82652;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tigerin-2.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RC TISSUE=Skin;
RX PubMed=11031261;
RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaram N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST B.SUBTILIS, E.COLI,
CC S.AUREUS, M.LUTEUS, P.PUTIDA AND S.CEREVISIAE.
CC -!- SUBCELLULAR LOCATION: SKIN.
CC -!- TISSUE SPECIFICITY: SKIN.
CC -!- MASS SPECTROMETRY: MW=1368; METHOD=MALDI.
KW Amphibian skin; Antibiotic; Amidation.
FT DISULFID 3 11
FT MOD_RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1369 MW; C2627D8EFD37605D CRC64;

Query Match 22.8%; Score 21; DB 1; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPV 4
|:|:
Db 7 PLPI 10

RESULT 11
TIN3_HOPTI STANDARD; PRT; 12 AA.
ID BP37_LEUMA
AC P82653;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tigerin-3.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RC TISSUE=Skin;
RX PubMed=11031261;
RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaram N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST B.SUBTILIS, E.COLI,
CC S.AUREUS, M.LUTEUS, P.PUTIDA AND S.CEREVISIAE.
CC -!- SUBCELLULAR LOCATION: SKIN.
CC -!- TISSUE SPECIFICITY: SKIN.
CC -!- MASS SPECTROMETRY: MW=1409; METHOD=MALDI.
KW Amphibian skin; Antibiotic; Amidation.
FT DISULFID 3 11
FT MOD_RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1411 MW; C0717D8EFD37605D CRC64;

Query Match 22.8%; Score 21; DB 1; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPV 4
|:|:
Db 7 PLPI 10

RESULT 12
BP37_LEUMA STANDARD; PRT; 13 AA.
ID BP37_LEUMA
AC P81754;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Brain protein 37F3.
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Brain;
RX MEDLINE=97269266; PubMed=9114447;
RA Muren J.E., Naessel D.R.;
RT "Seven tachykinin-related peptides isolated from the brain of the
RT madeira cockroach; evidence for tissue-specific expression of
RT isoforms.";
RL Peptides 18:7-15(1997).


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CC -!- TISSUE SPECIFICITY: BRAIN.
CC -!- MASS SPECTROMETRY: MW=1435.7; METHOD=MALDI.
SQ SEQUENCE 13 AA; 1436 MW; 8E532C9DE9A7D1B5 CRC64;

Query Match      22.8%; Score 21; DB 1; Length 13;
Best Local Similarity 62.5%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 LLKEFTVS 15
   | : | | |
Db 2 LFEESTVS 9

RESULT 13
CRBL_VESTR      STANDARD;      PRT;      13 AA.
AC P17231;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Vespid chemotactic peptide T (VESP-T).
OS Vespa tropica (Hornet).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Vespoidea; Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7450;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Yasuhara T., Nakajima T., Erspaer V.;
RL (In) Sakakibara S. (eds.);
RL Peptide chemistry 1982, pp.213-218, Protein Research Foundation,
RL Osaka (1983).
CC -!- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. INDUCES THE CHEMOTAXIS
CC OF NEUTROPHILS.
KW Mast cell degranulation; Chemotaxis; Venom; Amidation.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1354 MW; 220140365DFE5338 CRC64;

Query Match      22.8%; Score 21; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LPVPGVLL 9
   | | : |
Db 2 LPILGKIL 9

RESULT 14
CRTC_BOVIN      STANDARD;      PRT;      13 AA.
AC P28489;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Calreticulin (CRP55) (Calregulin) (HACBP) (ERP60) (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=91201375; PubMed=2016321;
RA Milner R.E., Baksh S., Shemanko C., Carpenter M.R., Smillie L.,
RA Vance J.E., Opas M., Michalak M.;
RT "Calreticulin, and not calsequestrin, is the major calcium binding
RT protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic
RT reticulum.";
RL J. Biol. Chem. 266:7155-7165(1991).
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CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
DR PIR; A33208; A33208.
DR InterPro; IPR001580; Calreticulin.
DR PROSITE; PS00803; CALRETICULIN_1; PARTIAL.
DR PROSITE; PS00804; CALRETICULIN_2; PARTIAL.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; PARTIAL.
KW Endoplasmic reticulum; Calcium-binding.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1557 MW; C85DDA6993CA1339 CRC64;

Query Match      22.8%; Score 21; DB 1; Length 13;
Best Local Similarity 33.3%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 PGVLLKEFTVSG 16
   | : | | : |
Db 2 PAIFYKEQFLDG 13

RESULT 15
SA2A_ONCMY      STANDARD;      PRT;      13 AA.
AC P82238;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Salmocidin 2A (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Serum;
RA Henry M.A., Secombes C.J.;
RT "Purification and partial characterization of antibacterial peptides
RT from rainbow trout, Oncorhynchus mykiss.";
RL Submitted (DEC-1999) to the SWISS-PROT data bank.
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-NEGATIVE BACTERIA.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma serum.
KW Antibiotic.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1416 MW; 5FFB792AFC645873 CRC64;

Query Match      22.8%; Score 21; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 GVLLKEFT 13
   | : | | : |
Db 2 GFVLKGYT 9

Search completed: July 3, 2002, 11:41:55
Job time: 836 sec
```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:41:20 ; Search time 100.54 Seconds
(without alignments)
30.972 Million cell updates/sec

Title: US-09-165-546A-10
Perfect score: 92
Sequence: 1 PLPVPGVLLKEFTVSGNI 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 4250

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	27	29.3	18	6	P79214	P79214 oryctolagus
2	25	27.2	15	4	Q9UCC2	Q9ucc2 homo sapien
3	25	27.2	16	2	Q47605	Q47605 escherichia
4	25	27.2	17	4	Q9UC89	Q9uc89 homo sapien
5	24	26.1	13	13	P82848	P82848 rana pipien
6	23	25.0	11	11	Q9QYF6	Q9qyf6 mus musculu
7	23	25.0	12	4	Q9BZ49	Q9bz49 homo sapien
8	23	25.0	13	8	Q957T7	Q957t7 trichopsis
9	23	25.0	15	2	O69173	O69173 yersinia pe
10	23	25.0	15	6	Q28822	Q28822 oryctolagus
11	23	25.0	16	4	Q96RT5	Q96rt5 homo sapien
12	23	25.0	17	6	Q9TRU8	Q9tru8 bos taurus
13	23	25.0	17	12	Q9IHJ0	Q9ihj0 human polio
14	23	25.0	17	12	Q9IH19	Q9ih19 human polio
15	23	25.0	17	12	Q9IH18	Q9ih18 human polio
16	23	25.0	17	12	Q9IH17	Q9ih17 human polio

17	23	25.0	17	12	Q9IH16	Q9ih16 human polio
18	23	25.0	17	12	Q9IH15	Q9ih15 human polio
19	23	25.0	17	12	Q9IH14	Q9ih14 human polio
20	23	25.0	17	12	Q9IH13	Q9ih13 human polio
21	23	25.0	17	12	Q9IH12	Q9ih12 human polio
22	23	25.0	17	12	Q9IH11	Q9ih11 human polio
23	23	25.0	17	12	Q9IH10	Q9ih10 human polio
24	23	25.0	17	12	Q9IHH9	Q9ihh9 human polio
25	23	25.0	17	12	Q9IHH8	Q9ihh8 human polio
26	23	25.0	17	12	Q9IHH7	Q9ihh7 human polio
27	23	25.0	17	12	Q9IHH6	Q9ihh6 human polio
28	23	25.0	17	12	Q9IHH5	Q9ihh5 human polio
29	23	25.0	17	12	Q9IHH4	Q9ihh4 human polio
30	23	25.0	17	12	Q9IHH3	Q9ihh3 human polio
31	23	25.0	17	12	Q9IHH2	Q9ihh2 human polio
32	23	25.0	17	12	Q9IHH1	Q9ihh1 human polio
33	23	25.0	17	12	Q9IHH0	Q9ihh0 human polio
34	23	25.0	17	12	Q9IHG9	Q9ihg9 human polio
35	23	25.0	17	12	Q9IHG8	Q9ihg8 human polio
36	23	25.0	17	12	Q9IHG7	Q9ihg7 human polio
37	23	25.0	17	12	Q9IHG6	Q9ihg6 human polio
38	23	25.0	17	12	Q9IHG5	Q9ihg5 human polio
39	23	25.0	17	12	Q9IHG4	Q9ihg4 human polio
40	23	25.0	17	12	Q9IHG3	Q9ihg3 human polio
41	23	25.0	17	12	Q9IHG2	Q9ihg2 human polio
42	22	23.9	9	5	Q9TWV0	Q9twv0 anthopleura
43	22	23.9	10	2	Q9X529	Q9x529 citrobacter
44	22	23.9	10	2	Q9X531	Q9x531 escherichia
45	22	23.9	10	2	Q9X532	Q9x532 comamonas t

ALIGNMENTS

RESULT 1
P79214
ID P79214 PRELIMINARY; PRT: 18 AA.
AC P79214;
DT 01-MAY-1997 (TremBLrel. 03, Created)
DT 01-MAY-1997 (TremBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE CFTR PROTEIN.
GN CFTR.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97254985; PubMed=9100367;
RA Vuillaume S., Kaltenboeck B., Lecointre G., Lehn P., Denamur E.;
RT "Phylogenetic analysis of cystic fibrosis transmembrane conductance
RT regulator gene in mammalian species argues for the development of a
RT rabbit model for cystic fibrosis."
RL Mol. Biol. Evol. 14:372-380(1997).
DR EMBL; X95931; CAA65172.1; -.
SQ SEQUENCE 18 AA; 2080 MW; 4D1C55056C1CE1B5 CRC64;

Query Match 29.3%; Score 27; DB 6; Length 18;
Best Local Similarity 58.3%; Pred. No. 1e+03;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEF 12
|| ||| | |
Db 5 PLEKAGVLSKLF 16

RESULT 2
Q9UCC2
ID Q9UCC2 PRELIMINARY; PRT: 15 AA.
AC Q9UCC2;
DT 01-MAY-2000 (TremBLrel. 13, Created)

DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE 35 KDA HEPARIN-RELEASABLE PROTEIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=94059921; PubMed=8241100;
RA Novotny W.F., Maffi T., Mehta R.L., Milner P.G.;
RT "Identification of novel heparin-releasable proteins, as well as the
RT cytokines midkine and pleiotrophin, in human postheparin plasma.";
RL Arterioscler. Thromb. 13:1798-1805(1993).
SQ SEQUENCE 15 AA; 1454 MW; 0585FEF4FE8F6265 CRC64;

Query Match 27.2%; Score 25; DB 4; Length 15;
Best Local Similarity 60.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVP 5
Db 5 PVPIP 9

RESULT 3
Q47605 ID Q47605 PRELIMINARY; PRT; 16 AA.
AC Q47605;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE C (FRAGMENT).
GN C.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91139577; PubMed=1995588;
RA Tao T., Bourne J.C., Blumenthal R.M.;
RT "A family of regulatory genes associated with type II restriction-
RT modification systems.";
RL J. Bacteriol. 173:1367-1375(1991).
DR EMBL; M63622; AAA24561.1; .
FT NON_TER 1 1
SQ SEQUENCE 16 AA; 1853 MW; E46774511496607C CRC64;

Query Match 27.2%; Score 25; DB 2; Length 16;
Best Local Similarity 55.6%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 LKEFTVSGN 17
Db 3 LLDFTTIGN 11

RESULT 4
Q9UC89 ID Q9UC89 PRELIMINARY; PRT; 17 AA.
AC Q9UC89;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE ONCOFETAL-LAMININ BINDING COLLAGEN ALPHA 1(III)CHAIN, OF-LB COLLAGEN
DE ALPHA 1(III).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

RN [1]
RP SEQUENCE.
RX MEDLINE=95169134; PubMed=7864881;
RA Minafra I.P., Andriolo M., Basirico L., Aquino A., Minafra S.,
RA Boutillon M.M., van der Rest M.;
RT "Onco-fetal/laminin-binding collagen from colon carcinoma: detection
RT of new sequences.";
RL Biochem. Biophys. Res. Commun. 207:852-859(1995).
SQ SEQUENCE 17 AA; 1566 MW; 8436525120A9B421 CRC64;

Query Match 27.2%; Score 25; DB 4; Length 17;
Best Local Similarity 66.7%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLPVP 6
Db 6 PLGIPG 11

RESULT 5
P82848 ID P82848 PRELIMINARY; PRT; 13 AA.
AC P82848;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE TEMPORIN-1P.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=SKIN;
RX MEDLINE=20117700; PubMed=10651828;
RA Goraya J., Wang Y., Li Z., O'Flaherty M., Knoop F.C., Platz J.E.,
RA Conlon J.M.;
RT "Peptides with antimicrobial activity from four different families
RT isolated from the skins of the North American frogs Rana luteiventris,
RT Rana berlandieri and Rana pipiens.";
RL Eur. J. Biochem. 267:894-900(2000).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
CC S.AUREUS.
CC -!- MASS SPECTROMETRY: MW=1368; METHOD=ELECTROSPRAY.
CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC FAMILY.
KW Antibiotic; Amidation.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1370 MW; 3EF3402B9DF92338 CRC64;

Query Match 26.1%; Score 24; DB 13; Length 13;
Best Local Similarity 62.5%; Pred. No. 2.4e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LPVPGVLL 9
Db 2 LPVGVKLL 9

RESULT 6
Q9QYF6 ID Q9QYF6 PRELIMINARY; PRT; 11 AA.
AC Q9QYF6;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE PANCREAS TRANSCRIPTION FACTOR1 P48 SUBUNIT (FRAGMENT).
GN PTF1P48.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.


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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129SV;
RA Obata J., Mimura H., Goto T., Nakayama R., Kondo M., Oka C.,
RA Kawaichi M.;
RT "p48 subunit of mouse PTF1 binds to RBP-Jkappa/CBF-1, the
RT intracellular mediator of Notch signaling, and is expressed in the
RT neural tube of the early stage embryos.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB035674; BAA88247.1; -.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1327 MW; CA4662F8E3372732 CRC64;

Query Match 25.0%; Score 23; DB 11; Length 11;
Best Local Similarity 83.3%; Pred. No. 2.9e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 VLLKEF 12.
   |||||
Db 4 VLLKHF 9

RESULT 7
Q9BZ49
ID Q9BZ49 PRELIMINARY; PRT; 12 AA.
AC Q9BZ49;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE GLYCOPHORIN C (FRAGMENT).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Patel S.S., Mehlotra R.K., Kastens W., Mgone C.S., Kazura J.W.,
RA Zimmerman P.A.;
RT "The association of the glycoporphin C exon 3 deletion with
RT ovalocytosis and malaria susceptibility in the Wosera, Papua New
RT Guinea.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF342984; AAK01459.1; -.
FT NON_TER 1 1
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1361 MW; 2A07044DB8377378 CRC64;

Query Match 25.0%; Score 23; DB 4; Length 12;
Best Local Similarity 80.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLPVP 5
   |||
Db 7 PLPPP 11

RESULT 8
Q957T7
ID Q957T7 PRELIMINARY; PRT; 13 AA.
AC Q957T7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CYTOCHROME B (FRAGMENT).
OS Trichopsis pumila (pygmy gourami).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Anabantoidae; Belontiidae; Trichopsis.
```

```
OX NCBI_TaxID=158454;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang T.Y., Tzeng C.S., Shen S.C.;
RT "Conservation and Phylogeography of Taiwan Paradise Fish, Macropodus
RT opercularis Linnaeus.";
RL Acta Zool. Taiwanica 10:121-134(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Wang T.Y., Tzeng C.S., Shen S.C.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF359378; AAK51458.1; -.
KW Mitochondrion.
FT NON_TER 1 1
SQ SEQUENCE 13 AA; 1443 MW; 55430C67982AAB17 CRC64;

Query Match 25.0%; Score 23; DB 8; Length 13;
Best Local Similarity 66.7%; Pred. No. 3.5e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 PVPGV 8
   |||
Db 1 PVAGIL 6

RESULT 9
O69173
ID O69173 PRELIMINARY; PRT; 15 AA.
AC O69173;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PUTATIVE FERROCHELATASE HEMH (FRAGMENT).
GN HEMH.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RA Munier-Lehmann H.;
RT "Adenylate kinase from Yersinia pestis and Escherichia coli:
RT structural relatedness and differences linked to growth properties of
RT these two organisms.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065382; AAC17437.1; -.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1606 MW; C8763FC5C9CCF10B CRC64;

Query Match 25.0%; Score 23; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 4.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 PGVLL 9
   |||
Db 6 PGVLM 10

RESULT 10
Q28822
ID Q28822 PRELIMINARY; PRT; 15 AA.
AC Q28822;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE VOLTAGE-DEPENDENT DIHYDROPYRIDINE-SENSITIVE CALCIUM CHANNEL ALPHA 1
DE SUBUNIT 155 KDA ISOFORM (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
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[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92265303; PubMed=1316766;
RA Malouf N.N., McMahon D.K., Hainsworth C.N., Kay B.K.;
RT "A two-motif isoform of the major calcium channel subunit in skeletal
RT muscle.";
RL Neuron 8:899-906(1992).
DR EMBL; S36895; AAB22180.1; -.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1796 MW; 841B2DB08BFE99DB CRC64;

Query Match 25.0%; Score 23; DB 6; Length 15;
Best Local Similarity 62.5%; Pred. No. 4.1e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 VLLKEFTV 14
Db 2 VLLSLFTI 9

RESULT 11
Q96RT5
ID Q96RT5 PRELIMINARY; PRT; 16 AA.
AC Q96RT5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE TUBEROUS SCLEROSIS 1 (FRAGMENT).
GN TSC1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Fang L., Wu Z.Y., Wang N., MuRong S.X., Lin M.T., Chao D.R.,
RA Fang Z.M.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF274227; AAK60414.1; -.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1826 MW; 895C250451E3BBEE CRC64;

Query Match 25.0%; Score 23; DB 4; Length 16;
Best Local Similarity 55.6%; Pred. No. 4.4e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LPVPGVLLK 10
Db 7 LNTPGQLLR 15

RESULT 12
Q9TRU8
ID Q9TRU8 PRELIMINARY; PRT; 17 AA.
AC Q9TRU8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE LEUKEMIA INHIBITORY FACTOR, LIF=INHIBITOR OF AORTIC ENDOTHELIAL CELL
DE GROWTH.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=92115728; PubMed=1370585;
RA Ferrara N., Winer J., Henzel W.J.;
RT "Pituitary follicular cells secrete an inhibitor of aortic endothelial
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cell growth: identification as leukemia inhibitory factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:698-702(1992).
SQ SEQUENCE 17 AA; 1763 MW; BE06BF41F3A2BF94 CRC64;

Query Match 25.0%; Score 23; DB 6; Length 17;
Best Local Similarity 50.0%; Pred. No. 4.7e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLPVPGV 8
Db 2 PLPTPVV 9

RESULT 13
Q9IHJ0
ID Q9IHJ0 PRELIMINARY; PRT; 17 AA.
AC Q9IHJ0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE CORE PROTEIN 2C (FRAGMENT).
OS Human poliovirus 1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=12080;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2677USA81D23;
RX MEDLINE=20366294; PubMed=10906191;
RA Gavrillin G.V., Cherkasova E.A., Lipskaya G.Y., Kew O.M., Agol V.I.;
RT "Evolution of circulating wild poliovirus and of vaccine-derived
RT poliovirus in an immunodeficient patient: a unifying model.";
RL J. Virol. 74:7381-7390(2000).
DR EMBL; AF233165; AAF35069.1; -.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1826 MW; 6B3DEB222D713050 CRC64;

Query Match 25.0%; Score 23; DB 12; Length 17;
Best Local Similarity 55.6%; Pred. No. 4.7e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 9 LKEFTVSGN 17
Db 5 LKKFTEACN 13

RESULT 14
Q9IH19
ID Q9IH19 PRELIMINARY; PRT; 17 AA.
AC Q9IH19;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE CORE PROTEIN 2C (FRAGMENT).
OS Human poliovirus 1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=12080;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2677USA81D48;
RX MEDLINE=20366294; PubMed=10906191;
RA Gavrillin G.V., Cherkasova E.A., Lipskaya G.Y., Kew O.M., Agol V.I.;
RT "Evolution of circulating wild poliovirus and of vaccine-derived
RT poliovirus in an immunodeficient patient: a unifying model.";
RL J. Virol. 74:7381-7390(2000).
DR EMBL; AF233166; AAF35070.1; -.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1826 MW; 6B3DEB222D713050 CRC64;
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Query Match 25.0%; Score 23; DB 12; Length 17;
Best Local Similarity 55.6%; Pred. No. 4.7e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 9 LKEFTVSGN 17
||:|:| : |
Db 5 LKKFTEACN 13

RESULT 15
Q9IHI8 PRELIMINARY: PRT; 17 AA.
AC Q9IHI8;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE CORE-PROTEIN 2C (FRAGMENT).
OS Human poliovirus 1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=12080;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3038USA81D126;
RX MEDLINE=20366294; PubMed=10906191;
RA Gavrilin G.V., Cherkasova E.A., Lipskaya G.Y., Kew O.M., Agol V.I.;
RT "Evolution of circulating wild poliovirus and of vaccine-derived
RT poliovirus in an immunodeficient patient: a unifying model.";
RL J. Virol. 74:7381-7390(2000).
DR EMBL; AF233167; AAF35071.1; -.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1826 MW; 6B3DEB222D713050 CRC64;

Query Match 25.0%; Score 23; DB 12; Length 17;
Best Local Similarity 55.6%; Pred. No. 4.7e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 9 LKEFTVSGN 17
||:|:| : |
Db 5 LKKFTEACN 13

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:26:58 ; Search time 128.9 Seconds
(without alignments)
15.511 Million cell updates/sec

Title: US-09-165-546A-10
Perfect score: 92
Sequence: 1 PLPVPGVLLKEFTVSGNI 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 214377

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802:*
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2: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*
4: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*
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19: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1998.DAT:*
20: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
21: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92	100.0	18	AAU01541	HLA-DR53 recognisi
2	92	100.0	18	AAB69941	Human NY-ESO-1 HLA
3	82	89.1	16	AAE07779	Human NY ESO-1 pep
4	82	89.1	17	AAE07753	Human NY ESO-1 pep
5	80	87.0	16	AAE07754	Human NY ESO-1 rel
6	76	82.6	17	AAE07719	Human NY ESO-1 MHC
7	75	81.5	15	AAE07721	Human NY ESO-1 MHC
8	75	81.5	15	AAE07780	Human NY ESO-1 pep
9	72	78.3	16	AAE07720	Human NY ESO-1 MHC
10	71	77.2	14	AAE07722	Human NY ESO-1 MHC
11	71	77.2	14	AAE07781	Human NY ESO-1 pep

12	68	73.9	15	22	AAE07748	Human NY ESO-1 pep
13	64	69.6	13	22	AAE07723	Human NY ESO-1 MHC
14	64	69.6	13	22	AAE07782	Human NY ESO-1 pep
15	63	68.5	14	22	AAE07749	Human NY ESO-1 pep
16	60	65.2	12	22	AAE07724	Human NY ESO-1 MHC
17	60	65.2	12	22	AAE07783	Human NY ESO-1 pep
18	57	62.0	13	22	AAE07750	Human NY ESO-1 pep
19	57	62.0	18	22	AAE07769	Human NY ESO-1 HLA
20	57	62.0	18	22	AAU01540	HLA-DR53 recognisi
21	57	62.0	18	22	AAB69940	Human NY-ESO-1 HLA
22	53	57.6	11	22	AAE07725	Human NY ESO-1 MHC
23	53	57.6	11	22	AAE07784	Human NY ESO-1 pep
24	53	57.6	15	22	AAE07726	Human NY ESO-1 MHC
25	53	57.6	15	22	AAE07786	Human NY ESO-1 pep
26	52	56.5	10	20	AA05998	Human cancer antig
27	52	56.5	10	22	AAG67195	Cancer testis tumo
28	52	56.5	10	22	AAB69927	Human NY-ESO-1 HLA
29	52	56.5	12	22	AAE07751	Human NY ESO-1 pep
30	49	53.3	15	22	AAE07727	Human NY ESO-1 MHC
31	49	53.3	15	22	AAE07787	Human NY ESO-1 pep
32	47	51.1	10	22	AAE07730	Human NY ESO-1 MHC
33	47	51.1	10	22	AAE07785	Human NY ESO-1 pep
34	47	51.1	11	22	AAE07752	Human NY ESO-1 pep
35	47	51.1	12	22	AAE07716	Human NY ESO-1 MHC
36	45	48.9	9	20	AA06026	Human cancer antig
37	45	48.9	9	22	AAG67182	Cancer testis tumo
38	45	48.9	9	22	AAB69914	Human NY-ESO-1 HLA
39	45	48.9	14	22	AAE07728	Human NY ESO-1 MHC
40	45	48.9	14	22	AAE07788	Human NY ESO-1 pep
41	43	46.7	9	20	AA06027	Human cancer antig
42	43	46.7	10	22	AAG67197	Cancer testis tumo
43	43	46.7	10	22	AAG67203	Cancer testis tumo
44	43	46.7	10	22	AAB69929	Human NY-ESO-1 HLA
45	43	46.7	10	22	AAB69935	Human NY-ESO-1 HLA

ALIGNMENTS

RESULT 1
AAU01541
ID AAU01541 standard; Peptide; 18 AA.
XX
AC AAU01541;
XX
DT 18-JUL-2001 (first entry)
XX
DE HLA-DR53 recognising NY-ESO-1 peptide #3.
XX
KW NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
KW human leukocyte antigen-determining region; disease progression;
KW disease regression; disease onset; body tissue; body fluid; enzyme label;
KW radioactive label; monoclonal antibody.
XX Homo sapiens.
XX
PN WO200123560-A2.
XX
PD 05-APR-2001.
XX
PF 26-SEP-2000; 2000WO-US26411.
XX
PR 29-SEP-1999; 99US-0408036.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Tureci O, Sahin U, Pfreundschuh M;
XX
DR WPI; 2001-266156/27.
XX
PT polypeptides binding to major histocompatibility complex class II human
leukocyte antigen-determining region molecule having amino acid

PT sequence found in tumour rejection antigen precursor used for
PT stimulating proliferation of helper T cells -
XX Example 13; Page 19; 62pp; English.
PS
XX
CC The sequence represents a human NY-ESO-1 tumour rejection antigen
CC precursor fragment which recognises and binds to HLA-DR53. NY-ESO-1 and
CC SSX-2 polypeptides, or fragments of, bind to major histocompatibility
CC complex (MHC) Class II molecules such as human leukocyte
CC antigen-determining region (HLA-DR) molecules and stimulate proliferation
CC of helper T cells. The peptides can be administered to an HLA-DR positive
CC subject in order to stimulate the helper T cells. An MHC Class II
CC HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell or
CC present in free form is useful for this stimulation. The nucleic acid is
CC useful for screening for a cancerous condition, which involves contacting
CC a subject sample to a cell line transfected with the immunoreactive cell
CC (helper T cell), where interaction is indicative of cancer. In addition,
CC a sample from a patient (for example, a body fluid or tissue) can be
CC monitored for the amount of the complex present in the bloodstream. This
CC is useful for determining regression, progression or onset of a cancerous
CC condition. The method involves contacting the sample with a radioactive
CC labelled or enzyme labelled monoclonal antibody which specifically binds
CC with the complex.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 92; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
Db 1 plpvpgvllkeftvsgni 18

RESULT 2
AAB69941
ID AAB69941 standard; Peptide; 18 AA.
XX AAB69941;
AC
XX
DT 27-APR-2001 (first entry)
XX
DE Human NY-ESO-1 HLA-DR53 binding motif #3.
XX
KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW non-small cell lung carcinoma; tumour status determination.
XX
OS Homo sapiens.
XX
PN WO200107917-A1.
XX
PD 01-FEB-2001.
XX
PF 14-JUL-2000; 2000WO-US19220.
XX
PR 23-JUL-1999; 99US-0359503.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.
XX
PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
XX
DR WPI; 2001-182822/18.
XX
PT Method useful for determining the status (e.g. progression, regression
PT or stability of the disease) of a cancerous condition, involves
PT determining the levels of NY-ESO-1 specific antibodies in a sample
PT taken from a patient -
XX

PS Example 16; Page 27; 50pp; English.
XX
CC The present sequence is given in a specification relating to a method
CC for determining the status of a cancerous condition in a patient
CC with a tumour that expresses NY-ESO-1. The method comprises assaying a
CC sample taken from the patient for antibodies that specifically bind to
CC the NY-ESO-1 and comparing the value obtained to a prior value obtained
CC from assay of a prior sample taken from the patient. Any difference
CC between the values is indicative of a change in status of the cancerous
CC condition. The method is useful for determining whether a cancerous
CC condition is progressing, regressing or remaining stable, in particular
CC in patients receiving treatment for a melanoma, adenocarcinoma,
CC non-small cell lung carcinoma or bladder carcinoma.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 92; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSGNI 18
Db 1 plpvpgvllkeftvsgni 18

RESULT 3
AAE07779
ID AAE07779 standard; peptide; 16 AA.
XX
AC AAE07779;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human NY ESO-1 peptide #13 to characterise epitope recognised by TE4-1.
XX
KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.
XX
OS Homo sapiens.
XX
PN WO200155393-A2.
XX
PD 02-AUG-2001.
XX
PF 26-JAN-2001; 2001WO-US02765.
XX
PR 28-JAN-2000; 2000US-0179004.
PR 29-SEP-2000; 2000US-0237107.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang R, Rosenberg SA, Zeng G;
XX
DR WPI; 2001-496851/54.
XX
PT New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -
XX
PS Example 6; Fig 6A; 134pp; English.
XX
CC The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and

CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or haptens and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is human
CC NY ESO-1 peptide used in the characterisation of the NY ESO-1 epitope
CC recognised by TE4-1.
XX
SQ Sequence 16 AA;

Query Match 89.1%; Score 82; DB 22; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSG 16
| | | | | | | | | | | | | | | |
Db 1 plpvpgvllkeftvsg 16

RESULT 4
AAE07753
ID AAE07753 standard; peptide; 17 AA.
XX
AC AAE07753;
XX

DT 06-NOV-2001 (first entry)
XX Human NY ESO-1 peptide #6 to characterise epitope recognised by TE4-1.
DE
DE Human; major histocompatibility complex; MHC; vaccine; metastasis;
XX class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.
XX
OS Homo sapiens.
XX WO200155393-A2.
PN
XX 02-AUG-2001.
PD
XX 26-JAN-2001; 2001WO-US02765.
PF
XX 28-JAN-2000; 2000US-0179004.
PR
XX 29-SEP-2000; 2000US-0237107.
PR
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
XX Wang R, Rosenberg SA, Zeng G;
PI WPI; 2001-496851/54.
PI
XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis
PT
XX

PS Example 6; Fig 6A; 134pp; English.
XX
CC The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of

CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or haptens and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is human
CC NY ESO-1 peptide used in the characterisation of the NY ESO-1 epitope
CC recognised by TE4-1.
XX
SQ Sequence 17 AA;

Query Match 89.1%; Score 82; DB 22; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSG 16
| | | | | | | | | | | | | | | |
Db 2 plpvpgvllkeftvsg 17

RESULT 5
AAE07754
ID AAE07754 standard; peptide; 16 AA.
XX
AC AAE07754;
XX

DT 06-NOV-2001 (first entry)
XX Human NY ESO-1 related peptide.
DE
DE Human; major histocompatibility complex; MHC; vaccine; metastasis;
XX class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.
XX
OS Homo sapiens.
XX WO200155393-A2.
PN
XX 02-AUG-2001.
PD
XX 26-JAN-2001; 2001WO-US02765.
PF
XX 28-JAN-2000; 2000US-0179004.
PR
XX 29-SEP-2000; 2000US-0237107.
PR
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
XX Wang R, Rosenberg SA, Zeng G;
PI WPI; 2001-496851/54.
PI
XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis
PT
XX

PS Disclosure; Page 125; 134pp; English.
XX
CC The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any

CC given target antigen and/or hapten and to induce tumour-specific.
CC humoral-mediated immunity against cancer. The present sequence is human
CC NY ESO-1 related peptide.
XX
SQ Sequence 16 AA;

Query Match 87.0%; Score 80; DB 22; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.1e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVSG 16
|:||||||||||||||
Db 1 pipvpgvllkeftvsg 16

RESULT 6
AAE07719
ID AAE07719 standard; peptide; 17 AA.
XX
AC AAE07719;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human NY ESO-1 MHC class II restricted T cell epitope #5.
XX
KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.
XX
OS Homo sapiens.
XX
PN WO200155393-A2.
XX
PD 02-AUG-2001.
XX
PF 26-JAN-2001; 2001WO-US02765.
XX
PR 28-JAN-2000; 2000US-0179004.
PR 29-SEP-2000; 2000US-0237107.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang R, Rosenberg SA, Zeng G;
XX
DR WPI; 2001-496851/54.
XX
PT New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -
XX
PS Claim 4; Page 16; 134pp; English.
XX
CC The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC humoral-mediated immunity against cancer. The present sequence is MHC
CC class II restricted T cell epitope of human NY ESO-1 protein.

SQ Sequence 17 AA;

Query Match 82.6%; Score 76; DB 22; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTVS 15
||||||||||||||
Db 3 plpvpgvllkeftvs 17

RESULT 7
AAE07721
ID AAE07721 standard; peptide; 15 AA.
XX
AC AAE07721;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human NY ESO-1 MHC class II restricted T cell epitope #7.
XX
KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.
XX
OS Homo sapiens.
XX
PN WO200155393-A2.
XX
PD 02-AUG-2001.
XX
PF 26-JAN-2001; 2001WO-US02765.
XX
PR 28-JAN-2000; 2000US-0179004.
PR 29-SEP-2000; 2000US-0237107.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang R, Rosenberg SA, Zeng G;
XX
DR WPI; 2001-496851/54.
XX
PT New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -
XX
PS Claim 4; Page 16; 134pp; English.
XX
CC The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or hapten and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is MHC
CC class II restricted T cell epitope of human NY ESO-1 protein.

Query Match 81.5%; Score 75; DB 22; Length 15;

Best Local Similarity 100.0%; Pred. No. 2.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPVPGVLLKEFTVSG 16
| | | | | | | | | | | | | | | |
Db 1 lpvpvgvllkeftvsg 15

RESULT 8
AAE07780
ID AAE07780 standard; peptide; 15 AA.
XX
AC AAE07780;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human NY ESO-1 peptide #14 to characterise epitope recognised by TE4-1.
XX
KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
tumour-specific humoral-mediated immunity; cancer; cytostatic;
immunotherapy.
XX Homo sapiens.
OS
XX WO200155393-A2.
PN
PD 02-AUG-2001.
XX
PF 26-JAN-2001; 2001WO-US02765.
XX
PR 28-JAN-2000; 2000US-0179004.
XX
XX 29-SEP-2000; 2000US-0237107.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang R, Rosenberg SA, Zeng G;
XX WPI; 2001-496851/54.
DR
XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -
XX
PS Example 6; Fig 6A; 134pp; English.
XX
CC The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or hapten and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is human
CC NY ESO-1 peptide used in the characterisation of the NY ESO-1 epitope
XX recognised by TE4-1.
SQ Sequence 15 AA;

Query Match 81.5%; Score 75; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTV 14
| | | | | | | | | | | | | | | |
Db 3 plpvpvgvllkeftv 16

QY 2 LPVPGVLLKEFTVSG 16
| | | | | | | | | | | | | | | |
Db 1 lpvpvgvllkeftvsg 15

RESULT 9
AAE07720
ID AAE07720 standard; peptide; 16 AA.
XX
AC AAE07720;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human NY ESO-1 MHC class II restricted T cell epitope #6.
XX
KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
tumour-specific humoral-mediated immunity; cancer; cytostatic;
immunotherapy.
XX Homo sapiens.
OS
XX WO200155393-A2.
PN
PD 02-AUG-2001.
XX
PF 26-JAN-2001; 2001WO-US02765.
XX
PR 28-JAN-2000; 2000US-0179004.
PR 29-SEP-2000; 2000US-0237107.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
PI Wang R, Rosenberg SA, Zeng G;
XX WPI; 2001-496851/54.
DR
XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -
XX
PS Claim 4; Page 16; 134pp; English.
XX
CC The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or hapten and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is MHC
CC class II restricted T cell epitope of human NY ESO-1 protein.
XX
SQ Sequence 16 AA;

Query Match 78.3%; Score 72; DB 22; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.9e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFTV 14
| | | | | | | | | | | | | | | |
Db 3 plpvpvgvllkeftv 16

```

RESULT 10
AAE07722
ID AAE07722 standard; peptide; 14 AA.
XX
XX
AC AAE07722;
XX
XX
DT 06-NOV-2001 (first entry)
XX
XX
DE Human NY ESO-1 MHC class II restricted T cell epitope #8.
XX
KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.
XX
OS Homo sapiens.
XX
PN WO200155393-A2.
XX
PD 02-AUG-2001.
XX
PN WO200155393-A2.
XX
PD 02-AUG-2001.
XX
PF 26-JAN-2001; 2001WO-US02765.
XX
PR 28-JAN-2000; 2000US-0179004.
PR 29-SEP-2000; 2000US-0237107.
XX
PF 26-JAN-2001; 2001WO-US02765.
XX
PR 28-JAN-2000; 2000US-0179004.
PR 29-SEP-2000; 2000US-0237107.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang R, Rosenberg SA, Zeng G;
XX
PI WPI; 2001-496851/54.
XX
PT New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -
XX
PS Claim 4; Page 16; 134pp; English.
XX
CC The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or hapten and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is MHC
CC class II restricted T cell epitope of human NY ESO-1 protein.
XX
SQ Sequence 14 AA;

Query Match 77.2%; Score 71; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PVPGVLLKEFTVSG 16
   |||||
Db 1 pvpgvllkeftvsg 14

RESULT 11
AAE07781
ID AAE07781 standard; peptide; 14 AA.
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XX AAE07781;
XX
DT 06-NOV-2001 (first entry)
XX
XX
DE Human NY ESO-1 peptide #15 to characterise epitope recognised by TE4-1.
XX
KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.
XX
OS Homo sapiens.
XX
PN WO200155393-A2.
XX
PD 02-AUG-2001.
XX
PF 26-JAN-2001; 2001WO-US02765.
XX
PR 28-JAN-2000; 2000US-0179004.
PR 29-SEP-2000; 2000US-0237107.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang R, Rosenberg SA, Zeng G;
XX
PI WPI; 2001-496851/54.
XX
PT New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -
XX
PS Example 6; Fig 6A; 134pp; English.
XX
CC The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or hapten and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is human
CC NY ESO-1 peptide used in the characterisation of the NY ESO-1 epitope
CC recognised by TE4-1.
XX
SQ Sequence 14 AA;

Query Match 77.2%; Score 71; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PVPGVLLKEFTVSG 16
   |||||
Db 1 pvpgvllkeftvsg 14

RESULT 12
AAE07748
ID AAE07748 standard; peptide; 15 AA.
XX
XX AAE07748;
XX
```


DT 06-NOV-2001 (first entry)
XX Human NY ESO-1 peptide #1 to characterise epitope recognised by TE4-1.
DE
XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.
KW Homo sapiens.
XX WO200155393-A2.
XX 02-AUG-2001.
XX 26-JAN-2001; 2001WO-US02765.
XX 28-JAN-2000; 2000US-0179004.
PR 29-SEP-2000; 2000US-0237107.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA Wang R, Rosenberg SA, Zeng G;
XX WPI; 2001-496851/54.
PI New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -
XX Example 6; Fig 6A; 134pp; English.
PS The invention relates to the identification and isolation of major
XX histocompatibility (MHC) class II restricted T cell epitope (MHC-II
XX epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or haptens and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is human
CC NY ESO-1 peptide used in the characterisation of the NY ESO-1 epitope
XX recognised by TE4-1.
SQ Sequence 15 AA;

Query Match 73.9%; Score 68; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLPVPGVLLKEFT 13
Db 3 plpvpvgvllkeft 15

RESULT 13
AAE07723
ID AAE07723 standard; peptide; 13 AA.
XX AAE07723;
XX 06-NOV-2001 (first entry)
DT Human NY ESO-1 MHC class II restricted T cell epitope #9.
XX

XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.
XX Homo sapiens.
XX WO200155393-A2.
XX 02-AUG-2001.
XX 26-JAN-2001; 2001WO-US02765.
XX 28-JAN-2000; 2000US-0179004.
PR 29-SEP-2000; 2000US-0237107.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA Wang R, Rosenberg SA, Zeng G;
XX WPI; 2001-496851/54.
PI New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -
XX Claim 4; Page 16; 134pp; English.
PS The invention relates to the identification and isolation of major
XX histocompatibility (MHC) class II restricted T cell epitope (MHC-II
XX epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or haptens and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is MHC
CC class II restricted T cell epitope of human NY ESO-1 protein.
XX Sequence 13 AA;
SQ

Query Match 69.6%; Score 64; DB 22; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VPGVLLKEFTVSG 16
Db 1 vpgvllkeftvsg 13

RESULT 14
AAE07782
ID AAE07782 standard; peptide; 13 AA.
XX AAE07782;
XX 06-NOV-2001 (first entry)
DT Human NY ESO-1 peptide #16 to characterise epitope recognised by TE4-1.
XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;

KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
XX immunotherapy.
OS Homo sapiens.
XX WO200155393-A2.
PN 02-AUG-2001.
XX 26-JAN-2001; 2001WO-US02765.
PD 28-JAN-2000; 2000US-0179004.
XX 29-SEP-2000; 2000US-0237107.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA Wang R, Rosenberg SA, Zeng G;
XX WPI; 2001-496851/54.
PI New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
XX useful as immunogen and vaccine for inhibiting cancer in a mammal or as
XX protection from metastasis -
PT Example 6; Fig 6A; 134pp; English.
PS The invention relates to the identification and isolation of major
XX histocompatibility (MHC) class II restricted T cell epitope (MHC-II
XX epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
XX from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
XX antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
XX restricted. The products of the gene are promising candidates for
XX immunotherapeutic strategies for the prevention, treatment and diagnosis
XX of patients with cancer. The cancer epitopes are useful as immunogen and
XX vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
XX lymphocytes resulting in protection of the recipient from development of
XX cancer and protection from metastasis, or by inhibiting the growth of
XX cells expressing the NY-ESO-1 gene product. The cancer peptides are also
XX useful as diagnostic agent to detect the presence of cancer, to enhance
XX the generation of antibody and/or CD8+ T cell responses against any
XX given target antigen and/or haptens and to induce tumour-specific
XX humoral-mediated immunity against cancer. The present sequence is human
XX NY ESO-1 peptide used in the characterisation of the NY ESO-1 epitope
XX recognised by TE4-1.
SQ Sequence 13 AA;
Query Match 69.6%; Score 64; DB 22; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 VPGVLLKEFTVSG 16
Db 1 vpgvllkeftvsg 13
RESULT 15
AAE07749
ID AAE07749 standard; peptide; 14 AA.
XX AAE07749;
AC
XX 06-NOV-2001 (first entry)
DT
XX Human NY ESO-1 peptide #2 to characterise epitope recognised by TE4-1.
XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
XX immunotherapy.

OS Homo sapiens.
XX WO200155393-A2.
PN 02-AUG-2001.
XX 26-JAN-2001; 2001WO-US02765.
PD 28-JAN-2000; 2000US-0179004.
XX 29-SEP-2000; 2000US-0237107.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA Wang R, Rosenberg SA, Zeng G;
XX WPI; 2001-496851/54.
PI New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
XX useful as immunogen and vaccine for inhibiting cancer in a mammal or as
XX protection from metastasis -
PT Example 6; Fig 6A; 134pp; English.
PS The invention relates to the identification and isolation of major
XX histocompatibility (MHC) class II restricted T cell epitope (MHC-II
XX epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
XX from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
XX antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
XX restricted. The products of the gene are promising candidates for
XX immunotherapeutic strategies for the prevention, treatment and diagnosis
XX of patients with cancer. The cancer epitopes are useful as immunogen and
XX vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
XX lymphocytes resulting in protection of the recipient from development of
XX cancer and protection from metastasis, or by inhibiting the growth of
XX cells expressing the NY-ESO-1 gene product. The cancer peptides are also
XX useful as diagnostic agent to detect the presence of cancer, to enhance
XX the generation of antibody and/or CD8+ T cell responses against any
XX given target antigen and/or haptens and to induce tumour-specific
XX humoral-mediated immunity against cancer. The present sequence is human
XX NY ESO-1 peptide used in the characterisation of the NY ESO-1 epitope
XX recognised by TE4-1.
SQ Sequence 14 AA;
Query Match 68.5%; Score 63; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PLPVPVGVLKEF 12
Db 3 plpvpvgvllkef 14
Search completed: July 3, 2002, 11:26:58
Job time: 955 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 11:39:32 ; Search time 61.64 Seconds
(without alignments)
29.545 Million cell updates/sec

Title: US-09-165-546A-10
Perfect score: 92
Sequence: 1 PLPVPGVLLKEFTVSGNI 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 308740 seqs, 101176262 residues

Total number of hits satisfying chosen parameters: 45157

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	56.5	10	6 US-10-117-937-183	Sequence 183, App
2	52	56.5	10	6 US-10-117-937-191	Sequence 191, App
3	47	51.1	9	6 US-10-117-937-178	Sequence 178, App
4	47	51.1	10	6 US-10-117-937-179	Sequence 179, App
5	47	51.1	10	6 US-10-117-937-188	Sequence 188, App
6	45	48.9	9	6 US-10-117-937-182	Sequence 182, App
7	45	48.9	9	6 US-10-117-937-190	Sequence 190, App
8	43	46.7	9	6 US-10-117-937-187	Sequence 187, App
9	43	46.7	9	6 US-10-117-937-189	Sequence 189, App
10	40	43.5	8	6 US-10-117-937-180	Sequence 180, App
11	40	43.5	8	6 US-10-117-937-184	Sequence 184, App
12	35	38.0	9	5 US-09-344-040C-120	Sequence 120, App
13	35	38.0	10	6 US-10-117-937-186	Sequence 186, App
14	29	31.5	9	5 US-09-344-040C-125	Sequence 125, App
15	29	31.5	9	6 US-10-117-937-185	Sequence 185, App
16	28	30.4	7	5 US-09-563-286B-286	Sequence 286, App
17	28	30.4	7	5 US-09-563-286B-287	Sequence 287, App
18	28	30.4	8	6 US-10-044-844-52	Sequence 52, Appl
19	28	30.4	10	6 US-10-044-844-214	Sequence 214, App
20	28	30.4	11	1 PCT-US02-12753-1	Sequence 1, Appli
21	28	30.4	14	6 US-10-125-187-19	Sequence 19, Appl
22	28	30.4	14	6 US-10-125-187-20	Sequence 20, Appl
23	28	30.4	14	6 US-10-125-187-21	Sequence 21, Appl
24	28	30.4	14	6 US-10-125-187-53	Sequence 53, Appl
25	28	30.4	14	6 US-10-125-187-54	Sequence 54, Appl
26	28	30.4	14	6 US-10-125-187-55	Sequence 55, Appl

27	27	29.3	10	6 US-10-014-340-471	Sequence 471, App
28	27	29.3	12	6 US-10-027-961A-7	Sequence 7, Appli
29	27	29.3	18	6 US-10-012-034A-20	Sequence 20, Appl
30	26	28.3	12	4 US-08-945-917B-22	Sequence 22, Appl
31	26	28.3	16	6 US-10-014-340-491	Sequence 491, App
32	26	28.3	16	7 US-60-372-557-10	Sequence 10, Appl
33	26	28.3	17	5 US-09-563-286B-273	Sequence 273, App
34	26	28.3	18	6 US-10-012-034A-21	Sequence 21, Appl
35	25	27.2	9	6 US-10-067-632-42	Sequence 42, Appl
36	25	27.2	11	1 PCT-US02-09671-197	Sequence 197, App
37	25	27.2	15	6 US-10-139-841-43	Sequence 43, Appl
38	25	27.2	16	5 US-09-641-353B-7	Sequence 7, Appli
39	25	27.2	18	5 US-09-855-604-182	Sequence 182, App
40	25	27.2	18	5 US-09-855-604-244	Sequence 244, App
41	25	27.2	18	6 US-10-006-593-39	Sequence 39, Appl
42	25	27.2	18	6 US-10-006-593-66	Sequence 66, Appl
43	24	26.6	11	4 US-08-945-917B-17	Sequence 17, Appl
44	24	26.1	9	5 US-09-454-033-52	Sequence 52, Appl
45	24	26.1	10	5 US-09-436-469-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-10-117-937-183
; Sequence 183, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 183
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-183

Query Match 56.5%; Score 52; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 3 PVPGVLLKEF 12
Db 1 PVPGVLLKEF 10
|||||

RESULT 2
US-10-117-937-191
; Sequence 191, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937

; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 191
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-191

Query Match 56.5%; Score 52; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PVPGVLLKEF 12
Db 1 PVPGVLLKEF 10

RESULT 3
US-10-117-937-178
; Sequence 178, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-178

Query Match 51.1%; Score 47; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PLPVPGVLL 9
Db 1 PLPVPGVLL 9

RESULT 4
US-10-117-937-179
; Sequence 179, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLLIMM.027A

; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 179
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-179

Query Match 51.1%; Score 47; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PLPVPGVLL 9
Db 2 PLPVPGVLL 10

RESULT 5
US-10-117-937-188
; Sequence 188, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 188
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-188

Query Match 51.1%; Score 47; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 VLLKEFTVSG 16
Db 1 VLLKEFTVSG 10

RESULT 6
US-10-117-937-182
; Sequence 182, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES

; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/1117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 182
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-182

Query Match 48.9%; Score 45; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VPGVLLKEF 12
|||||
Db 1 VPGVLLKEF 9

RESULT 7
US-10-117-937-190
; Sequence 190, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 190
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-190

Query Match 48.9%; Score 45; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VPGVLLKEF 12
|||||
Db 1 VPGVLLKEF 9

RESULT 8
US-10-117-937-187
; Sequence 187, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong

; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/1117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 187
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-187

Query Match 46.7%; Score 43; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GVLLKEFTV 14
|||||
Db 1 GVLLKEFTV 9

RESULT 9
US-10-117-937-189
; Sequence 189, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 189
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-189

Query Match 46.7%; Score 43; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LLKEFTVSG 16
|||||
Db 1 LLKEFTVSG 9

RESULT 10
US-10-117-937-180
; Sequence 180, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping

```
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 180
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-180
```

```
Query Match      43.5%; Score 40; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 LPVPGVLL 9
      |||||
Db      1 LPVPGVLL 8
```

```
RESULT 11
US-10-117-937-184
; Sequence 184, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 184
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-184
```

```
Query Match      43.5%; Score 40; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 LPVPGVLL 9
      |||||
Db      1 LPVPGVLL 8
```

```
RESULT 12
US-09-344-040C-120
; Sequence 120, Application US/09344040C
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
```

```
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Deter.
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gen
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 120
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-120
```

```
Query Match      38.0%; Score 35; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      12 FTVSGNI 18
      |||||
Db      1 FTVSGNI 7
```

```
RESULT 13
US-10-117-937-186
; Sequence 186, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 186
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-186
```

```
Query Match      38.0%; Score 35; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      12 FTVSGNI 18
      |||||
Db      1 FTVSGNI 7
```

```
RESULT 14
US-09-344-040C-125
; Sequence 125, Application US/09344040C
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
```


APPLICANT: Ramensee, Hans Georg
APPLICANT: Stevanovic, Stefan
TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determining Expression of an SSX Gene, Peptides Derived From Said SSX Gene and Uses Thereof
FILE REFERENCE: LUD 5556.1
CURRENT APPLICATION NUMBER: US/09/344,040C
CURRENT FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 09/105,839
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 08/851,130
PRIOR FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 132
SEQ ID NO 125
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-344-040C-125

Query Match 31.5%; Score 29; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 TVSGNI 18
Db 1 TVSGNI 6

RESULT 15
US-10-117-937-185
Sequence 185, Application US/10117937
GENERAL INFORMATION:
APPLICANT: CTL IMMUNO THERAPIES CORP.
APPLICANT: SIMARD, John, J.L.
APPLICANT: DIAMOND, David, C.
APPLICANT: LIU, Liping
APPLICANT: XIE, Zhidong
TITLE OF INVENTION: EPITOPE SEQUENCES
FILE REFERENCE: CTLIMM.027A
CURRENT APPLICATION NUMBER: US/10/117,937
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/282,211
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/337,017
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: US 60/363,210
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 602
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 185
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-10-117-937-185

Query Match 31.5%; Score 29; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 TVSGNI 18
Db 1 TVSGNI 6

Search completed: July 3, 2002, 11:39:32
Job time: 883 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:28:57 ; Search time 57.51 Seconds
(without alignments)
30.075 Million cell updates/sec

Title: US-09-165-546A-11
Perfect score: 105
Sequence: 1 GAASGLNGCCRCGARGPE 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 3210

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	34.5	32.9	16	2	A59042	alpha-conotoxin Ep
2	33.5	31.9	16	2	A54877	alpha-conotoxin Pn
3	33	31.4	11	2	T06383	hypothetical prote
4	32	30.5	16	2	PH1790	T cell receptor al
5	30	28.6	11	2	PT0214	T-cell receptor be
6	29	27.6	13	2	A61210	antibiotic GE2270
7	28.5	27.1	12	1	A53709	alpha-conotoxin Im
8	28	26.7	18	2	C59089	theta defensin-1 -
9	27.5	26.2	16	2	B54877	alpha-conotoxin Pn
10	27	25.7	14	2	PH1306	Ig heavy chain DJ
11	26.5	25.2	13	2	PH1309	Ig heavy chain DJ
12	25	23.8	7	2	PT0663	T-cell receptor be
13	25	23.8	15	2	D48394	major fat-globule
14	25	23.8	17	2	S15778	insulin chain B -
15	25	23.8	17	2	S16929	flavodoxin A - Azo
16	25	23.8	17	2	PH1331	Ig heavy chain DJ
17	24	22.9	5	2	A33882	cadmium-binding pe
18	24	22.9	7	2	B33882	cadmium-binding he
19	24	22.9	13	2	PH0805	T-cell receptor al
20	24	22.9	14	2	PH1305	Ig heavy chain DJ
21	24	22.9	14	2	PH0804	T-cell receptor al
22	24	22.9	15	2	B59045	alpha-conotoxin Au
23	24	22.9	16	2	A59046	alpha-conotoxin MI
24	24	22.9	16	2	C59045	alpha-conotoxin Au
25	24	22.9	16	2	A59045	alpha-conotoxin Au
26	24	22.9	16	2	JQ2306	hypothetical 1.7K
27	24	22.9	16	2	JQ2316	hypothetical 1.7K
28	24	22.9	16	4	I79565	hypothetical TGL3/
29	23	21.9	10	2	PT0632	T-cell receptor be

30	23	21.9	13	2	A28953	alpha-conotoxin SI
31	23	21.9	13	2	JH0460	corticostatic pept
32	23	21.9	14	2	A17150	glucose 1-dehydrog
33	23	21.9	15	2	PH1310	Ig heavy chain DJ
34	23	21.9	16	2	PH1580	Ig H chain V-D-J r
35	23	21.9	17	2	E40442	integrase homolog
36	22	21.0	8	2	S59622	metallothionein is
37	22	21.0	10	2	S26506	collagen alpha 1(V
38	22	21.0	12	2	PN0162	malate dehydrogena
39	22	21.0	12	2	PH1181	T-cell receptor al
40	22	21.0	13	1	NTKN2G	alpha-conotoxin GI
41	22	21.0	13	1	NTKNAS	alpha-conotoxin SI
42	22	21.0	14	1	NTKNLM	alpha-conotoxin MI
43	22	21.0	14	2	A58963	alpha-conotoxin Cn
44	22	21.0	14	2	PH0765	T-cell receptor be
45	22	21.0	15	1	NTKNAG	alpha-conotoxin GI

ALIGNMENTS

RESULT 1
A59042
alpha-conotoxin Epi - cone shell (Conus episcopatus)
C;Species: Conus episcopatus (bishop's cone)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 13-Aug-1999
C;Accession: A59042
R;Loughnan, M.; Bond, T.; Atkins, A.; Cuevas, J.; Adams, D.J.; Broxton, N.M.; Livett, J. Biol. Chem. 273, 15667-15674, 1998
A;Title: Alpha-conotoxin EPI, a novel sulfated peptide from Conus episcopatus that se
A;Reference number: A59042; MUID:98288307
A;Accession: A59042
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 <LOU>
C;Superfamily: alpha-conotoxin
C;Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neu
F;1-16/Product: alpha-conotoxin EPI #status experimental <NAT>
F;2-8,3-16/Disulfide bonds: #status experimental
F;15/Binding site: sulfate (Tyr) (covalent) #status experimental
F;16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 32.9%; Score 34.5; DB 2; Length 16;
Best Local Similarity 42.9%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 3; Gaps 1;
QY 8 GCC---RCGARGPE 18
||| || |:
Db 1 GCCSDPRCNMNNPD 14
RESULT 2
A54877
alpha-conotoxin PnIA [validated] - cone shell (Conus pennaceus)
N;Alternate names: alpha-CTX-PnIA
C;Species: Conus pennaceus
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 15-Sep-2000
C;Accession: A54877
R;Fainzilber, M.; Hasson, A.; Oren, R.; Burlingame, A.L.; Gordon, D.; Spira, M.E.; Zl
Biochemistry 33, 9523-9529, 1994
A;Title: New mollusc-specific alpha-conotoxins block Aplysia neuronal acetylcholine r
A;Reference number: A54877; MUID:94347719
A;Accession: A54877
A;Molecule type: protein
A;Residues: 1-16 <FAI>
R;Hu, S.H.; Gehrmann, J.; Guddat, L.W.; Alewood, P.F.; Craik, D.J.; Martin, J.L.
submitted to the Brookhaven Protein Data Bank, January 1996
A;Reference number: A66355; PDB:IPEN
A;Contents: annotation; X-ray crystallography, 1.1 angstroms; residues 1-16
C;Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsyn
C;Superfamily: alpha-conotoxin
C;Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neu

F;2-8,3-16/Disulfide bonds: #status experimental
F;16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 31.9%; Score 33.5; DB 2; Length 16;
Best Local Similarity 42.9%; Pred. No. 2.7e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

QY 8 GCCR---CGARGPE 18
||| | | | |
Db 1 GCCSLPPCAANNPD 14

RESULT 3
T06383
hypothetical protein - soybean
C;Species: Glycine max (soybean)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-May-2000
C;Accession: T06383
R;Dewey, R.E.; Wilson, R.F.; Novitzky, W.P.; Goode, J.H.
Plant Cell 6, 1495-1507, 1994
A;Title: The AAPt1 gene of soybean complements a cholinephosphotransferase-deficient mutant
A;Reference number: Z06169; MUID:95086383
A;Accession: T06383
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-11 <DEW>
A;Cross-references: EMBL:U12735; NID:g530086; PIDN:AAA67718.1; PID:g530087
A;Experimental source: strain Dare; seed

Query Match 31.4%; Score 33; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CCRCGA 14
|||| |
Db 6 CCRCEA 11

RESULT 4
PH1790
T cell receptor alpha chain V region (clone 2PBL V alpha 24-6) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: PH1790
R;Porcellini, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A;Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood lymphocytes

A;Reference number: PH1754; MUID:93301585
A;Accession: PH1790
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-16 <POR>

Query Match 30.5%; Score 32; DB 2; Length 16;
Best Local Similarity 83.3%; Pred. No. 4.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CGARGP 17
|| |||
Db 3 CGERGP 8

RESULT 5
PT0214
T-cell receptor beta chain V-J region (4-1-L.6) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
C;Accession: PT0214
R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991
A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not rest
A;Reference number: PT0209; MUID:91217621
A;Accession: PT0214
A;Molecule type: mRNA
A;Residues: 1-11 <NAK>
C;Keywords: T-cell receptor

Query Match 28.6%; Score 30; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CGARG 16
|||||
Db 1 CGARG 5

RESULT 6
A61210
antibiotic GE2270 - Planobispora rosea (ATCC 53773)
C;Species: Planobispora rosea
C;Date: 13-May-1994 #sequence_revision 05-Apr-1995 #text_change 07-May-1999
C;Accession: A61210
R;Kettenring, J.; Colombo, L.; Ferrari, P.; Tavecchia, P.; Nebuloni, M.; Vekey, K.; G
J. Antibiot. 44, 702-715, 1991
A;Title: Antibiotic GE2270 A: a novel inhibitor of bacterial protein synthesis. II. S
A;Reference number: A61210; MUID:91349090
A;Accession: A61210
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-13 <KEP>
C;Keywords: amidated carboxyl end; methylated amino acid; oxazole/thiazole ring
F;1-10/Cross-link: thiazole amino end (Cys-Lys) (by 10-C6) #status experimental
F;2-3/Cross-link: 5-methoxythiazole (Val-Cys) #status experimental
F;4-5/Cross-link: 5-methylthiazole (Asn-Cys) #status experimental
F;4/Modified site: N4-methylasparagine (Asn) #status experimental
F;7-8/Cross-link: thiazole (Phe-Cys) #status experimental
F;7/Modified site: 3-hydroxyphenylalanine (Phe) #status experimental
F;8-9/Cross-link: thiazole (Cys-Cys) #status experimental
F;9-10/Cross-link: pyridine (Cys-Lys) #status experimental
F;10-11/Cross-link: thiazole (Lys-Cys) #status experimental
F;11-12/Cross-link: 2-oxazoline (Cys-Ser) #status experimental
F;13/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 27.6%; Score 29; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 9.2e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 CCRC 12
||:|
Db 8 CCKC 11

RESULT 7
A53709
alpha-conotoxin ImI - cone shell (Conus imperialis)
N;Alternate names: alpha-Ctx-ImI
C;Species: Conus imperialis (imperial cone)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A53709
R;McIntosh, J.M.; Yoshikami, D.; Mahe, E.; Nielsen, D.B.; Rivier, J.E.; Gray, W.R.; O
J. Biol. Chem. 269, 16733-16739, 1994
A;Title: A nicotinic acetylcholine receptor ligand of unique specificity, alpha-conot
A;Reference number: A53709; MUID:94266889
A;Accession: A53709
A;Molecule type: protein
A;Residues: 1-12 <MCI>
A;Note: structure confirmed by chemical synthesis
A;Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsyn
C;Superfamily: alpha-conotoxin
C;Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neu

F;2-8,3-12/Disulfide bonds: #status experimental
F;12/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 27.1%; Score 28.5; DB 1; Length 12;
Best Local Similarity 54.5%; Pred. No. 1e+03;
Matches 6; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

QY 8 GCC---RCGAR 15
||| || |
Db 1 GCCSDPRCAWR 11

RESULT 8
C59089
theta defensin-1 - rhesus macaque
N;Alternate names: RTD-1
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: C59089
R;Tang, Y.Q.; Yuan, J.; Osapay, G.; Osapay, K.; Tran, D.; Miller, C.J.; Ouellette, A.J.;
Science 286, 498-502, 1999
A;Title: A cyclic antimicrobial peptide produced in primate leukocytes by the ligation o
A;Reference number: A59089; MUID:99453140
A;Accession: C59089
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-18 <SEL>
A;Note: this sequence is cyclically permuted by -6 residues from the sequence presented
C;Comment: For the two contributing precursor sequences, see PIR:A59089 and PIR:B59089.
C;Keywords: antibacterial; antibiotic; antifungal; leukocyte; protein splicing
F;1-9/Region: theta defensin 1a-derived
F;10-18/Region: theta defensin 1b-derived
F;1-18/Cross-link: cyclopeptide (Arg-Cys) #status experimental
F;2-11,4-9,13-18/Disulfide bonds: #status experimental
F;9-10/Cross-link: cyclopeptide (Cys-Arg) #status experimental

Query Match 26.7%; Score 28; DB 2; Length 18;
Best Local Similarity 62.5%; Pred. No. 1.6e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 GCCRCGAR 15
| ||| |
Db 7 GFCRCLCR 14

RESULT 9
B54877
alpha-conotoxin PnIB - cone shell (Conus pennaceus)
C;Species: Conus pennaceus
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-May-1997
C;Accession: B54877
R;Fainzilber, M.; Hasson, A.; Oren, R.; Burlingame, A.L.; Gordon, D.; Spira, M.E.; Zlotk
Biochemistry 33, 9523-9529, 1994
A;Title: New mollusc-specific alpha-conotoxins block Aplysia neuronal acetylcholine rece
A;Reference number: A54877; MUID:94347719
A;Accession: B54877
A;Molecule type: protein.
A;Residues: 1-16 <FAI>
C;Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynapt
C;Superfamily: alpha-conotoxin
C;Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro
F;2-8,3-16/Disulfide bonds: #status experimental
F;16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 26.2%; Score 27.5; DB 2; Length 16;
Best Local Similarity 35.7%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 5; Indels 3; Gaps 1;

QY 8 GCCR---CGARGPE 18
||| | |

Db 1 GCCSLPPCALSNPD 14

RESULT 10
PH1306

Ig heavy chain DJ region (clone C96-100) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PH1306
R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A;Title: Predominance of fetal type DJH joining in young children with B precursor ly
A;Reference number: PH1302; MUID:93094761
A;Accession: PH1306
A;Molecule type: DNA
A;Residues: 1-14 <WAS>
C;Keywords: heterotetramer; immunoglobulin

Query Match 25.7%; Score 27; DB 2; Length 14;
Best Local Similarity 53.8%; Pred. No. 1.8e+03;
Matches 7; Conservative 0; Mismatches 4; Indels 2; Gaps 1;

QY 7 NGCC--RCGARGP 17
|| | ||| |
Db 2 NGVCYTTTGAREP 14

RESULT 11
PH1309

Ig heavy chain DJ region (clone C770-101) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PH1309
R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A;Title: Predominance of fetal type DJH joining in young children with B precursor ly
A;Reference number: PH1302; MUID:93094761
A;Accession: PH1309
A;Molecule type: DNA
A;Residues: 1-13 <WAS>
C;Keywords: heterotetramer; immunoglobulin

Query Match 25.2%; Score 26.5; DB 2; Length 13;
Best Local Similarity 54.5%; Pred. No. 2e+03;
Matches 6; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

QY 10 CRC---GARGP 17
| | ||| |
Db 3 CACPTTGARDP 13

RESULT 12
PT0663

T-cell receptor beta chain V-D-J region (121-3L) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0663
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0663
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-7 <FEE>
A;Experimental source: day 4 postnatal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 23.8%; Score 25; DB 2; Length 7;
Best Local Similarity 71.4%; Pred. No. 2.8e+05;

Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 2 AASGLNG 8
|:|:|:| I
Db 1 ASSGLGG 7

RESULT 13
D48394
major fat-globule membrane protein GP 55 - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997
C;Accession: D48394
R;Mather, I.H.; Banghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
II-like sequences.
A;Reference number: A48394; MUID:93250576
A;Accession: D48394
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <MAT>
A;Experimental source: milk
A;Note: sequence extracted from NCBI backbone (NCBIP:131448)
C;Superfamily: milk fat globule protein; discoidin I amino-terminal homology; EGF homolo

Query Match 23.8%; Score 25; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LNGC 9
|:|:|:|
Db 8 LNGC 11

RESULT 14
S15778
insulin chain B - bovine (fragments)
C;Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: S15778; S15779
R;Bergman, T.; Agerberth, B.; Joernvall, H.
FEBS Lett. 283, 100-103, 1991
A;Title: Direct analysis of peptides and amino acids from capillary electrophoresis.
A;Reference number: S15778; MUID:91243852
A;Accession: S15778
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <FEB1>
A;Accession: S15779
A;Status: preliminary
A;Molecule type: protein
A;Residues: 9-17 <FEB2>
C;Superfamily: insulin
C;Keywords: hormone; pancreas

Query Match 23.8%; Score 25; DB 2; Length 17;
Best Local Similarity 80.0%; Pred. No. 3.8e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CGARG 16
|:|:|:|
Db 6 CGERG 10

RESULT 15
S16929
flavodoxin A - Azotobacter chroococcum (fragment)
N;Alternate names: AcF1dA
C;Species: Azotobacter chroococcum
C;Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999

C;Accession: S16929
R;Bagby, S.; Barker, P.D.; Hill, H.A.O.; Sanghera, G.S.; Dunbar, B.; Ashby, G.A.; Ead
Biochem. J. 277, 313-319, 1991
A;Title: Direct electrochemistry of two genetically distinct flavodoxins isolated fro
A;Reference number: S16929; MUID:91315397
A;Accession: S16929
A;Molecule type: protein
A;Residues: 1-17 <BAG>
A;Experimental source: strain MCD1155
C;Function:
A;Description: acts as an electron donor to the Mo-containing nitrogenase
C;Keywords: electron transfer; flavoprotein; FMN

Query Match 23.8%; Score 25; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 3.8e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAASGLNG 8
|:|:|:| I
Db 8 GSSSGVTG 15.

Search completed: July 3, 2002, 11:28:57
Job time: 398 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:41:55 ; Search time 27.94 Seconds
(without alignments)
24.945 Million cell updates/sec

Title: US-09-165-546A-11
Perfect score: 105
Sequence: 1 GAASGLNGCCRCGARGPE 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 923

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	34.5	32.9	16	1 CXA1_CONEP	P56638 conus episc
2	33.5	31.9	16	1 CXAA_CONPE	P50984 conus penna
3	29.5	28.1	15	1 CXA2_CONAL	P56640 conus aulic
4	28.5	27.1	12	1 CXA1_CONIM	P50983 conus imper
5	27.5	26.2	16	1 CXAB_CONPE	P50985 conus penna
6	25	23.8	15	1 TAI1_TREBR	P34070 tremella br
7	25	23.8	17	1 FLAW_AZOCH	P23002 azotobacter
8	24	22.9	16	1 CXA1_CONAL	P56639 conus aulic
9	24	22.9	16	1 CXA2_CONMA	P56636 conus magus
10	24	22.9	16	1 CXA3_CONAL	P56641 conus aulic
11	23	21.9	13	1 CXA1_CONST	P15471 conus stria
12	23	21.9	15	1 DIDH_PSESP	P80701 pseudomonas
13	22	21.0	12	1 PVK2_PERAM	P81555 periplaneta
14	22	21.0	13	1 CXA2_CONGE	P01520 conus geogr
15	22	21.0	13	1 CXAA_CONST	P28878 conus stria
16	22	21.0	14	1 CXA1_CONCN	P56973 conus conso
17	22	21.0	14	1 CXA1_CONMA	P01521 conus magus
18	22	21.0	15	1 CX1B_CONBE	P58624 conus betul
19	22	21.0	15	1 CXA1_CONGE	P01519 conus geogr
20	22	21.0	16	1 BAI1_EUBSP	P32371 eubacterium
21	21.5	20.5	18	1 CXA1_CONER	P50982 conus ermin
22	21	20.0	12	1 RR16_GINBI	P36207 ginkgo bilo
23	21	20.0	13	1 CXET_CONTE	P81755 conus texti
24	21	20.0	15	1 UC06_MAIZE	P80612 zea mays (m
25	21	20.0	17	1 RUBR_CHLTE	P58025 chlorobium
26	20	19.0	14	1 CX1A_CONBE	P58623 conus betul
27	19	18.1	12	1 TAI0_TREME	P01371 tremella me
28	19	18.1	14	1 SAP2_ARBPU	P11760 arabacia pun
29	19	18.1	14	1 UC04_MAIZE	P80610 zea mays (m
30	19	18.1	17	1 ITHB_HIRME	P28502 hirudo medi
31	19	18.1	18	1 AGI_EUPCH	P33888 euphorbia c
32	19	18.1	18	1 AGI_EUPMA	P33889 euphorbia m
33	18	17.1	9	1 DSIP_RABIT	P01158 oryctolagus

34	18	17.1	10	1 TRP8_LEUMA	P81740 leucophaea
35	18	17.1	11	1 PVK1_PERAM	P41837 periplaneta
36	18	17.1	12	1 FRE1_LITIN	P82021 litoria inf
37	18	17.1	13	1 BPPL_BOTJA	P01020 bothrops ja
38	18	17.1	15	1 ESTB_SCHGA	P81011 schizaphis
39	18	17.1	17	1 PATS_ANASP	O52748 anabaena sp
40	18	17.1	18	1 HSTB_ECOLI	P01560 escherichia
41	18	17.1	18	1 SODM_MYCHA	P80582 mycobacteri
42	17.5	16.7	17	1 LCK_RAT	Q01621 rattus norv
43	17	16.2	8	1 VGLG_HSV2B	P81780 herpes simp
44	17	16.2	9	1 OXYA_SCYCA	P42996 scylliorhinu
45	17	16.2	9	1 OXYA_SQUAC	P42999 squalus aca

ALIGNMENTS

RESULT 1

CXAA_CONEP
ID CXA1_CONEP STANDARD; PRT; 16 AA.
AC P56638;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-conotoxin Epi.
OS Conus episcopatus (Bishop's cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=88764;
RN [1]
RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
RX MEDLINE=98376423; PubMed=9708977;
RA Hu S.H., Loughnan M., Miller R., Weeks C.M., Blessing R.H.,
RA Alewood P.F., Lewis R.J., Martin J.L.;
RT "The 1.1-A resolution crystal structure of [Tyr15]Epi, a novel
RT alpha-conotoxin from Conus episcopatus, solved by direct methods.";
RL Biochemistry 37:11425-11433(1998).
CC -!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC
CC ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-2 AND ALPHA-
CC 3/BETA-4 SUBUNITS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE ALPHA-TYPE CONOTOXIN FAMILY.
DR PDB; 1A0M; 13-JAN-99.
KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
KW Venom; Sulfation; 3D-structure.
FT DISULFID 2 8
FT DISULFID 3 16
FT MOD_RES 15 15 SULFATION.
FT MOD_RES 16 16 AMIDATION.
SQ SEQUENCE 16 AA; 1792 MW; C63385F376C99B4C CRC64;

Query Match 32.9%; Score 34.5; DB 1; Length 16;
Best Local Similarity 42.9%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

QY 8 GCC---RCGARGPE 18

||| || |

Db 1 GCCSDPRCNMNPD 14

RESULT 2

CXAA_CONEP
ID CXAA_CONPE STANDARD; PRT; 16 AA.
AC P50984;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-conotoxin PnIA.
OS Conus pennaceus (Feathered cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;


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OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=37335;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=94347719; PubMed=8058627;
RA Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D.,
RA Spira M.E., Zlotkin E.;
RT "New mollusc-specific alpha-conotoxins block Aplysia neuronal
RT acetylcholine receptors.";
RL Biochemistry 33:9523-9529(1994).
RN [2]
RP SULFATION OF TYR-15.
RX MEDLINE=99242956; PubMed=10226369;
RA Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M.,
RA Baldwin M.A., Burlingame A.L.;
RT "Identification of tyrosine sulfation in Conus pennaceus conotoxins
RT alpha-PnIA and alpha-PnIB: further investigation of labile sulfo- and
RT phosphopeptides by electrospray, matrix-assisted laser
RT desorption/ionization (MALDI) and atmospheric pressure MALDI mass
RT spectrometry.";
RL J. Mass Spectrom. 34:447-454(1999).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
RX MEDLINE=96311277; PubMed=8740364;
RA Hu S.-H., Gehrmann J., Guddat L.W., Alewood P.F., Craik D.J.,
RA Martin J.L.;
RT "The 1.1 A crystal structure of the neuronal acetylcholine receptor
RT antagonist, alpha-conotoxin PnIA from Conus pennaceus.";
RL Structure 4:417-423(1996).
CC -!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM. IN CONTRAST TO OTHER ALPHA-CONOTOXINS, WHICH ARE
CC SELECTIVE FOR VERTEBRATE SKELETAL MUSCLE NACHR, THE CONUS
CC PENNACEUS ALPHA-CONOTOXINS BLOCK NACHR IN MOLLUSCS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE ALPHA-TYPE CONOTOXIN FAMILY.
CC PDB; IPEN; 2I-APR-97.
DR Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
KW Sulfation; Venom; 3D-structure.
KW DISULFID 2 8
FT DISULFID 3 16
FT DISULFID 15 15 SULFATION.
FT MOD_RES 16 16 AMIDATION.
SQ SEQUENCE 16 AA; 1628 MW; 05310FF95EC99005 CRC64;

Query Match 31.9%; Score 33.5; DB 1; Length 16;
Best Local Similarity 42.9%; Pred. No. 64;
Matches 6; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

QY 8 GCCR---CGARGPE 18
   ||| | | |
Db 1 GCCSLPPCAANNPD 14

RESULT 3
CXA2_CONAL
ID CXA2_CONAL STANDARD; PRT; 15 AA.
AC P56640;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-conotoxin AuIB.
OS Conus aulicus (Court cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89437;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Venom;
RX MEDLINE=99003392; PubMed=9786965;
RA Luč.S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D.,
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RA Olivera B.M., McIntosh J.M.;
RT "Alpha-conotoxin AuIB selectively blocks alpha3 beta4 nicotinic
RT acetylcholine receptors and nicotine-evoked norepinephrine release.";
RL J. Neurosci. 18:8571-8579(1998).
CC -!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC
CC ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-4 SUBUNITS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1572.5; METHOD=Electrospray.
CC -!- SIMILARITY: BELONGS TO THE ALPHA-TYPE CONOTOXIN FAMILY.
KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
KW Venom.
FT DISULFID 2 8
FT DISULFID 3 15
FT MOD_RES 15 15 AMIDATION.
SQ SEQUENCE 15 AA; 1578 MW; 84EFE95FDC700155 CRC64;

Query Match 28.1%; Score 29.5; DB 1; Length 15;
Best Local Similarity 42.9%; Pred. No. 2.2e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

QY 8 GCCR---CGARGPE 18
   ||| | | |
Db 1 GCCSYPPCFATNPD 14

RESULT 4
CXAL_CONIM
ID CXAL_CONIM STANDARD; PRT; 12 AA.
AC P50983;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-conotoxin ImI.
OS Conus imperialis (Imperial cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=35631;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Venom;
RX MEDLINE=94266889; PubMed=8206995;
RA McIntosh J.M., Yoshikami D., Mahe E., Nielsen D.B., Rivier J.E.,
RA Gray W.R., Olivera B.M.;
RT "A nicotinic acetylcholine receptor ligand of unique specificity,
RT alpha-conotoxin ImI.";
RL J. Biol. Chem. 269:16733-16739(1994).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=95379776; PubMed=7651351;
RA Johnson D.S., Martinez J., Elgoyhen A.B., Heinemann S.F.,
RA McIntosh J.M.;
RT "Alpha-conotoxin ImI exhibits subtype-specific nicotinic
RT acetylcholine receptor blockade: preferential inhibition of homomeric
RT alpha 7 and alpha 9 receptors.";
RL Mol. Pharmacol. 48:194-199(1995).
RN [3]
RP STRUCTURE BY NMR.
RX MEDLINE=99212205; PubMed=10194298;
RA Rogers J.P., Luginbuhl P., Shen G.S., McCabe R.T., Stevens R.C.,
RA Wemmer D.E.;
RT "NMR solution structure of alpha-conotoxin ImI and comparison to
RT other conotoxins specific for neuronal nicotinic acetylcholine
RT receptors.";
RL Biochemistry 38:3874-3882(1999).
RN [4]
RP STRUCTURE BY NMR.
RX MEDLINE=99158061; PubMed=10050774;
RA Maslennikov I.V., Shenkarev Z.O., Zhmak M.N., Ivanov V.T.,
RA Methfessel C., Tsetlin V.I., Arseniev A.S.;
RT "NMR spatial structure of alpha-conotoxin ImI reveals a common
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RT scaffold in snail and snake toxins recognizing neuronal nicotinic
RT acetylcholine receptors.";
RL FEBS Lett. 444:275-280(1999).
RN [5]
RP STRUCTURE BY NMR.
RX MEDLINE=99324017; PubMed=10395477;
RA Gehrman J., Daly N.L., Alewood P.F., Craik D.J.;
RT "Solution structure of alpha-conotoxin IMI by 1H nuclear magnetic
RT resonance.";
RL J. Med. Chem. 42:2364-2372(1999).
CC -!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM. IT IS HIGHLY ACTIVE AGAINST THE NEUROMUSCULAR
CC RECEPTOR IN FROG BUT NOT IN MICE. IN CONTRAST, IT INDUCES SEIZURES
CC WHEN INJECTED CENTRALLY IN MICE AND RATS. IT TARGETS NEURONAL
CC NACHRS IN MAMMALS. BLOCKS HOMOMERIC ALPHA-7 NICOTINIC RECEPTORS
CC WITH THE HIGHEST APPARENT AFFINITY AND HOMOMERIC ALPHA-9 RECEPTORS
CC WITH 8-FOLD LOWER AFFINITY. HAS NO EFFECT ON RECEPTORS COMPOSED OF
CC ALPHA-2/BETA-2, ALPHA-3/BETA-2, ALPHA-4/BETA-2, ALPHA-2/BETA-4,
CC ALPHA-3/BETA-4, OR ALPHA-4/BETA-4 SUBUNIT COMBINATIONS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE ALPHA-TYPE CONOTOXIN FAMILY.
DR PDB; 1IMI; 15-JUN-99.
DR PDB; 1IMI; 23-APR-99.
DR PDB; 1CNL; 27-MAY-99.
KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
KW Venom; 3D-structure.
FT DISULFID 2 8
FT DISULFID 3 12
FT MOD_RES 12 12
FT SEQUENCE 12 AA; 1357 MW; 9C29CEA545A4176A CRC64;
AMIDATION.
Query Match 27.1%; Score 28.5; DB 1; Length 12;
Best Local Similarity 54.5%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 3; Gaps 1;
QY 8 GCC---RCGAR 15
 | | | | |
Db 1 GCCSDPRCAWR 11
RESULT 5
CXAB_CONPE
ID CXAB_CONPE STANDARD; PRT; 16 AA.
AC P50985;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-conotoxin PnIB.
OS Conus pennaceus (Feathered cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=37335;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=94347719; PubMed=8068627;
RA Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D.,
RA Spira M.E., Zlotkin E.;
RT "New mollusc-specific alpha-conotoxins block Aplysia neuronal
RT acetylcholine receptors.";
RL Biochemistry 33:9523-9529(1994).
RN [2]
RP SULFATION OF TYR-15.
RX MEDLINE=99242956; PubMed=10226369;
RA Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M.,
RA Baldwin M.A., Burlingame A.L.;
RT "Identification of tyrosine sulfation in Conus pennaceus conotoxins
RT alpha-PnIA and alpha-PnIB: further investigation of labile sulfo- and
RT phosphopeptides by electrospray, matrix-assisted laser
RT desorption/ionization (MALDI) and atmospheric pressure MALDI mass
RT spectrometry.";

RL J. Mass Spectrom. 34:447-454(1999).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
RX MEDLINE=97444322; PubMed=9298951;
RA Hu S.H., Gehrman J., Alewood P.F., Craik D.J., Martin J.L.;
RT "Crystal structure at 1.1-A resolution of alpha-conotoxin PnIB:
RT comparison with alpha-conotoxins PnIA and GI.";
RL Biochemistry 36:11323-11330(1997).
CC -!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM. IN CONTRAST TO OTHER ALPHA-CONOTOXINS, WHICH ARE
CC SELECTIVE FOR VERTEBRATE SKELETAL MUSCLE NACHR, THE CONUS
CC PENNACEUS ALPHA-CONOTOXINS BLOCK NACHR IN MOLLUSCS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE ALPHA-TYPE CONOTOXIN FAMILY.
DR PDB; 1AKG; 20-MAY-98.
KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
KW Sulfation; Venom; 3D-structure.
FT DISULFID 2 8
FT DISULFID 3 16
FT MOD_RES 15 15
FT MOD_RES 16 16
FT SEQUENCE 16 AA; 1643 MW; 05310FF95ED86AF5 CRC64;
SULFATION.
AMIDATION.
Query Match 26.2%; Score 27.5; DB 1; Length 16;
Best Local Similarity 35.7%; Pred. No. 4.4e+02;
Matches 5; Conservative 1; Mismatches 5; Indels 3; Gaps 1;
QY 8 GCCR---CGARGPE 18
 | | | | |
Db 1 GCCSLPPCALSNPD 14
RESULT 6
TAL_TREBR
ID TAL_TREBR STANDARD; PRT; 15 AA.
AC P34070;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Tremorogen A-I.
OS Tremella brasiliensis (Jelly fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Tremella.
OX NCBI_TaxID=29896;
RN [1]
RP SEQUENCE.
RA Ishibashi Y., Sakagami Y., Isoqai A., Suzuki A.;
RT "Structures of Tremorogens A-9291-I and A-9291-VIII: peptidyl sex
RT hormones of Tremella brasiliensis.";
RL Biochemistry 23:1399-1404(1984).
CC -!- FUNCTION: TREMEROGEN A-I IS PRODUCED BY THE A MATING-TYPE CELLS
CC AND INDUCES FORMATION OF CONJUGATION TUBES IN A MATING-TYPE CELLS.
KW Pheromone; Prenylation; Lipoprotein.
FT LIPID 15 15
FT SEQUENCE 15 AA; 1339 MW; 3AABA4FC2D605333 CRC64;
FARNESYL.
Query Match 23.8%; Score 25; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 9.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
QY 1 GAASGLNGC 9
 | | | | |
Db 9 GASSG--GC 15
RESULT 7
FLAW_AZOC
ID FLAW_AZOC STANDARD; PRT; 17 AA.
AC P23002;
DT 01-AUG-1991 (Rel. 19, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Flavodoxin A (FLDA) (Fragment).
OS Azotobacter chroococcum mcd 1.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Azotobacter.
OX NCBI_TaxID=355;
RN [1]
RP SEQUENCE.
RC STRAIN=MCD 1155;
RX MEDLINE=91315397; PubMed=1859358;
RA Bagby S., Barker P.D., Hill H.A.O., Sanghera G.S., Dunbar B.,
RA Ashby G.A., Eady R.R., Thorneley R.N.F.;
RT "Direct electrochemistry of two genetically distinct flavodoxins
RT isolated from Azotobacter chroococcum grown under nitrogen-fixing
RT conditions.";
RL Biochem. J. 277:313-319(1991).
CC -!- FUNCTION: LOW-POTENTIAL ELECTRON DONOR TO A NUMBER OF REDOX
CC ENZYMES.
CC -!- COFACTOR: FMN.
CC -!- SIMILARITY: BELONGS TO THE FLAVODOXIN FAMILY.
DR PIR; S16929; S16929.
DR InterPro; IPR001226; Flavodoxin.
DR PROSITE; PS00201; FLAVODOXIN; PARTIAL.
KW Electron transport; Flavoprotein; FMN.
FT NON_TER 17
SQ SEQUENCE 17 AA; 1692 MW; DE7B6D4A36B2A4C7 CRC64;

Query Match 23.8%; Score 25; DB 1; Length 17;
Best Local Similarity 50.0%; Pred. No. 1e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAASGLNG 8
Db 8 GSSSGVTG 15

RESULT 8
CXAL_CONAL STANDARD; PRT; 16 AA.
AC P56639;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-conotoxin Au1A.
OS Conus aulicus (Court cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89437;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Venom;
RX MEDLINE=99003392; PubMed=9786965;
RA Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D.,
RA Olivera B.M., McIntosh J.M.;
RT "Alpha-conotoxin Au1B selectively blocks alpha3 beta4 nicotinic
RT acetylcholine receptors and nicotine-evoked norepinephrine release.";
RL J. Neurosci. 18:8571-8579(1998).
CC -!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC
CC ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-4 SUBUNITS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1725.6; METHOD=Electrospray.
CC -!- SIMILARITY: BELONGS TO THE ALPHA-TYPE CONOTOXIN FAMILY.
DR HSSP; P50984; 1PEN.
KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
KW Venom.
FT DISULFID 2 8
FT DISULFID 3 16
FT MOD_RES 16 16 AMIDATION.
SQ SEQUENCE 16 AA; 1731 MW; 1E310FEB8FDC7001 CRC64;

Query Match 22.9%; Score 24; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GCC 10
Db 1 GCC 3

RESULT 9
CXA2_CONMA STANDARD; PRT; 16 AA.
ID CXA2_CONMA
AC P56636;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-conotoxin MII (M2).
OS Conus magus (Magus cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6492;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Venom;
RX MEDLINE=96205934; PubMed=8631783;
RA Cartier G.E., Yoshikami D., Gray W.R., Luo S., Olivera B.M.,
RA McIntosh J.M.;
RT "A new alpha-conotoxin which targets alpha3beta2 nicotinic
RT acetylcholine receptors.";
RL J. Biol. Chem. 271:7522-7528(1996).
RN [2]
RP STRUCTURE BY NMR.
RX MEDLINE=98062282; PubMed=9398298;
RA Shon K.-J., Koerber S.C., Rivier J.E., Olivera B.M., McIntosh J.M.;
RT "Three-dimensional solution structure of alpha-conotoxin MII, an
RT alpha3beta2 neuronal nicotinic acetylcholine receptor-targeted
RT ligand.";
RL Biochemistry 36:15693-15700(1997).
RN [3]
RP STRUCTURE BY NMR.
RX MEDLINE=99060038; PubMed=9843366;
RA Hill J.M., Oomen C.J., Miranda L.P., Bingham J.-P., Alewood P.F.,
RA Craik D.J.;
RT "Three-dimensional solution structure of alpha-conotoxin MII by NMR
RT spectroscopy: effects of solution environment on helicity.";
RL Biochemistry 37:15621-15630(1998).
CC -!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC
CC ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-2 SUBUNITS. IT
CC HAS AN ACTIVITY 2 TO 4 ORDERS OF MAGNITUDE LESS POTENT ON OTHER
CC NACHR SUBUNIT COMBINATIONS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE ALPHA-TYPE CONOTOXIN FAMILY.
DR PDB; 1MII; 21-OCT-98.
DR PDB; 1M2C; 13-JAN-99.
KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
KW Venom; 3D-structure.
FT DISULFID 2 8
FT DISULFID 3 16
FT MOD_RES 16 16 AMIDATION.
SQ SEQUENCE 16 AA; 1716 MW; 282AEF190166CAF9 CRC64;

Query Match 22.9%; Score 24; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GCC 10
Db 1 GCC 3

RESULT 10
CXA3_CONAL STANDARD; PRT; 16 AA.
AC P56641;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-conotoxin AuIC.
OS Conus aulicus (Court cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89437;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE-Venom;
RX MEDLINE=99003392; PubMed=9786965;
RA Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D.,
RA Olivera B.M., McIntosh J.M.;
RT "Alpha-conotoxin AuIB selectively blocks alpha3 beta4 nicotinic
acetylcholine receptors and nicotine-evoked norepinephrine release.";
RL J. Neurosci. 18:8571-8579(1998).
CC -!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC
CC ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-4 SUBUNITS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1667.6; METHOD=Electrospray.
CC -!- SIMILARITY: BELONGS TO THE ALPHA-TYPE CONOTOXIN FAMILY.
DR HSSP; P50984; IPEN.
KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
KW Venom.
FT DISULFID 2 8
FT DISULFID 3 16
FT MOD_RES 16 16 AMIDATION.
SQ SEQUENCE 16 AA; 1673 MW; 1E310D3B8FDC7001 CRC64;

Query Match 22.9%; Score 24; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GCC 10
Db 1 GCC 3

RESULT 11
CXAL_CONST STANDARD; PRT; 13 AA.
AC P15471;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-conotoxin SI (S1).
OS Conus striatus (Striated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6493;
RN [1]
RP SEQUENCE.
RX MEDLINE=89062448; PubMed=3196703;
RA Zafaralla G.C., Ramilo C., Gray W.R., Karlstroem R., Olivera B.M.,
RA Cruz L.J.;
RT "Phylogenetic specificity of cholinergic ligands: alpha-conotoxin
SI.";
RL Biochemistry 27:7102-7105(1988).
CC -!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE ALPHA-TYPE CONOTOXIN FAMILY.

DR PIR; A28953; A28953.
DR HSSP; P01519; 1NOT.
KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
KW Venom.
FT DISULFID 2 7
FT DISULFID 3 13
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1359 MW; DEE90F8EF2457EBD CRC64;

Query Match 21.9%; Score 23; DB 1; Length 13;
Best Local Similarity 44.4%; Pred. No. 1.6e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 9 CCR--CGAR 15
Db 2 CCNPACGPK 10

RESULT 12
DIDH_PSESP STANDARD; PRT; 15 AA.
AC P80701;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE 3-alpha-hydroxysteroid dehydrogenase (EC 1.1.1.50) (3-alpha-HSD)
DE (Hydroxyprostaglandin dehydrogenase) (HSD29) (Fragment).
OS Pseudomonas sp.
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=306;
RN [1]
RP SEQUENCE.
RX MEDLINE=97100200; PubMed=8944761;
RA Oppermann U.C.T., Maser E.;
RT "Characterization of a 3 alpha-hydroxysteroid dehydrogenase/carbonyl
reductase from the Gram-negative bacterium Comamonas testosteroni.";
RL Eur. J. Biochem. 241:744-749(1996).
CC -!- FUNCTION: ALONG WITH THE 3 ALPHA-HYDROXYSTEROID DEHYDROGENASE AND
CC 3-OXO-REDUCTASE ACTIVITIES TOWARDS A VARIETY OF CIS OR TRANS FUSED
CC A/B RING STEROIDS, IT ALSO REDUCES SEVERAL XENOBIOTIC CARBONYL
CC COMPOUNDS, INCLUDING A METYRAPONE-BASED CLASS OF INSECTICIDES, TO
CC THE RESPECTIVE ALCOHOL METABOLITES.
CC -!- CATALYTIC ACTIVITY: Androstosterone + NAD(P)(+) = 5-alpha-androstane-
CC 3,17-dione + NAD(P)H.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR InterPro; IPR002198; ADH_short.
DR PROSITE; PS00061; ADH_SHORT; PARTIAL.
KW Oxidoreductase; NAD.
FT DOMAIN 6 >15 INVOLVED IN COFACTOR BINDING
FT NON_TER 15 15 (BY SIMILARITY).
SQ SEQUENCE 15 AA; 1315 MW; 95068660D070A7790 CRC64;

Query Match 21.9%; Score 23; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.8e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGL 6
Db 7 GSASGI 12

RESULT 13
PVK2_PERAM STANDARD; PRT; 12 AA.
ID PVK2_PERAM
AC P81555;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

```
DE Periviscerokinin-2 (Pea-PVK-2).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattoidea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Abdominal perisymphathetic organs;
RX MEDLINE=98326577; PubMed=9663444;
RA Predel R., Rapus J., Eckert M., Holman G.M., Nachman R.J., Wang Y.,
RA Penzlin H.;
RT "Isolation of periviscerokinin-2 from the abdominal perisymphathetic
RT organs of the American cockroach, Periplaneta americana.";
RL Peptides 19:801-809(1998).
CC -!- FUNCTION: MYOACTIVE PEPTIDE; HAS EXCITATORY ACTIONS ON THE
CC HYPERNEURAL MUSCLE.
CC -!- MASS SPECTROMETRY: MW=1189.3; METHOD=MALDI.
KW Neuropeptide; Amidation.
FT MOD_RES 12 12
SQ SEQUENCE 12 AA; 1190 MW; 2F4D8EEE1EB05728 CRC64;

Query Match 21.0%; Score 22; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 2e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGL 6
Db 1 GSSSGL 6

RESULT .14
CXAA2_CONGE STANDARD; PRT; 13 AA.
AC P01520;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-conotoxin GII.
OS Conus geographus (Geography cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6491;
RN [1]
RP SEQUENCE.
RX MEDLINE=81191854; PubMed=7014556;
RA Gray W.R., Luque A., Olivera B.M., Barrett J., Cruz L.J.;
RA "Peptide toxins from Conus geographus venom.";
RL J. Biol. Chem. 256:4734-4740(1981).
RN [2]
RP DISULFIDE BONDS.
RX MEDLINE=84032400; PubMed=6630187;
RA Gray W.R., Rivier J.E., Galyean R., Cruz L.J., Olivera B.M.;
RT "Conotoxin MI. Disulfide bonding and conformational states.";
RL J. Biol. Chem. 258:12247-12251(1983).
RN [3]
RP REVIEW.
RX MEDLINE=89024586; PubMed=3052286;
RA Gray W.R., Olivera B.M., Cruz L.J.;
RT "Peptide toxins from venomous Conus snails.";
RL Annu. Rev. Biochem. 57:665-700(1988).
CC -!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE ALPHA-TYPE CONOTOXIN FAMILY.
DR PIR; A01783; NTKN2G.
DR HSSP; P01519; 1NOT.
KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
KW Venom.
FT DISULFID 2 7
FT DISULFID 3 13
```

```
FT MOD_RES 13 13
SQ SEQUENCE 13 AA; 1422 MW; DEEE831C39297EBD CRC64;

Query Match 21.0%; Score 22; DB 1; Length 13;
Best Local Similarity 57.1%; Pred. No. 2.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 9 CCR--CG 13
Db 2 CCHPACG 8

RESULT 15
CXAA_CONST STANDARD; PRT; 13 AA.
AC P28878;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-conotoxin SIA (S1A).
OS Conus striatus (Striated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6493;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=91369955; PubMed=1892838;
RA Myers R.A., Zafarella G.C., Gray W.R., Abbot J., Cruz L.J.,
RA Olivera B.M.;
RT "Alpha-conotoxins, small peptide probes of nicotinic acetylcholine
RT receptors.";
RL Biochemistry 30:9370-9377(1991).
CC -!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE ALPHA-TYPE CONOTOXIN FAMILY.
DR PIR; A40312; NTKNAS.
KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
KW Venom.
FT DISULFID 2 7
FT DISULFID 3 13
FT MOD_RES 13 13
SQ SEQUENCE 13 AA; 1461 MW; DEF1931982457EBD CRC64;

Query Match 21.0%; Score 22; DB 1; Length 13;
Best Local Similarity 57.1%; Pred. No. 2.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 9 CCR--CG 13
Db 2 CCHPACG 8
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Search completed: July 3, 2002, 11:41:55
Job time: 836 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:41:20 ; Search time 100.54 Seconds
(without alignments)
30.972 Million cell updates/sec

Title: US-09-165-546A-11
Perfect score: 105
Sequence: 1 GAASGLNGCCRCGARGPE 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 4250

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhcs:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archheap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	32.4	18	11 Q63136	Q63136 rattus norv
2	29.5	28.1	16	5 P82706	P82706 drosophila
3	29.5	28.1	18	4 Q14042	Q14042 homo sapien
4	28	26.7	18	13 Q90790	Q90790 gallus gall
5	26	24.8	14	2 P83077	P83077 bacillus ce
6	25	23.8	13	4 P82276	P82276 homo sapien
7	25	23.8	18	4 Q9UE38	Q9ue38 homo sapien
8	24	22.9	9	5 Q9TWD6	Q9twd6 leptinotars
9	24	22.9	10	13 P82084	P82084 limnodynast
10	24	22.9	11	11 Q99JC3	Q99jc3 rattus sp.
11	24	22.9	12	13 P82085	P82085 limnodynast
12	24	22.9	15	8 Q95773	Q95773 conolophus
13	24	22.9	16	4 Q15632	Q15632 homo sapien
14	24	22.9	16	6 Q9TRM0	Q9trm0 bos taurus
15	24	22.9	18	4 Q9Y6D8	Q9y6d8 homo sapien
16	24	22.9	18	10 Q9S8Q5	Q9s8q5 arabidopsis

17	23	21.9	13	11 Q9QVI3	Q9qvi3 cavia (guin
18	23	21.9	15	4 Q9Y4Z9	Q9y4z9 homo sapien
19	23	21.9	15	6 Q9TRP2	Q9trp2 sus scrofa
20	23	21.9	16	5 Q9TWK0	Q9twk0 mytilus edu
21	23	21.9	16	5 Q9TZR1	Q9tzt1 haliotis fu
22	23	21.9	16	13 Q9PTT5	Q9ptt5 gallus gall
23	23	21.9	17	10 Q9SMC7	Q9smc7 lycopersico
24	22	21.0	18	4 Q16053	Q16053 homo sapien
25	22	21.0	18	4 Q14009	Q14009 homo sapien
26	21	20.0	15	2 Q9R569	Q9r569 nitrosomona
27	21	20.0	15	8 Q78794	Q78794 pylaiella 1
28	21	20.0	16	4 Q9UC88	Q9uc88 homo sapien
29	21	20.0	16	6 Q9TRH0	Q9trh0 bos taurus
30	21	20.0	17	4 Q9UC89	Q9uc89 homo sapien
31	21	20.0	18	4 Q9UCN1	Q9ucn1 homo sapien
32	21	20.0	18	4 Q9UCL4	Q9ucl4 homo sapien
33	21	20.0	18	4 Q9UE43	Q9ue43 homo sapien
34	21	20.0	18	7 Q9MY73	Q9my73 homo sapien
35	21	20.0	18	7 Q30216	Q30216 homo sapien
36	21	20.0	18	10 Q9S8Y9	Q9s8y9 poa pratens
37	21	20.0	18	12 Q65539	Q65539 baboon herp
38	20	19.0	9	6 Q9XT05	Q9xt05 macropus ru
39	20	19.0	9	15 O12096	O12096 caprine art
40	20	19.0	9	15 O12098	O12098 caprine art
41	20	19.0	9	15 O12100	O12100 caprine art
42	20	19.0	9	15 O12102	O12102 caprine art
43	20	19.0	9	15 O12104	O12104 caprine art
44	20	19.0	10	9 Q9TOR6	Q9tor6 bacterioph
45	20	19.0	11	11 Q60807	Q60807 mus musculu

ALIGNMENTS

RESULT 1
Q63136
ID Q63136 PRELIMINARY; PRT; 18 AA.
AC Q63136;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ALPHA(B)-CRYSTALLIN PROTEIN.
GN ALPHA(B)-CRYSTALLIN
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91093055; Pubmed=2176207;
RA Iwaki A., Iwaki T., Goldman J.E., Liem R.K.H.;
RT "Multiple mRNAs of rat brain-alpha-crystallin B chain from alternative
transcriptional Initiation."
RL J. Biol. Chem. 265:22197-22203(1990).
DR EMBL; M55534; AAA40974.1; -.
SQ SEQUENCE 18 AA; 1963 MW; 1D4F384151EF1DDB CRC64;

Query Match 32.4%; Score 34; DB 11; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 5 GLNGCCRCGARGPE 18
| | | | | |
Db 2 GWVGATRCGQRASE 15

RESULT 2
P82706
ID P82706 PRELIMINARY; PRT; 16 AA.
AC P82706;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT	01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE	IMMUNE-INDUCED PROTEIN 1 (DIM-1).
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephydroidea; Drosophilidae; Drosophila.
OX	NCBI_TaxID=7227;
RN	[1]
RP	SEQUENCE
RC	STRAIN=OREGON-R; TISSUE=HEMOLYMPH;
RX	MEDLINE=98409659; PubMed=9736738;
RA	Uttenweiler-Joseph S., Moniatte M., Lagueux M., Van Dorselaer A.,
RA	Hoffmann J.A., Bulet P.;
RT	"Differential display of peptides induced during the immune response
RT	of Drosophila: a matrix-assisted laser desorption ionization time-of-
RT	flight mass spectrometry study.";
RL	Proc. Natl. Acad. Sci. U.S.A. 95:11342-11347(1998).
CC	-!- TISSUE SPECIFICITY: HEMOLYMPH.
CC	-!- INDUCTION: BY BACTERIAL INFECTION.
CC	-!- MASS SPECTROMETRY: MW=1687.7; METHOD=MALDI.
KW	Antibiotic; Insect immunity; Amidation.
FT	MOD_RES 16 16
FT	DISULFID 9 12
SQ	SEQUENCE 16 AA; 1670 MW; 5F22356839CD06AF CRC64;
Query Match 28.1%; Score 29.5; DB 5; Length 16;	
Best Local Similarity 50.0%; Pred. No. 5.6e+02;	
Matches 6; Conservative 1; Mismatches 4; Indels 1; Gaps 1;	
QY	6 LNGCCR-CGARG 16
Db	5 TNGDCRVCNVHG 16
RESULT 3	
Q14042	
ID	Q14042 PRELIMINARY; PRT; 18 AA.
AC	Q14042;
DT	01-NOV-1996 (TReMBLrel. 01, Created)
DT	01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT	01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE	TYPE II PROCOLLAGEN GENE.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Strom C.M., Upholt W.B.;
RT	"Isolation and characterization of genomic clones corresponding to the
RT	human type II procollagen gene.";
RL	Nucleic Acids Res. 11:1025-1037(1983).
DR	EMBL; X00299; CAA25082.1; -.
KW	Collagen.
SQ	SEQUENCE 18 AA; 1595 MW; 17789165A92EEB0F CRC64;
Query Match 28.1%; Score 29.5; DB 4; Length 18;	
Best Local Similarity 47.1%; Pred. No. 6.2e+02;	
Matches 8; Conservative 1; Mismatches 7; Indels 1; Gaps 1;	
QY	3 ASGLNGCC-RCGARGPE 18
Db	2 ATGFPGAAGRVGPPGPE 18
RESULT 4	
Q90790	
ID	Q90790 PRELIMINARY; PRT; 18 AA.
AC	Q90790;
DT	01-NOV-1996 (TReMBLrel. 01, Created)
DT	01-NOV-1996 (TReMBLrel. 01, Last sequence update)

DT	01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE	GENE ENCODING ALPHA-1 TYPE III COLLAGEN. THIS IS EXON 16.
OS	Gallus gallus (Chicken).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC	Gallus.
OX	NCBI_TaxID=9031;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=83135706; PubMed=6298201;
RA	Yamada Y., Mudryj M., Sullivan M., de Crombrughe B.;
RT	"Isolation and characterization of a genomic clone encoding chick
RT	alpha-1 type III collagen.";
RL	J. Biol. Chem. 258:2758-2761(1983).
DR	EMBL; V00391; CAA23689.1; -.
KW	Collagen.
SQ	SEQUENCE 18 AA; 1732 MW; 439C34D5A9329EBC CRC64;
Query Match 26.7%; Score 28; DB 13; Length 18;	
Best Local Similarity 100.0%; Pred. No. 1e+03;	
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	13 GARGP 17
Db	7 GARGP 11
RESULT 5	
P83077	
ID	P83077 PRELIMINARY; PRT; 14 AA.
AC	P83077;
DT	01-OCT-2001 (TReMBLrel. 18, Created)
DT	01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DT	01-OCT-2001 (TReMBLrel. 18, Last annotation update)
DE	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12) (GAPDH)
DE	(FRAGMENT).
OS	Bacillus cereus.
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;
OC	Bacillus/Staphylococcus group; Bacillus.
OX	NCBI_TaxID=1396;
RN	[1]
RP	SEQUENCE.
RC	STRAIN=NCIMB 11796;
RA	Browne N., Dowds B.C.A.;
RL	Submitted (JUL-2001) to the SWISS-PROT data bank.
CC	-!- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + ORTHOPHOSPHATE
CC	+ NAD(+) = 1,3-DIPHOSPHATEGLYCERATE + NADH.
CC	-!- PATHWAY: FIRST STEP IN THE SECOND PHASE OF GLYCOLYSIS.
CC	-!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC	-!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC	-!- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
CC	DEHYDROGENASE FAMILY.
DR	InterPro; IPR000173; GAP_DH.
DR	PROSITE; PS00071; GAPDH; PARTIAL.
KW	Glycolysis; Oxidoreductase; NAD; Multigene family.
FT	NON_TER 14 14
SQ	SEQUENCE 14 AA; 1604 MW; 209872BB19F5E0C8 CRC64;
Query Match 24.8%; Score 26; DB 2; Length 14;	
Best Local Similarity 55.6%; Pred. No. 1.7e+03;	
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;	
QY	5 GLNGCCRCG 13
Db	4 GINGFARRG 12
RESULT 6	
P82276	
ID	P82276 PRELIMINARY; PRT; 13 AA.
AC	P82276;

DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE TUBULIN-ASSOCIATED PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA Rossbacher J., Gartner W., Katinger H., Wagner L.;
RT "Haptoglobin mediated changes in cellular immune response.";
RL Submitted (JAN-2000) to the SWISS-PROT data bank.
CC -!- TISSUE SPECIFICITY: LEUKOCYTES AND HEPATOCYTES.
KW Microtubules.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1300 MW; 4FD05B1E478D62C7 CRC64;

Query Match 23.8%; Score 25; DB 4; Length 13;
Best Local Similarity 85.7%; Pred. No. 2.3e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AASGLNG 8
Db 2 AASGLVG 8
RESULT 7
Q9UE38
ID Q9UE38 PRELIMINARY; PRT; 18 AA.
AC Q9UE38;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE COLLAGEN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89325561; PubMed=2753125;
RA Vikkula M., Peltonen L.;
RT "Structural analyses of the polymorphic area in type II collagen gene.";
RL FEBS Lett. 250:171-174(1989).
DR EMBL; X16158; CAA34284.1; -.
SQ SEQUENCE 18 AA; 1683 MW; 7724306D60CA21B4 CRC64;

Query Match 23.8%; Score 25; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 3e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 13 GARGPE 18
Db 4 GEKGPE 9
RESULT 8
Q9TWD6
ID Q9TWD6 PRELIMINARY; PRT; 9 AA.
AC Q9TWD6;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE LED-NPF-1-NEUROPEPTIDE F-RELATED PEPTIDE.
OS Leptinotarsa decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Cucujiformia; Phytophaga; Chrysomeloidea; Chrysomelidae;

OC Chrysomelinae; Leptinotarsa.
OX NCBI_TaxID=7539;
RN [1]
RP SEQUENCE.
RX MEDLINE=96245438; PubMed=8814784;
RA Spittaels K., Verhaert P., Shaw C., Johnston R.N., Devreese B.,
RV Van Beeumen J., De Loof A.;
RT "Insect neuropeptide F (NPF)-related peptides: isolation from Colorado potato beetle (Leptinotarsa decemlineata) brain.";
RL Insect Biochem. Mol. Biol. 26:375-382(1996).
SQ SEQUENCE 9 AA; 1066 MW; 7E02340736C76864 CRC64;

Query Match 22.9%; Score 24; DB 5; Length 9;
Best Local Similarity 80.0%; Pred. No. 5.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 14 ARGPE 18
Db 1 ARGPQ 5
RESULT 9
P82084
ID P82084 PRELIMINARY; PRT; 10 AA.
AC P82084;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE DYNASTIN 6.
OS Limnodynastes salmini (Salmin's-striped frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Limnodynastes.
OX NCBI_TaxID=39404;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=SKIN SECRETION;
RA Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structure of the dynastins from Limnodynastes salmini and Fletcherin from Limnodynastes fletcheri.";
RL Aust. J. Chem. 46:1235-1244(1993).
CC -!- MASS SPECTROMETRY: MW=944; METHOD=FAB.
KW Amphibian skin.
SQ SEQUENCE 10 AA; 944 MW; D976CAA7272865A2 CRC64;

Query Match 22.9%; Score 24; DB 13; Length 10;
Best Local Similarity 83.3%; Pred. No. 2.6e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAASGL 6
Db 1 GAVSGL 6
RESULT 10
Q99JC3
ID Q99JC3 PRELIMINARY; PRT; 11 AA.
AC Q99JC3;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE LUTEINIZING HORMONE/CHORIONIC GONADOTROPIN RECEPTOR HOMOLOG (FRAGMENT).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RX MEDLINE=96147985; PubMed=8571710;

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RA Shen Q.X., Liu H.H., Chen W.Y., Bahl O.P.;
RT "[Cloning and overexpression of rat ovary LH/hCG receptor cDNA in
RT insect cells].";
RL Shih Yen Sheng Wu Hsueh Pao 28:283-290(1995).
DR EMBL; S80658; AAB50709.1; -.
KW Receptor; Chorion.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 994 MW; 333DCB137EB865B8 CRC64;

Query Match 22.9%; Score 24; DB 11; Length 11;
Best Local Similarity 80.0%; Pred. No. 2.8e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CGARG 16
   ||| |
Db 7 CGAAG 11

RESULT 11
P82085 PRELIMINARY; PRT; 12 AA.
AC P82085;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE DYNASTIN 7.
OS Limnodynastes salmini (Salmin's-striped frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Limnodynastes.
OX NCBI_TaxID=39404;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=SKIN SECRETION;
RA Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structure of the dynastins from
RT Limnodynastes salmini and Fletcherin from Limnodynastes fletcheri.";
RL Aust. J. Chem. 46:1235-1244(1993).
CC -1- MASS SPECTROMETRY: MW=1114; METHOD=FAB.
KW Amphibian skin.
SQ SEQUENCE 12 AA; 1114 MW; 3AB5A976CAA72728 CRC64;

Query Match 22.9%; Score 24; DB 13; Length 12;
Best Local Similarity 83.3%; Pred. No. 3e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAASGL 6
   || |||
Db 1 GAVSGL 6

RESULT 12
Q95773 PRELIMINARY; PRT; 15 AA.
AC Q95773;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NADH DEHYDROGENASE SUBUNIT 4 (FRAGMENT).
GN ND4.
OS Conolophus subcristatus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Conolophus.
OX NCBI_TaxID=31140;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97019047; PubMed=8865663;
RA Sites J.W. Jr., Davis S.K., Guerra T., Iverson J.B., Snell H.L.;
RT "Character congruence and phylogenetic signal in molecular and
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RT morphological data sets: a case study in the living Iguanas (Squamata,
RT Iguanidae).";
RL Mol. Biol. Evol. 13:1087-1105(1996).
DR EMBL; U66235; AAB07475.1; -.
KW Mitochondrion.
FT NON_TER 1 1
FT NON_TER 15 AA; 1839 MW; 9263179CE68523B1 CRC64;

Query Match 22.9%; Score 24; DB 8; Length 15;
Best Local Similarity 66.7%; Pred. No. 3.6e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 LNGCCR 11
   | : | | |
Db 5 LHGTCR 10

RESULT 13
Q15632 PRELIMINARY; PRT; 16 AA.
AC Q15632;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE TCL3 ONCOGENE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90222189; PubMed=2326274;
RA Zutter M., Hockett R.D., Roberts C.W., McGuire E.A., Bloomstone J.,
RA Morton C.C., Deaven L.L., Crist W.M., Carroll A.J., Korsmeyer S.J.;
RT "The t(10;14)(q24;q11) of T-cell acute lymphoblastic leukemia
RT juxtaposes the delta T-cell receptor with TCL3, a conserved and
RT activated locus at 10q24.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:3161-3165(1990).
DR EMBL; M33602; AAA66450.1; -.
FT NON_TER 1 1
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1812 MW; EBCF0A05EAE77D24 CRC64;

Query Match 22.9%; Score 24; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CGAR 15
   ||| |
Db 4 CGAR 7

RESULT 14
Q9TRM0 PRELIMINARY; PRT; 16 AA.
AC Q9TRM0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 41 KDA CA(2+)-DEPENDENT CARBOHYDRATE-BINDING PROTEIN (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=93015942; PubMed=1400371;
RA Kojima K., Ogawa H.K., Seno N., Yamamoto K., Irimura T., Osawa T.,
RA Matsumoto I.;
RT "Carbohydrate-binding proteins in bovine kidney have consensus amino
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RT acid sequences of annexin family proteins.";
RL J. Biol. Chem. 267:20536-20539(1992).
SQ SEQUENCE 16 AA; 1642 MW; 750143513F0045BE CRC64;

Query Match 22.9%; Score 24; DB 6; Length 16;
Best Local Similarity 83.3%; Pred. No. 3.8e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AASGLN 7
 |||||
Db 1 AASGFN 6

RESULT 15
Q9Y6D8 PRELIMINARY; PRT; 18 AA.
AC Q9Y6D8;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE MUTANT BETA-GLOBIN.
GN HBB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99250504; PubMed=10233364;
RA Cabeda J.M., Correia C., Estevinho A., Cardoso C., Amorim M.L.,
RA Cleto E., Vale L., Coimbra E., Pinho L., Justica B.;
RT "Unexpected pattern of beta-globin mutations in beta-thalassaemia
RT patients from northern Portugal.";
RL Br. J. Haematol. 105:68-74(1999).
DR EMBL; AF083884; AAD34034.1; -
SQ SEQUENCE 18 AA; 1952 MW; FFC4BB0AF3377D0A CRC64;

Query Match 22.9%; Score 24; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CGAR 15
 |||||
Db 15 CGAR 18

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:26:58 ; Search time 128.9 Seconds
(without alignments)
15.511 Million cell updates/sec

Title: US-09-165-546A-11
Perfect score: 105
Sequence: 1 GAASGLNGCCRCRGARGPE 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 214377

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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11: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:*
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22: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	105	100.0	18	21 AAY52438	Human tumour antig
2	105	100.0	18	22 AAU01542	HLA-DR53 recognisi
3	105	100.0	18	22 AAB69942	Human NY-ESO-1 HLA
4	64	61.0	10	20 AAY06012	Human cancer antig
5	63	60.0	10	20 AAY06063	Human cancer antig
6	63	60.0	10	20 AAY06008	Human cancer antig
7	59	56.2	9	20 AAY06044	Human cancer antig
8	57	54.3	10	20 AAY06060	Human cancer antig
9	57	54.3	10	20 AAY05994	Human cancer antig
10	53	50.5	9	20 AAY06047	Human cancer antig
11	47	44.8	10	20 AAY06059	Human cancer antig

12	47	44.8	10	20	AAY05993	Human cancer antig
13	42	40.0	10	14	AAR69313	Gp IiIb/IIia recept
14	42	40.0	10	19	AAW52088	Targeting peptide
15	42	40.0	10	21	AAW55511	GPIIb/IIia recepto
16	41	39.0	11	21	AAW97091	Tau conotoxin sequ
17	41	39.0	11	21	AAW97109	Tau conotoxin sequ
18	40	38.1	11	21	AAW82639	Influenza A virus
19	40	38.1	12	20	AAW41492	Fragment of human
20	39.5	37.6	15	16	AAR75282	A-lineage conotoxi
21	39	37.1	12	22	AAB68489	Peptide encoded by
22	37	35.2	15	20	AAW33078	Carbohydrate antig
23	36	34.3	10	22	AAB96032	HPV 18 E7 A2 MHC-b
24	36	34.3	14	22	AAB95966	HPV 18 E6 protein
25	36	34.3	15	18	AAW38912	Peptide resembling
26	36	34.3	15	18	AAW24889	Predatory cone sna
27	36	34.3	15	18	AAW12744	A-lineage conotoxi
28	35	33.3	15	10	AAP90207	Antigenic peptide
29	34	32.4	15	22	AAG80814	A fulgidus DtxR ho
30	34	32.4	18	22	AAG73116	Protease binding s
31	33.5	31.9	14	22	AAM98812	Human peptide #208
32	33.5	31.9	15	21	AAB03867	GIR receptor targe
33	33.5	31.9	16	20	AAW24163	Alpha-conotoxin pe
34	33	31.4	9	13	AAR26401	Sequence of techne
35	33	31.4	9	14	AAR69302	Gp IiIb/IIia recept
36	33	31.4	9	15	AAW08517	Endothelin metal c
37	33	31.4	9	19	AAW50585	GPIIb/IIia recepto
38	33	31.4	9	21	AAW95453	GPIIb/IIia recepto
39	33	31.4	9	21	AAW79751	NY-ESO-1 derived p
40	33	31.4	9	21	AAW54968	Peptide ligand for
41	33	31.4	9	22	AAG67174	Cancer testis tumo
42	33	31.4	9	22	AAG67180	Cancer testis tumo
43	33	31.4	9	22	AAG67184	Cancer testis tumo
44	33	31.4	9	22	AAB69906	Human NY-ESO-1 HLA
45	33	31.4	9	22	AAB69912	Human NY-ESO-1 HLA

ALIGNMENTS

RESULT 1
AAY52438
ID AAY52438 standard; Protein; 18 AA.
XX
AC AAY52438;
XX
DT 15-FEB-2000 (first entry)
XX Human tumour antigen NY-ESO-1 peptide #11.
DE
XX Cancer; tumour; antigen; MHC; major histocompatibility complex; Class II;
KW T-cell; helper; stimulation; proliferation; treatment;
KW diagnosis; prevention; melanoma; breast cancer; ovarian cancer;
KW prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer;
KW lymphoma.
XX Synthetic.
OS Homo sapiens.
XX
PN WO9953938-A1.
XX
PD 28-OCT-1999.
XX
PF 24-MAR-1999; 99WO-US06875.
XX
PR 17-APR-1998; 98US-0062422.
PR 02-OCT-1998; 98US-0165546.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
PI Gure A, Ritter G;
XX
DR WPI; 2000-038483/03.

CC with a tumour that expresses NY-ESO-1. The method comprises assaying a
CC sample taken from the patient for antibodies that specifically bind to
CC the NY-ESO-1 and comparing the value obtained to a prior value obtained
CC from assay of a prior sample taken from the patient. Any difference
CC between the values is indicative of a change in status of the cancerous
CC condition. The method is useful for determining whether a cancerous
CC condition is progressing, regressing or remaining stable, in particular
CC in patients receiving treatment for a melanoma, adenocarcinoma,
CC non-small cell lung carcinoma or bladder carcinoma.

XX Sequence 18 AA;

Query Match 100.0%; Score 105; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
Db 1 gaasglnccrcgargpe 18
|||||

RESULT 4
AAAY06012
ID AAY06012 standard; Peptide; 10 AA.
XX
AC AAY06012;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; human leukocyte antigen; HLA.

XX Homo sapiens.
OS
XX WO9918206-A2.
PN
XX 15-APR-1999.
PD
XX 21-SEP-1998; 98WO-US19609.
PF
XX
PR WO9918206-A2.
XX
PA 15-APR-1999.
XX
PI 21-SEP-1998; 98WO-US19609.
XX
PR 08-OCT-1997; 97US-0061428.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rosenberg SA, Wang RF;
XX
DR WPI; 1999-277270/23.
XX
PT Cancer antigen NY ESO1/CAG-3
XX
PS Example 10; Page 42; 88pp; English.

XX This peptide was identified as an HLA peptide motif following a
CC screen for epitopes from the coding region of human ESO-1/CAG-3
CC ORF1 (see AAX58599). 30 Epitopes (see AAY05988-Y06017) were identified.
CC The present peptide (ranked 25) corresponds to amino acid residues
CC 71-80 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent
CC tumour antigen capable of eliciting an antigen specific immune
CC response by T cells. Cancer peptides (see AAY05967-87) derived from
CC CAG-3, portions of CAG-3 and their variants, are useful as cancer
CC vaccines. A claimed method of preventing or inhibiting cancer
CC involves administering a cancer peptide, with or without an HLA
CC molecule. The cancer peptides form part of, or are derived
CC from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine

CC cancer, cervical cancer, bladder cancer, kidney cancer and
CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
CC thyroid cancers.

XX Sequence 10 AA;

Query Match 61.0%; Score 64; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GLNGCCRCGA 14
Db 1 glngccrcga 10
|||||

RESULT 5
AAAY06063
ID AAY06063 standard; Peptide; 10 AA.
XX
AC AAY06063;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 peptide ESO10-72.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; cytotoxic T lymphocyte; CTL.

XX Homo sapiens.
OS
XX WO9918206-A2.
PN
XX 15-APR-1999.
PD
XX 21-SEP-1998; 98WO-US19609.
PF
XX
PR 08-OCT-1997; 97US-0061428.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rosenberg SA, Wang RF;
XX
DR WPI; 1999-277270/23.
XX
PT Cancer antigen NY ESO1/CAG-3
XX
PS Example 10; Page 45; 88pp; English.

XX Peptide ESO10-72 corresponds to amino acid residues 72-81 of
CC human NY ESO-1/CAG-3 ORF1 (see AAY05965), a new and potent tumour
CC antigen capable of eliciting an antigen specific immune response
CC by T cells. It was examined for reactivity to a cytotoxic T
CC lymphocyte (CTL), measured as release of granulocyte macrophage
CC colony stimulating factor. Cancer peptides (see AAY05967-87) derived
CC from CAG-3, portions of CAG-3 and their variants, are useful as
CC cancer vaccines. A claimed method of preventing or inhibiting
CC cancer involves administering a cancer peptide, with or without an
CC HLA molecule. The cancer peptides form part of, or are derived
CC from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer and
CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
CC thyroid cancers.

XX Sequence 10 AA;

```

Query Match          60.0%; Score 63; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 LNGCCRCGAR 15
Db      1 lngccrcgar 10

RESULT 6
AAY06008
ID  AAY06008 standard; Peptide; 10 AA.
XX
AC  AAY06008;
XX
DT  16-AUG-1999 (first entry)
XX
DE  Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
KW  NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW  leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW  metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW  uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW  cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW  liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW  vaccine; human leukocyte antigen; HLA.
XX
OS  Homo sapiens.
XX
PN  WO9918206-A2.
XX
PD  15-APR-1999.
XX
PF  21-SEP-1998; 98WO-US19609.
XX
PR  08-OCT-1997; 97US-0061428.
XX
PA  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI  Rosenberg SA, Wang RF;
XX
DR  WPI; 1999-277270/23.
XX
PT  Cancer antigen NY ESO1/CAG-3
XX
PS  Example 10; Page 42; 88pp; English.
XX
CC  This peptide was identified as an HLA peptide motif following a
CC  screen for epitopes from the coding region of human ESO-1/CAG-3
CC  ORF1 (see AAX58599). 30 Epitopes (see AAY05988-Y06017) were identified.
CC  The present peptide (ranked 21) corresponds to amino acid residues
CC  72-81 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent
CC  tumour antigen capable of eliciting an antigen specific immune
CC  response by T cells. Cancer peptides (see AAY05967-87) derived from
CC  CAG-3, portions of CAG-3 and their variants, are useful as cancer
CC  vaccines. A claimed method of preventing or inhibiting cancer
CC  involves administering a cancer peptide, with or without an HLA
CC  molecule. The cancer peptides form part of, or are derived
CC  from, cancers such as primary or metastatic melanoma, thymoma,
CC  lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
CC  cancer, cervical cancer, bladder cancer, kidney cancer and
CC  adenocarcinomas such as breast, prostate, ovarian, pancreatic and
CC  thyroid cancers.
XX
SQ  Sequence 10 AA;

Query Match          60.0%; Score 63; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 LNGCCRCGAR 15
Db      1 lngccrcgar 10

RESULT 6
AAY06008
ID  AAY06008 standard; Peptide; 10 AA.
XX
AC  AAY06008;
XX
DT  16-AUG-1999 (first entry)
XX
DE  Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
KW  NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW  leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW  metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW  uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW  cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW  liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW  vaccine; human leukocyte antigen; HLA.
XX
OS  Homo sapiens.
XX
PN  WO9918206-A2.
XX
PD  15-APR-1999.
XX
PF  21-SEP-1998; 98WO-US19609.
XX
PR  08-OCT-1997; 97US-0061428.
XX
PA  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI  Rosenberg SA, Wang RF;
XX
DR  WPI; 1999-277270/23.
XX
PT  Cancer antigen NY ESO1/CAG-3
XX
PS  Example 10; Page 42; 88pp; English.
XX
CC  This peptide was identified as an HLA peptide motif following a
CC  screen for epitopes from the coding region of human ESO-1/CAG-3
CC  ORF1 (see AAX58599). 30 Epitopes (see AAY05988-Y06017) were identified.
CC  The present peptide (ranked 21) corresponds to amino acid residues
CC  72-81 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent
CC  tumour antigen capable of eliciting an antigen specific immune
CC  response by T cells. Cancer peptides (see AAY05967-87) derived from
CC  CAG-3, portions of CAG-3 and their variants, are useful as cancer
CC  vaccines. A claimed method of preventing or inhibiting cancer
CC  involves administering a cancer peptide, with or without an HLA
CC  molecule. The cancer peptides form part of, or are derived
CC  from, cancers such as primary or metastatic melanoma, thymoma,
CC  lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
CC  cancer, cervical cancer, bladder cancer, kidney cancer and
CC  adenocarcinomas such as breast, prostate, ovarian, pancreatic and
CC  thyroid cancers.
XX
SQ  Sequence 10 AA;

Query Match          60.0%; Score 63; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 LNGCCRCGAR 15
Db      1 lngccrcgar 10

RESULT 6
AAY06008
ID  AAY06008 standard; Peptide; 10 AA.
XX
AC  AAY06008;
XX
DT  16-AUG-1999 (first entry)
XX
DE  Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
KW  NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW  leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW  metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW  uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW  cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW  liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW  vaccine; human leukocyte antigen; HLA.
XX
OS  Homo sapiens.
XX
PN  WO9918206-A2.
XX
PD  15-APR-1999.
XX
PF  21-SEP-1998; 98WO-US19609.
XX
PR  08-OCT-1997; 97US-0061428.
XX
PA  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI  Rosenberg SA, Wang RF;
XX
DR  WPI; 1999-277270/23.
XX
PT  Cancer antigen NY ESO1/CAG-3
XX
PS  Example 10; Page 43; 88pp; English.
XX
CC  This peptide was identified as an HLA peptide motif following a
CC  screen for epitopes from the coding region of human ESO-1/CAG-3
CC  ORF1 (see AAX58599). 30 Epitopes (see AAY06018-47) were identified.
CC  The present peptide (ranked 27) corresponds to amino acid residues
CC  73-81 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent
CC  tumour antigen capable of eliciting an antigen specific immune
CC  response by T cells. Cancer peptides (see AAY05967-87) derived from
CC  CAG-3, portions of CAG-3 and their variants, are useful as cancer
CC  vaccines. A claimed method of preventing or inhibiting cancer
CC  involves administering a cancer peptide, with or without an HLA
CC  molecule. The cancer peptides form part of, or are derived
CC  from, cancers such as primary or metastatic melanoma, thymoma,
CC  lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
CC  cancer, cervical cancer, bladder cancer, kidney cancer and
CC  adenocarcinomas such as breast, prostate, ovarian, pancreatic and
CC  thyroid cancers.
XX
SQ  Sequence 9 AA;

Query Match          56.2%; Score 59; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 NGCCRCGAR 15
Db      1 ngccrcgar 9

RESULT 8
AAY06060
ID  AAY06060 standard; Peptide; 10 AA.
```

XX AAY06060;
AC
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 peptide ESO10-68.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; cytotoxic T lymphocyte; CTL.
XX
XX Homo sapiens..
OS
XX
XX WO9918206-A2.
PN
XX
XX 15-APR-1999.
PD
XX
XX 21-SEP-1998; 98WO-US19609.
PF
XX
XX 08-OCT-1997; 97US-0061428.
PR
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
XX
XX Rosenber SA, Wang RF;
PI
XX
XX WPI; 1999-277270/23.
DR
XX
XX Cancer antigen NY ESO1/CAG-3
PT
XX
XX Example 10; Page 45; 88pp; English.
PS
XX
XX Peptide ESO10-68 corresponds to amino acid residues 68-77 of
CC human NY ESO-1/CAG-3 ORF1 (see AAY05965), a new and potent tumour
CC antigen capable of eliciting an antigen specific immune response
CC by T cells. It was examined for reactivity to a cytotoxic T
CC lymphocyte (CTL), measured as release of granulocyte macrophage
CC colony stimulating factor. Cancer peptides (see AAY05967-87) derived
CC from CAG-3, portions of CAG-3 and their variants, are useful as
CC cancer vaccines. A claimed method of preventing or inhibiting
CC cancer involves administering a cancer peptide, with or without an
CC HLA molecule. The cancer peptides form part of, or are derived
CC from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer and
CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
CC thyroid cancers.
XX
SQ Sequence 10 AA;

Query Match 54.3%; Score 57; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AASGLNGCCR 11
Db 1 aasglnccr 10
|||||
1 aasglnccr 10

RESULT 9
AAY05994
ID AAY05994 standard; Peptide; 10 AA.
XX
AC AAY05994;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
XX

KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; human leukocyte antigen; HLA.
XX
XX Homo sapiens.
OS
XX
XX WO9918206-A2.
PN
XX
XX 15-APR-1999.
PD
XX
XX 21-SEP-1998; 98WO-US19609.
PF
XX
XX 08-OCT-1997; 97US-0061428.
PR
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
XX
XX Rosenber SA, Wang RF;
PI
XX
XX WPI; 1999-277270/23.
DR
XX
XX Cancer antigen NY ESO1/CAG-3
PT
XX
XX Example 10; Page 42; 88pp; English.
PS
XX
XX This peptide was identified as an HLA peptide motif following a
CC screen for epitopes from the coding region of human ESO-1/CAG-3
CC ORF1 (see AAX58599). 30 Epitopes (see AAY05988-Y06017) were identified.
CC The present peptide (ranked 7) corresponds to amino acid residues
CC 68-77 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent
CC tumour antigen capable of eliciting an antigen specific immune
CC response by T cells. Cancer peptides (see AAY05967-87) derived from
CC CAG-3, portions of CAG-3 and their variants, are useful as cancer
CC vaccines. A claimed method of preventing or inhibiting cancer
CC involves administering a cancer peptide, with or without an HLA
CC molecule. The cancer peptides form part of, or are derived
CC from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer and
CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
CC thyroid cancers.
XX
SQ Sequence 10 AA;

Query Match 54.3%; Score 57; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AASGLNGCCR 11
Db 1 aasglnccr 10
|||||
1 aasglnccr 10

RESULT 10
AAY06047
ID AAY06047 standard; Peptide; 9 AA.
XX
XX AAY06047;
AC
XX
XX 16-AUG-1999 (first entry)
DT
XX
DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; human leukocyte antigen; HLA.

KW vaccine; human leukocyte antigen; HLA.

OS Homo sapiens.

XX WO9918206-A2.

PN WO9918206-A2.

XX 15-APR-1999.

PD 21-SEP-1998; 98WO-US19609.

XX 08-OCT-1997; 97US-0061428.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Rosenberg SA, Wang RF;

XX WPI; 1999-277270/23.

XX Cancer antigen NY ESO1/CAG-3

PS Example 10; Page 43; 88pp; English.

XX This peptide was identified as an HLA peptide motif following a
CC screen for epitopes from the coding region of human ESO-1/CAG-3
CC ORF1 (see AAX58599). 30 Epitopes (see AAY06018-47) were identified.
CC The present peptide (ranked 30) corresponds to amino acid residues
CC 69-77 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent
CC tumour antigen capable of eliciting an antigen specific immune
CC response by T cells. Cancer peptides (see AAY05967-87) derived from
CC CAG-3, portions of CAG-3 and their variants, are useful as cancer
CC vaccines. A claimed method of preventing or inhibiting cancer
CC involves administering a cancer peptide, with or without an HLA
CC molecule. The cancer peptides form part of, or are derived
CC from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer and
CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
CC thyroid cancers.

XX SQ Sequence 9 AA;

Query Match 50.5%; Score 53; DB 20; Length 9;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASGLNGCCR 11

Db 1 asglngccr 9

RESULT 11

AAY06059

ID AAY06059 standard; Peptide; 10 AA.

XX AC AAY06059;

XX 16-AUG-1999 (first entry)

DT Human cancer antigen NY ESO-1/CAG-3 peptide ESO10-77.

XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; cytotoxic T lymphocyte; CTL.

XX OS Homo sapiens.

XX WO9918206-A2.

PN WO9918206-A2.

XX

PD 15-APR-1999.

XX 21-SEP-1998; 98WO-US19609.

XX 08-OCT-1997; 97US-0061428.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Rosenberg SA, Wang RF;

PI WPI; 1999-277270/23.

XX Cancer antigen NY ESO1/CAG-3

PT Example 10; Page 45; 88pp; English.

XX Peptide ESO10-77 corresponds to amino acid residues 77-86 of
CC human NY ESO-1/CAG-3 ORF1 (see AAY05965), a new and potent tumour
CC antigen capable of eliciting an antigen specific immune response
CC by T cells. It was examined for reactivity to a cytotoxic T
CC lymphocyte (CTL), measured as release of granulocyte macrophage
CC colony stimulating factor. Cancer peptides (see AAY05967-87) derived
CC from CAG-3, portions of CAG-3 and their variants, are useful as
CC cancer vaccines. A claimed method of preventing or inhibiting
CC cancer involves administering a cancer peptide, with or without an
CC HLA molecule. The cancer peptides form part of, or are derived
CC from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer and
CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
CC thyroid cancers.

XX SQ Sequence 10 AA;

Query Match 44.8%; Score 47; DB 20; Length 10;

Best Local Similarity 100.0%; Pred. No. 7.6;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RCGARGPE 18

Db 1 rcgargpe 8

RESULT 12

AAY05993

ID AAY05993 standard; Peptide; 10 AA.

XX AC AAY05993;

XX 16-AUG-1999 (first entry)

DT Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.

XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; human leukocyte antigen; HLA.

XX OS Homo sapiens.

XX WO9918206-A2.

XX 15-APR-1999.

XX 21-SEP-1998; 98WO-US19609.

XX 08-OCT-1997; 97US-0061428.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Rosenberg SA, Wang RF;
PI WPI; 1999-277270/23.
XX Cancer antigen NY ES01/CAG-3
PT Example 10; Page 42; 88pp; English.
XX
PS This peptide was identified as an HLA peptide motif following a
XX screen for epitopes from the coding region of human ESO-1/CAG-3
CC ORF1 (see AAX58599). 30 Epitopes (see AAY05988-Y06017) were identified.
CC The present peptide (ranked 6) corresponds to amino acid residues
CC 77-86 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent
CC tumour antigen capable of eliciting an antigen specific immune
CC response by T cells. Cancer peptides (see AAY05967-87) derived from
CC CAG-3, portions of CAG-3 and their variants, are useful as cancer
CC vaccines. A claimed method of preventing or inhibiting cancer
CC involves administering a cancer peptide, with or without an HLA
CC molecule. The cancer peptides form part of, or are derived
CC from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer and
CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
CC thyroid cancers.
XX
SQ Sequence 10 AA;

Query Match 44.8%; Score 47; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RCGARGPE 18
Db 1 rcgargpe 8

RESULT 13
AAR69313
ID AAR69313 standard; peptide; 10 AA.
XX
AC AAR69313;
XX
DT 24-JUN-1995 (first entry)
DE Gp IIb/IIIa receptor ligand used in scintigraphic imaging of thrombi.
XX
KW Scintigraphy; thrombus; thrombi; imaging; specific binding;
KW technetium-99m; radiolabelled; Gp IIb/IIIa receptor ligand.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 2 /note= "S-acetamidomethyl-Cys"
FT Modified-site 4
FT Modified-site 4 /note= "S-acetamidomethyl-Cys"
FT Modified-site 10
FT /note= "this residue is joined via the OH group
FT to tris(2-succinimidoethyl)amine (TSEA)
FT to form one of three such peptides
FT connected to the amine; i.e. forming a
FT product of formula (peptide)3-TSEA"
XX
PN WO9323085-A.
XX
PD 25-NOV-1993.
XX
PF 21-MAY-1993; 93WO-US04794.
XX
PR 21-MAY-1992; 92US-0886752.
XX

PA (DIAT-) DIATECH INC.
XX Dean RF, Lister-James J;
PI WPI; 1993-386229/48.
XX
DR Claim 19; Page 42; 61pp; English.
XX
PT Reagent for scintigraphic imaging of thrombi with 99m technetium
PT - comprises synthetic peptide which binds to thrombus, covalently
PT coupled to metal binding gp.; rapidly cleared from blood and
PT tissue
XX
PS Claim 19; Page 42; 61pp; English.
XX
CC The invention relates to reagents for scintigraphic imaging of a
CC thrombus in-vivo, comprising (A) a specific binding compound capable of
CC binding to at least one component of a thrombus, covalently linked
CC to (B) a technetium-99m-binding moiety. Specific peptides
CC constituting the reagents are claimed as new. The present peptide is
CC one such peptide, in which the Cys(Acm)-Gly-Cys(Acm) moiety is the
CC 99m-Tc binding moiety and the residue constitutes the thrombus-
CC binding component.
XX
SQ Sequence 10 AA;

Query Match 40.0%; Score 42; DB 14; Length 10;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 CCRCGARG 16
Db 1 ccgcggrg 8

RESULT 14
AAW52088
ID AAW52088 standard; peptide; 10 AA.
XX
AC AAW52088;
XX
DT 23-SEP-1998 (first entry)
DE Targetting peptide #16 useful as component of thrombolytic agent.
XX
KW Thrombolytic agent; thrombolytic proteinase; blood clot; fibrin;
KW thrombus; antithrombotic activity.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 2 /note= "The side-chain thiol of Cys is protected by
FT an acetamidomethyl group"
FT Modified-site 4 /note= "The side-chain thiol group of Cys is protected
FT by an acetamidomethyl group"
XX
PN WO9824917-A1.
XX
PD 11-JUN-1998.
XX
PF 02-DEC-1997; 97WO-US21918.
XX
PR 02-DEC-1996; 96US-0753781.
XX
PA (DIAT-) DIATIDE INC.
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Bush LR, Flores-Sanchez S E, Markland FS, Swenson S;
XX WPI; 1998-333336/29.
XX
PT New thrombolytic agents - comprise thrombolytic proteinase

PT covalently linked to targetting compound for binding to component of
PT thrombus
XX
PS Claim 10; Page 64; 79pp; English.
XX
CC The invention relates to new thrombolytic agents which comprise a
CC thrombolytic proteinase covalently linked to a targetting compound
CC capable of specifically binding to a component of a thrombus. The
CC thrombolytic agents can be used for eliminating thrombi in vivo in, e.g.
CC myocardial infarction, cerebral ischaemia, deep vein thrombosis or
CC pulmonary embolism. A labelled form of the thrombolytic agent can also
CC be used to image thrombi for diagnostic purposes. The thrombolytic
CC agents are specifically targetted to thrombus sites in vivo and have
CC minimal haemorrhagic side effects and side effects related to non-
CC specific proteolysis. The present sequence represents a specifically
CC claimed targetting peptide.
XX
SQ Sequence 10 AA;

Query Match 40.0%; Score 42; DB 19; Length 10;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 CCRCGARG 16
Db 1 ccgcggrg 8

RESULT 15
AAY95511
ID AAY95511 standard; Peptide; 10 AA.
XX
AC AAY95511;
XX
DT 10-OCT-2000 (first entry)
XX
DE GPIIb/IIIa receptor ligand with polyvalent linking moiety.
XX
KW Thrombus; imaging; radioimaging; thrombosis; thromboembolism;
KW embolism; diagnosis; technetium-99m; GPIIb/IIIa receptor ligand.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 2 /note= "Cys(Acm)"
FT Modified-site 4 /note= "Cys(Acm)"
FT Peptide 1..10
FT /note= "3 peptides of this sequence are joined
FT C-terminally to the polyvalent linking
FT moiety tris(succinimidylethyl)amine"
XX
PN US6083481-A.
XX
PD 04-JUL-2000.
XX
PF 27-AUG-1998; 98US-0141127.
XX
PR 21-MAY-1992; 92US-0886752.
PR 21-MAY-1993; 93WO-US04794.
PR 05-JAN-1995; 95US-0335832.
XX
PA (DIAT-) DIATIDE INC.
XX
PI Lister-James J, Dean RT;
XX
DR WPI; 2000-498061/44.
XX
PT Composition comprises technetium-99m and polyamide reagent which binds
PT to thrombi, useful as scintigraphic imaging agent for imaging sites of
PT thrombus formation in vivo

XX Disclosure; Column 10; 27pp; English.
PS
XX
CC The present sequence is that of a GPIIb/IIIa receptor ligand. The
CC invention relates to radiolabeled reagents that are scintigraphic
CC imaging agents for imaging sites of thrombus formation in vivo.
CC The reagents each comprise a specific binding compound, such as the
CC present peptide, that is capable of binding to at least 1 component
CC of a thrombus, and which is covalently linked to a radiolabel-binding
CC moiety and may include a polyvalent lining moiety. A method for
CC using such a reagent labeled with technetium-99m to image a thrombus
CC site in a mammalian body is claimed.
XX
SQ Sequence 10 AA;

Query Match 40.0%; Score 42; DB 21; Length 10;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 CCRCGARG 16
Db 1 ccgcggrg 8

Search completed: July 3, 2002, 11:26:58
Job time: 955 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:39:32 ; Search time 61.64 Seconds
(without alignments)
29.545 Million cell updates/sec

Title: US-09-165-546A-11
Perfect score: 105
Sequence: 1 GAASGLNGCCRCGARGPE 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 308740 seqs, 101176262 residues

Total number of hits satisfying chosen parameters: 45157

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New: *
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep: *
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep: *
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep: *
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep: *
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep: *
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep: *
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	49	46.7	9	6	US-10-117-937-354
2	45	42.9	14	1	PCT-US02-10880-2
3	45	42.9	14	1	PCT-US02-10881-2
4	45	42.9	14	1	PCT-US02-11064-2
5	39	37.1	12	6	US-10-111-245-18
6	39	37.1	18	5	US-09-913-996A-2
7	37	35.2	10	1	PCT-US02-10880-1
8	37	35.2	10	1	PCT-US02-10881-1
9	37	35.2	10	1	PCT-US02-11064-1
10	34.5	32.9	18	1	PCT-US02-12353-10
11	34.5	32.9	18	6	US-10-141-645-10
12	33	31.4	9	5	US-09-344-040C-118
13	32.5	31.0	16	6	US-10-007-280A-153
14	32	30.5	10	7	US-60-369-452-17
15	31.5	30.0	13	4	US-08-771-212A-26
16	31	29.5	14	5	US-09-658-517B-16
17	31	29.5	14	5	US-09-658-517B-17
18	31	29.5	15	5	US-09-547-938B-85
19	30.5	29.0	17	6	US-10-126-752-1
20	30.5	29.0	17	6	US-10-126-752-4
21	30	28.6	10	5	US-09-855-604-932
22	30	28.6	13	5	US-09-722-250-77
23	30	28.6	13	5	US-09-722-250-77
24	30	28.6	18	6	US-10-105-299-3801
25	29	27.6	12	6	US-10-004-860-873
26	29	27.6	13	4	US-08-771-212A-25

27	29	27.6	15	5	US-09-527-083C-128	Sequence 128, App
28	29	27.6	15	5	US-09-527-083C-129	Sequence 129, App
29	29	27.6	15	5	US-09-527-083D-128	Sequence 128, App
30	29	27.6	15	5	US-09-527-083D-129	Sequence 129, App
31	29	27.6	15	6	US-10-113-872-1927	Sequence 1927, Ap
32	28	26.7	7	5	US-09-527-083C-74	Sequence 74, Appl
33	28	26.7	7	5	US-09-527-083D-74	Sequence 74, Appl
34	28	26.7	9	6	US-10-117-937-356	Sequence 356, App
35	28	26.7	10	6	US-10-117-937-357	Sequence 357, App
36	28	26.7	11	6	US-10-004-860-1184	Sequence 1184, Ap
37	28	26.7	13	5	US-09-722-250-107	Sequence 107, App
38	28	26.7	13	5	US-09-722-250-107	Sequence 107, App
39	28	26.7	14	5	US-09-563-286B-65	Sequence 65, Appl
40	28	26.7	15	5	US-09-547-938B-202	Sequence 202, App
41	28	26.7	18	1	PCT-US02-12353-1	Sequence 1, Appli
42	28	26.7	18	1	PCT-US02-12353-2	Sequence 2, Appli
43	28	26.7	18	1	PCT-US02-12353-3	Sequence 3, Appli
44	28	26.7	18	1	PCT-US02-12353-4	Sequence 4, Appli
45	28	26.7	18	1	PCT-US02-12353-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-10-117-937-354
; Sequence 354, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 354
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-354

Query Match 46.7%; Score 49; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGC 9
| | | | | | | | | |
Db 1 GAASGLNGC 9

RESULT 2
PCT-US02-10880-2
; Sequence 2, Application PC/TUS0210880
; GENERAL INFORMATION:
; APPLICANT: Stanley F. Barnett
; APPLICANT: Andrew Pate Owens
; TITLE OF INVENTION: INHIBITORS OF AKT ACTIVITY
; FILE REFERENCE: 20837
; CURRENT APPLICATION NUMBER: PCT/US02/10880
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/282,825
; PRIOR FILING DATE: 2001-04-10

; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely Synthetic Amino Acid Sequence
PCT-US02-10880-2

Query Match 42.9%; Score 45; DB 1; Length 14;
Best Local Similarity 58.3%; Pred. No. 5.9;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRC 12
| | | | |
Db 1 GTACGGGGCCGC 12

RESULT 3
PCT-US02-10881-2
; Sequence 2, Application PC/TUS0210881
; GENERAL INFORMATION:
; APPLICANT: Stanley F. Barnett
; APPLICANT: Andrew Pate Owens
; TITLE OF INVENTION: INHIBITORS OF AKT ACTIVITY
; FILE REFERENCE: 20838
; CURRENT APPLICATION NUMBER: PCT/US02/10881
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/282,824
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely Synthetic Amino Acid Sequence
PCT-US02-10881-2

Query Match 42.9%; Score 45; DB 1; Length 14;
Best Local Similarity 58.3%; Pred. No. 5.9;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRC 12
| | | | |
Db 1 GTACGGGGCCGC 12

RESULT 4
PCT-US02-11064-2
; Sequence 2, Application PC/TUS0211064
; GENERAL INFORMATION:
; APPLICANT: Stanley F. Barnett
; APPLICANT: Samuel L. Graham
; APPLICANT: David C. Remy
; TITLE OF INVENTION: INHIBITORS OF AKT ACTIVITY
; FILE REFERENCE: 20840
; CURRENT APPLICATION NUMBER: PCT/US02/11064
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/282,781
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely Synthetic Amino Acid Sequence

PCT-US02-11064-2

Query Match 42.9%; Score 45; DB 1; Length 14;
Best Local Similarity 58.3%; Pred. No. 5.9;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRC 12
| | | | |
Db 1 GTACGGGGCCGC 12

RESULT 5
US-10-111-245-18
; Sequence 18, Application US/10111245
; GENERAL INFORMATION:
; APPLICANT: Tan, Carina
; APPLICANT: McKee, Karen Kulju
; TITLE OF INVENTION: DOG AND RABBIT MOTILIN RECEPTOR
; TITLE OF INVENTION: ORTHOLOGS
; FILE REFERENCE: 20390P
; CURRENT APPLICATION NUMBER: US/10/111,245
; CURRENT FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: PCT/US00/29426
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: 60/162,264
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Rabbit
US-10-111-245-18

Query Match 37.1%; Score 39; DB 6; Length 12;
Best Local Similarity 85.7%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 CGARGPE 18
| | | | |
Db 4 CGSRGPE 10

RESULT 6
US-09-913-996A-2
; Sequence 2, Application US/09913996A
; GENERAL INFORMATION:
; APPLICANT: JANSEN, Robert
; APPLICANT: de BOER, Kylie
; TITLE OF INVENTION: ISOLATING A CYTOPLASMIC FRACTION WITHOUT
; TITLE OF INVENTION: IMPAIRING THE VIABILITY OF OCCYTES AND EMBRYONIC CELLS
; FILE REFERENCE: GH-005
; CURRENT APPLICATION NUMBER: US/09/913,996A
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: PCT/AU00/00125
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: PP 8841
; PRIOR FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-913-996A-2

Query Match 37.1%; Score 39; DB 5; Length 18;
Best Local Similarity 53.8%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 AASGLNGCCRCGA 14
||| |
Db 2 AAGCGACACGCGA 14

RESULT 7
PCT-US02-10880-1
; Sequence 1, Application PC/TUS0210880
; GENERAL INFORMATION:
; APPLICANT: Stanley F. Barnett
; APPLICANT: Andrew Pate Owens
; TITLE OF INVENTION: INHIBITORS OF AKT ACTIVITY
; FILE REFERENCE: 20837
; CURRENT APPLICATION NUMBER: PCT/US02/10880
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/282,825
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely Synthetic Amino Acid Sequence
PCT-US02-10880-1

Query Match 35.2%; Score 37; DB 1; Length 10;
Best Local Similarity 55.6%; Pred. No. 49;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 SGLNGCCRC 12
:| ||| |
Db 2 TCGGCGCCG 10

RESULT 8
PCT-US02-10881-1
; Sequence 1, Application PC/TUS0210881
; GENERAL INFORMATION:
; APPLICANT: Stanley F. Barnett
; APPLICANT: Andrew Pate Owens
; TITLE OF INVENTION: INHIBITORS OF AKT ACTIVITY
; FILE REFERENCE: 20838
; CURRENT APPLICATION NUMBER: PCT/US02/10881
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/282,824
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely Synthetic Amino Acid Sequence
PCT-US02-10881-1

Query Match 35.2%; Score 37; DB 1; Length 10;
Best Local Similarity 55.6%; Pred. No. 49;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 SGLNGCCRC 12
:| ||| |
Db 2 TCGGCGCCG 10

RESULT 9
PCT-US02-11064-1
; Sequence 1, Application PC/TUS0211064
; GENERAL INFORMATION:

; APPLICANT: Stanley F. Barnett
; APPLICANT: Samuel L. Graham
; APPLICANT: David C. Remy
; TITLE OF INVENTION: INHIBITORS OF AKT ACTIVITY
; FILE REFERENCE: 20840
; CURRENT APPLICATION NUMBER: PCT/US02/11064
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/282,781
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely Synthetic Amino Acid Sequence
PCT-US02-11064-1

Query Match 35.2%; Score 37; DB 1; Length 10;
Best Local Similarity 55.6%; Pred. No. 49;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 SGLNGCCRC 12
:| ||| |
Db 2 TCGGCGCCG 10

RESULT 10
PCT-US02-12353-10
; Sequence 10, Application PC/TUS0212353
; GENERAL INFORMATION:
; APPLICANT: Robert Lehrer
; APPLICANT: Alan Waring
; APPLICANT: Alexander Cole
; APPLICANT: Teresa Hong
; TITLE OF INVENTION: Retrocyclins: Antiviral and
; FILE REFERENCE: UCLA-001WO
; CURRENT APPLICATION NUMBER: PCT/US02/12353
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 60/284,855
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic variant
PCT-US02-12353-10

Query Match 32.9%; Score 34.5; DB 1; Length 18;
Best Local Similarity 70.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 8 GC-CRCGARG 16
|| ||| ||
Db 2 GCICRCIGRG 11

RESULT 11
US-10-141-645-10
; Sequence 10, Application US/10141645
; GENERAL INFORMATION:
; APPLICANT: Robert Lehrer
; APPLICANT: Alan Waring
; APPLICANT: Alexander Cole
; APPLICANT: Teresa Hong
; TITLE OF INVENTION: Retrocyclins - Antiviral and

; TITLE OF INVENTION: Antimicrobial Peptides
; FILE REFERENCE: UCLA-001CIP
; CURRENT APPLICATION NUMBER: US/10/141,645
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/284,855
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: Unassigned
; PRIOR FILING DATE: 2002-04-18
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic variant
US-10-141-645-10

Query Match 32.9%; Score 34.5; DB 6; Length 18;
Best Local Similarity 70.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 8 GC-CRCGARG 16
|| ||| ||
Db 2 GCICRCIGRG 11

RESULT 12
US-09-344-040C-118
; Sequence 118, Application US/09344040C
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determin
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 118
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-118

Query Match 31.4%; Score 33; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GARGPE 18
|||||
Db 1 GARGPE 6

RESULT 13
US-10-007-280A-153
; Sequence 153, Application US/10007280A
; GENERAL INFORMATION:
; APPLICANT: Sun, Yongming
; APPLICANT: Recipon, Herve
; APPLICANT: Salceda, Susana
; APPLICANT: Chenghua, Liu
; TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Prd

; FILE REFERENCE: DEX-0257
; CURRENT APPLICATION NUMBER: US/10/007,280A
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/246,640
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 153
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-007-280A-153

Query Match 31.0%; Score 32.5; DB 6; Length 16;
Best Local Similarity 50.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 4 SGL---NGCCRC 12
||: ||| |
Db 5 SGIFPDRGCCSC 16

RESULT 14
US-60-369-452-17
; Sequence 17, Application US/60369452
; GENERAL INFORMATION:
; APPLICANT: Paul Roben
; APPLICANT: Anthony C. Stevens
; TITLE OF INVENTION: TISSUE-SPECIFIC ENDOTHELIAL MEMBRANE
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: TPTECH.006PR
; CURRENT APPLICATION NUMBER: US/60/369,452
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Sus scrofa
US-60-369-452-17

Query Match 30.5%; Score 32; DB 7; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GLNGCCRC 12
|: ||: |
Db 1 GVEGCTKC 8

RESULT 15
US-08-771-212A-26
; Sequence 26, Application US/08771212A
; GENERAL INFORMATION:
; APPLICANT: Berlin, V.
; APPLICANT: Damagnez, V.
; APPLICANT: Smith, S.
; TITLE OF INVENTION: NUCLEIC ACIDS FOR IDENTIFYING ANTI-FUNGAL AGENTS, AND USES REL
; TITLE OF INVENTION: THERETO
; FILE REFERENCE: GPCI-P03-074
; CURRENT APPLICATION NUMBER: US/08/771,212A
; CURRENT FILING DATE: 1996-12-20
; PRIOR APPLICATION NUMBER: 08/631,319
; PRIOR FILING DATE: 1996-04-10
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-771-212A-26

Query Match 30.08; Score 31.5; DB 4; Length 13;
Best Local Similarity 61.58; Pred. NO. 3.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

QY 4 SGLNGCCRCGARG 16
| | | | |
Db 4 SNLN---RCGFRG 13

Search completed: July 3, 2002, 11:39:32
Job time: 883 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:27:54 ; Search time 47.88 Seconds
(without alignments)
9.183 Million cell updates/sec

Title: US-09-165-546A-11
Perfect score: 105
Sequence: 1 GAASGLNGCCRCGARGPE 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 113617

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	105	100.0	18	4	US-09-359-503-11	Sequence 11, Appl
2	42	40.0	10	2	US-08-753-781-13	Sequence 13, Appl
3	36	34.3	15	1	US-08-137-800-22	Sequence 22, Appl
4	36	34.3	15	1	US-08-477-383-22	Sequence 22, Appl
5	36	34.3	15	1	US-08-487-174-22	Sequence 22, Appl
6	36	34.3	15	1	US-08-480-750-22	Sequence 22, Appl
7	36	34.3	15	4	US-08-602-999A-308	Sequence 308, App
8	34	32.4	13	4	US-08-737-841-8	Sequence 8, Appli
9	34	32.4	13	4	US-08-737-841-9	Sequence 9, Appli
10	34	32.4	13	4	US-08-737-841-11	Sequence 11, Appl
11	33.5	31.9	16	4	US-09-219-446B-9	Sequence 37, Appl
12	33	31.4	9	1	US-08-464-456-37	Sequence 37, Appl
13	33	31.4	9	1	US-08-463-052-37	Sequence 37, Appl
14	33	31.4	9	2	US-08-480-551-37	Sequence 37, Appl
15	33	31.4	9	2	US-08-335-832-9	Sequence 3, Appli
16	33	31.4	9	3	US-09-141-127-3	Sequence 3, Appli
17	33	31.4	10	2	US-08-753-781-3	Sequence 33, Appl
18	33	31.4	13	1	US-08-290-448A-33	Sequence 33, Appl
19	33	31.4	13	1	US-08-290-448A-33	Sequence 33, Appl
20	33	31.4	13	1	US-08-175-069A-33	Sequence 33, Appl
21	33	31.4	13	4	US-08-461-939B-33	Sequence 33, Appl
22	33	31.4	13	4	US-08-464-000-33	Sequence 33, Appl
23	33	31.4	14	2	US-08-335-832-10	Sequence 10, Appl
24	33	31.4	14	3	US-09-141-127-4	Sequence 4, Appli
25	33	31.4	15	2	US-08-753-781-4	Sequence 11, Appl
26	33	31.4	18	4	US-09-314-242-11	Sequence 11, Appl
27	32.5	31.0	16	4	US-09-219-446B-11	Sequence 11, Appl

28	32	30.5	10	1	US-08-000-931-3	Sequence 3, Appli
29	32	30.5	10	1	US-08-446-856A-12	Sequence 12, Appl
30	32	30.5	11	3	US-08-925-002-56	Sequence 56, Appl
31	32	30.5	12	1	US-08-446-856A-10	Sequence 10, Appl
32	32	30.5	16	2	US-08-692-257-2	Sequence 2, Appli
33	32	30.5	17	2	US-08-692-257-3	Sequence 3, Appli
34	32	30.5	18	2	US-08-692-257-4	Sequence 4, Appli
35	31.5	30.0	13	4	US-08-842-306B-30	Sequence 30, Appl
36	31.5	30.0	13	4	US-08-838-973B-30	Sequence 30, Appl
37	31	29.5	14	4	US-08-853-910-7	Sequence 7, Appli
38	31	29.5	16	1	US-08-322-962-6	Sequence 6, Appli
39	31	29.5	16	3	US-08-450-653-6	Sequence 6, Appli
40	30.5	29.0	17	2	US-08-955-206-1	Sequence 1, Appli
41	30.5	29.0	17	2	US-08-955-206-4	Sequence 4, Appli
42	30.5	29.0	17	3	US-08-955-050-1	Sequence 1, Appli
43	30.5	29.0	17	3	US-08-955-050-4	Sequence 4, Appli
44	30.5	29.0	17	4	US-09-382-950-3	Sequence 3, Appli
45	30.5	29.0	17	4	US-09-382-736B-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-359-503-11
; Sequence 11, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid


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;
; TOPOLOGY: linear
US-09-359-503-11

Query Match 100.0%; Score 105; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
Db 1 GAASGLNGCCRCGARGPE 18
|||||

RESULT 2
US-08-753-781-13
; Sequence 13, Application US/08753781C
; Patent No. 5951981
; GENERAL INFORMATION:
; APPLICANT: Markland Jr., Francis S.
; APPLICANT: Bush, Larry R.
; APPLICANT: Swenson, Stephen
; APPLICANT: Flores Sanchez, Eladio
; TITLE OF INVENTION: THROMBOLYTIC AGENTS WITH ANTITHROMBOTIC ACTIVITY
; FILE REFERENCE: DITI 124
; CURRENT APPLICATION NUMBER: US/08/753,781C
; CURRENT FILING DATE: 1996-12-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (2)
; OTHER INFORMATION: acetamidomethyl
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)
; OTHER INFORMATION: acetamidomethyl
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
; OTHER INFORMATION: peptide
US-08-753-781-13

Query Match 40.0%; Score 42; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 7.7;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 CCRCGARG 16
Db 1 CCGCGGRG 8
|||

RESULT 3
US-08-137-800-22
; Sequence 22, Application US/08137800
; Patent No. 5514774
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Hillyard, David R.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Santos, Ameurfina D.
; TITLE OF INVENTION: Conotoxin Peptides
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue N.W., Suite 1000
; CITY: Washington
; STATE: DC
; ZIP: 20005

Query Match 100.0%; Score 105; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAASGLNGCCRCGARGPE 18
Db 1 GAASGLNGCCRCGARGPE 18
|||||

RESULT 2
US-08-753-781-13
; Sequence 13, Application US/08753781C
; Patent No. 5951981
; GENERAL INFORMATION:
; APPLICANT: Markland Jr., Francis S.
; APPLICANT: Bush, Larry R.
; APPLICANT: Swenson, Stephen
; APPLICANT: Flores Sanchez, Eladio
; TITLE OF INVENTION: THROMBOLYTIC AGENTS WITH ANTITHROMBOTIC ACTIVITY
; FILE REFERENCE: DITI 124
; CURRENT APPLICATION NUMBER: US/08/753,781C
; CURRENT FILING DATE: 1996-12-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (2)
; OTHER INFORMATION: acetamidomethyl
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)
; OTHER INFORMATION: acetamidomethyl
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
; OTHER INFORMATION: peptide
US-08-753-781-13

Query Match 40.0%; Score 42; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 7.7;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 CCRCGARG 16
Db 1 CCGCGGRG 8
|||

RESULT 3
US-08-137-800-22
; Sequence 22, Application US/08137800
; Patent No. 5514774
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Hillyard, David R.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Santos, Ameurfina D.
; TITLE OF INVENTION: Conotoxin Peptides
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue N.W., Suite 1000
; CITY: Washington
; STATE: DC
; ZIP: 20005

Query Match 34.3%; Score 36; DB 1; Length 15;
Best Local Similarity 46.7%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 7 NGCC-----RCG 13
Db 1 NGCCRNPA CESHRCG 15
|||||

RESULT 4
US-08-477-383-22
; Sequence 22, Application US/08477383
; Patent No. 5589340
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Hillyard, David R.
; APPLICANT: Macintosh, J. Michael
; APPLICANT: Santos, Ameurfino S.
; TITLE OF INVENTION: Conotoxin Peptides
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,800
FILING DATE: 19-OCT-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-104763
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Conus striatus
US-08-137-800-22
```

NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107673
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Conus striatus
US-08-477-383-22

Query Match 34.3%; Score 36; DB 1; Length 15;
Best Local Similarity 46.7%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 1;

QY 7 NGCC-----RCG 13
|||||
Db 1 NGCCRNPACE\$HRCG 15

RESULT 5
US-08-487-174-22
Sequence 22, Application US/08487174
Patent No. 5595972
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameurfino S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,174
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107673
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Conus striatus
US-08-487-174-22

Query Match 34.3%; Score 36; DB 1; Length 15;
Best Local Similarity 46.7%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 1;

QY 7 NGCC-----RCG 13
|||||
Db 1 NGCCRNPACE\$HRCG 15

RESULT 6
US-08-480-750-22
Sequence 22, Application US/08480750
Patent No. 5633347
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameurfino S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,750
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107673
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Conus striatus
US-08-480-750-22

Query Match 34.3%; Score 36; DB 1; Length 15;

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Best Local Similarity 46.7%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 7 NGCC-----RCG 13
    ||||
Db 1 NGCCRNPA CESHRCG 15

RESULT 7
US-08-602-999A-308
; Sequence 308, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 308:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-308

Query Match 34.3%; Score 36; DB 4; Length 15;
Best Local Similarity 75.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CRCGARGP 17
    |||||
Db 1 CRCGRRLP 8

RESULT 8
US-08-737-841-8
; Sequence 8, Application US/08737841
; Patent No. 6150131
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; TITLE OF INVENTION: TREATMENT OF INFLUENZA VIRUS INFECTION
; TITLE OF INVENTION: USING ANTIVIRALS THAT INHIBIT ACYLATION/PALMITYLATION OF
```

```
; TITLE OF INVENTION: HEMAGGLUTININ
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,841
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-068
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-737-841-8

Query Match 32.4%; Score 34; DB 4; Length 13;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 NGCCRC 12
    |||||
Db 4 NGSCRC 9

RESULT 9
US-08-737-841-9
; Sequence 9, Application US/08737841
; Patent No. 6150131
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; TITLE OF INVENTION: TREATMENT OF INFLUENZA VIRUS INFECTION
; TITLE OF INVENTION: USING ANTIVIRALS THAT INHIBIT ACYLATION/PALMITYLATION OF
; TITLE OF INVENTION: HEMAGGLUTININ
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,841
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
```


REFERENCE/DOCKET NUMBER: 6923-068
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-737-841-9

Query Match 32.4%; Score 34; DB 4; Length 13;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 NGCCRC 12
II III
Db 4 NGSCRC 9

RESULT 10
US-08-737-841-11
Sequence 11, Application US/08737841
Patent No. 6150131
GENERAL INFORMATION:
APPLICANT: Palese, Peter
TITLE OF INVENTION: TREATMENT OF INFLUENZA VIRUS INFECTION
TITLE OF INVENTION: USING ANTIVIRALS THAT INHIBIT ACYLATION/PALMITYLATION OF
TITLE OF INVENTION: HEMAGGLUTININ
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,841
FILING DATE: 20-NOV-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6923-068
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-737-841-11

Query Match 32.4%; Score 34; DB 4; Length 13;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 NGCCRC 12
II III
Db 4 NGSCRC 9

RESULT 11
US-09-219-446B-9
Sequence 9, Application US/09219446B
Patent No. 6265541
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Yoshikami, Doju
APPLICANT: Cartier, G. Edward
APPLICANT: Luo, Siqin
APPLICANT: University of Utah Research Foundation
TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
FILE REFERENCE: Uses of Alpha-Conotoxins
CURRENT APPLICATION NUMBER: US/09/219,446B
CURRENT FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 60/080,588
PRIOR FILING DATE: 1998-04-03
PRIOR APPLICATION NUMBER: US 60/070,153
PRIOR FILING DATE: 1997-12-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 16
TYPE: PRT
ORGANISM: Conus purpurascens
US-09-219-446B-9

Query Match 31.9%; Score 33.5; DB 4; Length 16;
Best Local Similarity 42.9%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

QY 8 GCCR---CGARGPE 18
III I I I
Db 1 GCCSLPPCAANNPD 14

RESULT 12
US-08-464-456-37
Sequence 37, Application US/08464456
Patent No. 5681541
GENERAL INFORMATION:
APPLICANT: Dean, Richard T
TITLE OF INVENTION: Technetium-99m Labeled Polypeptides for
TITLE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,456
FILING DATE: 05-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: No. 5681541nan, Kevin, E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1104-V
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312 715 1000
TELEFAX: 312 715 1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 37:

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;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 1
;; OTHER INFORMATION: /label= Cys-Acm
;; OTHER INFORMATION: /note= "This cysteine residue is protected by
;; OTHER INFORMATION: esterification with acetic a..."
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 3
;; OTHER INFORMATION: /label= Cys-Acm
;; OTHER INFORMATION: /note= "This cysteine residue is protected by
;; OTHER INFORMATION: esterification with acetic a..."
US-08-464-456-37
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Query Match 31.4%; Score 33; DB 1; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 10 CRCGARG 16
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Db 1 CGCGGRG 7
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RESULT 13
US-08-463-052-37
; Sequence 37, Application US/08463052
; Patent No. 578960
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; TITLE OF INVENTION: Technetium-99m Labeled Polypeptides for
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
```

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,052
FILING DATE: 05-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: No. 5788960nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1104-V
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312 715 1000
TELEFAX: 312 715 1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /label= Cys-Acm
OTHER INFORMATION: /note= "This cysteine residue is protected by
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;; OTHER INFORMATION: esterification with acetic a..."
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 3
;; OTHER INFORMATION: /label= Cys-Acm
;; OTHER INFORMATION: /note= "This cysteine residue is protected by
;; OTHER INFORMATION: esterification with acetic a..."
US-08-463-052-37
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Query Match 31.4%; Score 33; DB 1; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 10 CRCGARG 16
| | | | |
Db 1 CGCGGRG 7
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RESULT 14
US-08-480-551-37
; Sequence 37, Application US/08480551
; Patent No. 5811394
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; TITLE OF INVENTION: Technetium-99m Labeled Polypeptides for
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Drive Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
```

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,551
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/264,176
FILING DATE:
APPLICATION NUMBER: US 07/653,012
FILING DATE: 08-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 90,1104
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312 715 1000
TELEFAX: 312 715 1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /label= Cys-Acm
OTHER INFORMATION: /note= "This cysteine residue is protected by
OTHER INFORMATION: esterification with acetic a..."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /label= Cys-Acm
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OTHER INFORMATION: /note= "This cysteine residue is protected by
OTHER INFORMATION: esterification with acetic a..."
US-08-480-551-37

Query Match 31.4%; Score 33; DB 2; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 10 CRCGARG 16
| | | | |
Db 1 CGCGGRG 7

RESULT 15
US-08-335-832-9
; Sequence 9, Application US/08335832
; Patent No. 5925331
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Lister-James, John
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; TITLE OF INVENTION: Thrombus Imaging
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335,832
; FILING DATE: 05-JAN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5925331nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,216-I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= Acn
; OTHER INFORMATION: /note= "This cysteine residue is blocked at the
; OTHER INFORMATION: sidechain sulfur by covalent linkage to an
; OTHER INFORMATION: acetamido group"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /label= Acn
; OTHER INFORMATION: /note= "This cysteine residue is blocked at the
; OTHER INFORMATION: sidechain sulfur by covalent linkage to an
; OTHER INFORMATION: acetamido group"
US-08-335-832-9

Query Match 31.4%; Score 33; DB 2; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.7e+05;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 10 CRCGARG 16
| | | | |
Db 1 CGCGGRG 7
Search completed: July 3, 2002, 11:27:55
Job time: 411 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 11:28:57 ; Search time 57.51 seconds
(without alignments)
30.075 Million cell updates/sec

Title: US-09-165-546A-12
Perfect score: 91
Sequence: 1 SRLLEFYLAMPFATPMEA 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 3210

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	27	29.7	15	2 B45115	peptidylprolyl iso
2	26	28.6	13	2 PH1596	Ig H chain V-D-J r
3	24	26.4	15	2 AF0832	phe leader peptide
4	23	25.3	13	2 PH1593	Ig H.chain V-D-J r
5	23	25.3	15	2 B61457	alpha-glucosidase
6	23	25.3	18	2 A48550	hexon - canine ade
7	23	25.3	18	2 B49048	T-cell receptor be
8	21	23.1	14	2 S09721	2S albumin small c
9	21	23.1	14	2 PA0104	protein QF200070 -
10	21	23.1	14	2 C48394	major fat-globule
11	21	23.1	15	1 LFECF	phe operon leader
12	21	23.1	16	2 PH1580	Ig H chain V-D-J r
13	21	23.1	16	2 S68730	bleomycin-binding
14	21	23.1	18	2 PH1368	Ig heavy chain DJ
15	21	23.1	18	2 A59137	protein Pil - gold
16	20	22.0	11	2 I52980	glucocerebrosidase
17	20	22.0	12	2 S43957	Ig mu chain V regi
18	20	22.0	14	2 PH1597	Ig H chain V-D-J r
19	20	22.0	14	2 PH1601	Ig H chain V-D-J r
20	20	22.0	14	2 PH1608	Ig H chain V-D-J r
21	20	22.0	15	2 A54397	Ig H chain V-D-J r
22	20	22.0	15	2 E91061	ubiquitin-carrier
23	20	22.0	15	2 PA0027	hypothetical prote
24	20	22.0	15	2 PH1610	protein QAI00006 -
25	20	22.0	16	2 PH1588	Ig H chain V-D-J r
26	20	22.0	16	2 PH1604	Ig H chain V-D-J r
27	20	22.0	16	2 S24667	protein-tyrosine k
28	20	22.0	17	2 PH1607	Ig H chain V-D-J r
29	20	22.0	18	1 DRUFPD	pigment-dispersing

30 20 22.0 18 2 S29166 quinaldine oxidore
31 20 22.0 18 2 S09722 2S albumin small c
32 20 22.0 18 2 S09723 2S albumin small c
33 20 22.0 18 2 A45590 beta-pigment-dispe
34 19 20.9 11 2 C58501 42K bile stone pro
35 19 20.9 12 4 JX0315 aminotransferase c
36 19 20.9 13 2 B61620 locustamyotropin I
37 19 20.9 14 2 PA0015 seed storage prote
38 19 20.9 14 2 B20872 alpha-2-macroglobu
39 19 20.9 14 2 A23996 beta-granin - rat
40 19 20.9 15 2 I49407 placental calcium-
41 19 20.9 15 2 PW0004 chlorophyll a/b-bl
42 19 20.9 15 2 B41436 ovostatin - green
43 19 20.9 15 2 PH1613 Ig H chain V-D-J r
44 19 20.9 16 2 A60551 leukocyte elastase
45 19 20.9 16 2 A25213 antifreeze glycopr

ALIGNMENTS

RESULT 1
B45115
peptidylprolyl isomerase (EC 5.2.1.8) FKBP51 - human (fragment)
N:Alternate names: FK506-binding protein FKBP51; peptidylprolyl cis-trans isomerase F
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997
C:Accession: B45115
R:Wiederrecht, G.; Hung, S.; Chan, H.K.; Marcy, A.; Martin, M.; Calaycay, J.; Boulton
J. Biol. Chem. 267, 21753-21760, 1992
A:Title: Characterization of high molecular weight FK-506 binding activities reveals
A:Reference number: A45115; MUID:93016131
A:Accession: B45115
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <WIE>
A:Experimental source: JURKAT cells
A:Note: sequence extracted from NCBI backbone (NCBIP:116748)
C:Keywords: cis-trans-isomerase; cyclosporin A binding

Query Match 29.7%; Score 27; DB 2; Length 15;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 YLAMPFA 13
||| |:
Db 7 YLAPPYA 13

RESULT 2
PH1596
Ig H chain V-D-J region (wild-type clone 303) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1596
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less m
A:Reference number: PH1580; MUID:93301609
A:Accession: PH1596
A:Molecule type: DNA
A:Residues: 1-13 <LEV>
A:Experimental source: bone marrow pre-B lymphocyte
C:Keywords: immunoglobulin

Query Match 28.6%; Score 26; DB 2; Length 13;
Best Local Similarity 41.7%; Pred. No. 2.7e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 SRLLEFYLAMPF 12
:| | :| | :

Db 2 ARRLGYYAMDY 13

RESULT 3

AF0832

phe leader peptide [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain C;Species: Salmonella enterica subsp. enterica serovar Typhi

A;Note: this species has also been called Salmonella typhi

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001

C;Accession: AF0832

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, , S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A;Reference number: AB0502; PMID:11677608

A;Accession: AF0832

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-15 <PAR>

A;Cross-references: GB:AL513382; PIDN:CAD05845.1; PID:gl6503820; GSPDB:GN00176

C;Genetics:

A;Gene: STY2853a

Query Match 26.4%; Score 24; DB 2; Length 15;

Best Local Similarity 35.7%; Pred. No. 7.1e+02;

Matches 5; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 RLLEFYLAMPFATP 15

:| | | | |

Db 2 KLTRFFFAFFFIFF 15

RESULT 4

PH1593

Ig H chain V-D-J region (wild-type clone 144) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C;Accession: PH1593

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice

A;Reference number: PH1580; MUID:93301609

A;Accession: PH1593

A;Molecule type: DNA

A;Residues: 1-13 <LEV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 25.3%; Score 23; DB 2; Length 13;

Best Local Similarity 41.7%; Pred. No. 9.2e+02;

Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 SRLLEFYLAMPF 12

:| | | | |

Db 2 ARPLRHHYAMDY 13

RESULT 5

B61457

alpha-glucosidase (EC 3.2.1.20) - Tetrahymena pyriformis (strain W) (fragment)

C;Species: Tetrahymena pyriformis

C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 07-Dec-1999

C;Accession: B61457

R;Banno, Y.; Sasaki, N.; Yoshino, T.; Mochizuki, J.I.; Hirata, H.; Nozawa, Y.

J. Protozool. 36, 562-567, 1989

A;Title: A thermostable acid alpha-glucosidase from Tetrahymena thermophila: purification

A;Reference number: A61457; MUID:90095988

A;Accession: B61457

A;Molecule type: protein

A;Residues: 1-15 <BAN>

C;Genetics:

A;Genetic code: SGC5

C;Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; lysosome; mo

Query Match 25.3%; Score 23; DB 2; Length 15;

Best Local Similarity 42.9%; Pred. No. 1.1e+03;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 11 PFATPME 17

|| |::

Db 4 PFTPLQ 10

RESULT 6

A48550

hexon - canine adenovirus 1 (fragment)

C;Species: Mastadenovirus can1 (canine adenovirus 1)

C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 26-Aug-1999

C;Accession: A48550

R;Cai, F.; Weber, J.M.

Virus Genes 6, 307-312, 1992

A;Title: Nucleotide and deduced amino acid sequence of the canine adenovirus type 1 p

A;Reference number: A48550; MUID:93033182

A;Accession: A48550

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-18 <CAI>

A;Cross-references: GB:M72715; NID:g210022; PIDN:AAA42528.1; PID:g210023

A;Note: sequence extracted from NCBI backbone (NCBIN:114644, NCBIP:114646)

C;Superfamily: adenovirus hexon protein

Query Match 25.3%; Score 23; DB 2; Length 18;

Best Local Similarity 57.1%; Pred. No. 1.3e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 YLAMPFA 13

|| |::

Db 6 YLRTPPFS 12

RESULT 7

B49048

T-cell receptor beta chain V region (CDR3 junction, clone Vbeta20.1) - human (fragmen

C;Species: Homo sapiens (man)

C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997

C;Accession: B49048

R;Sioud, M.; Kjeldsen-Kragh, J.; Suleyman, S.; Vinje, O.; Natvig, J.B.; Forre, O.

Eur. J. Immunol. 22, 2413-2418, 1992

A;Title: Limited heterogeneity of T cell receptor variable region gene usage in juven

A;Reference number: A49048; MUID:92387250

A;Accession: B49048

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-18 <SIO>

A;Experimental source: patient EV, IL-2R+ synovial T-cells

A;Note: sequence extracted from NCBI backbone (NCBIP:113264)

C;Keywords: T-cell receptor

Query Match 25.3%; Score 23; DB 2; Length 18;

Best Local Similarity 66.7%; Pred. No. 1.3e+03;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 FYLAMP 11

|| | |

Db 4 FYLCAP 9

RESULT 8

S09721

2S albumin small chain nIII - rape (fragments)
C;Species: Brassica napus (rape)
C;Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
C;Accession: S09721
R;Monsalve, R.I.; Menendez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.
FEBS Lett. 263, 209-212, 1990
A;Title: beta-Turns as structural motifs for the proteolytic processing of seed proteins
A;Reference number: S09720; MUID:90242974
A;Accession: S09721
A;Molecule type: protein
A;Residues: 1-9;10-14 <MON>
A;Experimental source: seed

Query Match 23.1%; Score 21; DB 2; Length 14;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 9 AMPFATPMEA 18
I I I I ::
Db 2 AGFRIPKQS 11

RESULT 9
PA0104
protein QF200070 - fungus (Fusarium sporotrichioides) (fragment)
C;Species: Fusarium sporotrichioides
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C;Accession: PA0104
R;Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides
A;Reference number: PA0051
A;Accession: PA0104
A;Molecule type: protein
A;Residues: 1-14 <CHO>

Query Match 23.1%; Score 21; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 MPFATPME 17
I I I I :
Db 4 MXFAXPRO 11

RESULT 10
C48394
major fat-globule membrane protein GP 55 - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
C;Accession: C48394
R;Mather, I.H.; Banghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig II-like sequences.
A;Reference number: A48394; MUID:93250576
A;Accession: C48394
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14 <MAT>
A;Experimental source: milk
A;Note: sequence extracted from NCBI backbone (NCBIP:131446)

Query Match 23.1%; Score 21; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 12 FATPME 17
I : I I
Db 4 FSAPLE 9

RESULT 11
LFECF
phe operon leader peptide - Escherichia coli
A;Alternate names: attenuator peptide
C;Species: Escherichia coli
C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
C;Accession: A03593; B36494; A65038
R;Zurawski, G.; Brown, K.; Killingly, D.; Yanofsky, C.
Proc. Natl. Acad. Sci. U.S.A. 75, 4271-4275, 1978
A;Title: Nucleotide sequence of the leader region of the phenylalanine operon of Esch
A;Reference number: A03593; MUID:79033820
A;Accession: A03593
A;Molecule type: DNA
A;Residues: 1-15 <ZUR>
A;Cross-references: GB:V00314; GB:J01658; NID:g42378; PIDN:CAA23600.1; PID:g42379
R;Gavini, N.; Davidson, B.E.
J. Biol. Chem. 265, 21532-21535, 1990
A;Title: pheAo mutants of Escherichia coli have a defective pheA attenuator.
A;Reference number: A36494; MUID:91072346
A;Accession: B36494
A;Molecule type: DNA
A;Residues: 1-15 <GAV>
A;Cross-references: GB:M58024; GB:J05694; NID:g147178; PIDN:AAA62783.1; PID:g147180
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Accession: A65038
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-15 <BLAT>
A;Cross-references: GB:AE000346; GB:U00096; NID:g2367141; PIDN:AAC75647.1; PID:g17889
A;Experimental source: strain K-12, substrain MGL655
C;Genetics:
A;Gene: pheL; pheAe
A;Map position: 56 min
C;Superfamily: pheA leader peptide

Query Match 23.1%; Score 21; DB 1; Length 15;
Best Local Similarity 33.3%; Pred. No. 2.4e+03;
Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 4 LEFYLAMPFATP 15
: I : I I
Db 4 IPFFFAFFFTFP 15

RESULT 12
PH1580
Ig H chain V-D-J region (wild-type clone 3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1580
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less m
A;Reference number: PH1580; MUID:93301609
A;Accession: PH1580
A;Molecule type: DNA
A;Residues: 1-16 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 23.1%; Score 21; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 FYLAM 10

Db 10 FYIAM 14

|| ||

RESULT 13

S68730

bleomycin-binding protein - Streptomyces verticillus (fragment)

C;Species: Streptomyces verticillus

C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 17-Mar-1999

C;Accession: S68730

R;Sugiyama, M.; Kumagai, T.; Matsuo, H.; Bhuiyan, M.Z.A.; Ueda, K.; Mochizuki, H.; Nakamura, S.; Lett, 362, 80-84, 1995

A;Title: Overproduction of the bleomycin-binding proteins from bleomycin-producing Streptomyces verticillus

A;Reference number: S68730; MUID:95212588

A;Accession: S68730

A;Molecule type: protein

A;Residues: 1-16 <SUG>

A;Experimental source: ATCC 15003

C;Keywords: antibiotic resistance

Query Match 23.1%; Score 21; DB 2; Length 16;

Best Local Similarity 26.7%; Pred. No. 2.6e+03;

Matches 4; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 3 LLEFYLAMPFATPME 17

:::| |::| |::

Db 1 VVKELGAVPVLTAVD 15

RESULT 14

PH1368

Ig heavy chain DJ region (clone C111-112) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C;Accession: PH1368

R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G. J. Exp. Med. 176, 1577-1581, 1992

A;Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma

A;Reference number: PH1302; MUID:93094761

A;Accession: PH1368

A;Molecule type: DNA

A;Residues: 1-18 <WAS>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match 23.1%; Score 21; DB 2; Length 18;

Best Local Similarity 42.9%; Pred. No. 2.9e+03;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 LEFYLAM 10

:::| |

Db 5 MEYYIGM 11

RESULT 15

A59137

protein Pil - golden needle mushroom (fragment)

C;Species: Flammulina velutipes (golden needle mushroom)

C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 12-Nov-1999

C;Accession: A59137

R;Sakamoto, Y.; Ando, A.; Tamai, Y.; Miura, K.

A;Title: Submitted to the Protein Sequence Database, November 1999

A;Description: Differences of proteins expressed in the fruiting dikaryon and the non-fructifying dikaryon

A;Reference number: A59137

A;Accession: A59137

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-18 <SAK>

Query Match 23.1%; Score 21; DB 2; Length 18;

Best Local Similarity 28.6%; Pred. No. 2.9e+03;

Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 11 PFATPME 17

:::| |::| |::

Db 2 PYTSPVQ 8

Search completed: July 3, 2002, 11:28:57

Job time: 398 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:41:55 ; Search time 27.94 Seconds
(without alignments)
24.945 Million cell updates/sec

Title: US-09-165-546A-12

Perfect score: 91
Sequence: 1 SRLLEFYLAMPPFATPMEA 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 923

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	26.4	14	1 ECDC_LYMDI	P80940 lymantria d
2	23	25.3	18	1 HEX_ADECU	P35985 canine aden
3	22	24.2	14	1 MARI_ALTSP	P29399 alteromonas
4	21	23.1	15	1 LPF_ECOLI	P03057 escherichia
5	21	23.1	15	1 UN01_PINPS	P81106 pinus pinas
6	20	22.0	13	1 CRBL_ICASP	P17237 icaria sp.
7	20	22.0	18	1 DRPH_UCAPU	P08871 uca pugilat
8	19	20.9	9	1 MGMT_BOVIN	P29177 bos taurus
9	19	20.9	10	1 COXQ_SHEEP	P80337 ovis aries
10	19	20.9	12	1 PA2B_VIPBO	P31859 vipera beru
11	19	20.9	13	1 LMT4_LOCMI	P41490 locusta mig
12	19	20.9	15	1 MCRA_METTE	P22948 methanosarc
13	19	20.9	16	1 ANP8_ELEGR	P11921 eleginus gr
14	18	19.8	8	1 UPAA_HUMAN	P30096 homo sapien
15	18	19.8	10	1 NS1_MYCTU	P81135 mycobacteri
16	18	19.8	11	1 PQQC_PSEFL	P55173 pseudomonas
17	18	19.8	12	1 TIN2_HOPTI	P82652 hoplobatrac
18	18	19.8	17	1 ATPI_PAVLU	P28529 pavlova lut
19	18	19.8	17	1 PH4_PERAM	P82697 periplaneta
20	17	18.7	8	1 ALL7_CARMA	P81809 carcinus ma
21	17	18.7	8	1 PPK2_PERAM	P82692 periplaneta
22	17	18.7	10	1 ANGI_BOTJA	Q10581 bothrops ja
23	17	18.7	10	1 LPK2_LOCMI	P41488 locusta mig
24	17	18.7	11	1 LPW_THETH	P05624 thermus aqu
25	17	18.7	12	1 HS9A_RAT	P82995 rattus norv
26	17	18.7	13	1 YPNP_PHOLU	P41122 photorhabdu
27	17	18.7	14	1 HY14_PIG	P01155 sus scrofa
28	17	18.7	15	1 ACEA_ACICA	P28467 acinetobact
29	17	18.7	15	1 PGTS_PELAC	P80564 pelobacter
30	17	18.7	15	1 UBL1_MONDO	P50103 monodelphis
31	17	18.7	15	1 UC25_MAIZE	P80631 zea mays (m
32	17	18.7	18	1 A2M_OCTVU	P30800 octopus vul
33	17	18.7	18	1 NPA_BOVIN	P15506 bos taurus

34	16	17.6	5	1 EI03_LITRU	P82099 litoria rub
35	16	17.6	5	1 RE21_LITRU	P82071 litoria rub
36	16	17.6	5	1 RE31_LITRU	P82072 litoria rub
37	16	17.6	5	1 SUGA_ACHDO	P19991 acheta dome
38	16	17.6	7	1 CARP_MYTED	P10420 mytilus edu
39	16	17.6	7	1 UN06_PINPS	P81675 pinus pinas
40	16	17.6	10	1 COXQ_RABIT	P80336 oryctolagus
41	16	17.6	11	1 TKND_RANCA	P22691 rana catesb
42	16	17.6	13	1 GER2_HORVU	P28526 hordeum vul
43	16	17.6	13	1 PSAJ_PEA	P17229 pisum sativ
44	16	17.6	14	1 TKNM_RANMA	P40951 rana margar
45	16	17.6	14	1 UHA1_CANFA	P99503 canis famil

ALIGNMENTS

RESULT 1					
ECDC_LYMDI					
ID ECDC_LYMDI	STANDARD;	PRT;	14 AA.		
AC P80940;					
DT 15-JUL-1998	(Rel. 36, Created)				
DT 15-JUL-1998	(Rel. 36, Last sequence update)				
DT 15-JUL-1998	(Rel. 36, Last annotation update)				
DE Testis ecdysiotropin peptide C (TE).					
OS Lymantria dispar (Gypsy moth).					
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;					
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;					
OC Noctuoidea; Lymantriidae; Lymantria.					
OX NCBI_TaxID=13123;					
RN [1]					
RP SEQUENCE.					
RC TISSUE=Brain;					
RX MEDLINE=97387807; PubMed=9243792;					
RA Loeb M.J., Wagner R.M., Woods C.W., Gelman D.G., Harrison D.,					
RA Bell R.A.;					
RT "Naturally occurring analogs of Lymantria testis ecdysiotropin, a					
RT gonadotropin isolated from brains of Lymantria dispar pupae.";					
RL Arch. Insect Biochem. Physiol. 36:37-50(1997).					
CC -!- FUNCTION: STIMULATES SYNTHESIS OF ECDYSTEROID IN THE TESTES					
CC OF LARVAE AND PUPAE.					
SQ SEQUENCE 14 AA; 1553 MW; 17F479531A685CBB CRC64;					

Query Match 26.4%; Score 24; DB 1; Length 14;
Best Local Similarity 57.1%; Pred. No. 4.1e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy	7 YLAMPPFA 13
	:
Db	7 YTPLPFA 13

RESULT 2

HEX_ADECU					
ID HEX_ADECU	STANDARD;	PRT;	18 AA.		
AC P35985;					
DT 01-JUN-1994	(Rel. 29, Created)				
DT 01-JUN-1994	(Rel. 29, Last sequence update)				
DT 01-NOV-1997	(Rel. 35, Last annotation update)				
DE Hexon protein (Late protein 2) (Fragment).					
GN PII.					
OS Canine adenovirus type 1 (strain Utrecht).					
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.					
OX NCBI_TaxID=36364;					
RN [1]					
RP SEQUENCE FROM N.A.					
RX MEDLINE=93033182; PubMed=1413543;					
RA Cai F., Weber J.M.;					
RT "Nucleotide and deduced amino acid sequence of the canine adenovirus					
RT type 1 proteinase.";					
RL Virus Genes 6:307-312(1992).					
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE STRUCTURAL PROTEINS IN THE					

```
CC VIRAL COAT AND IS SYNTHESIZED DURING LATE INFECTION.
CC -!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -----
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CC -----
DR EMBL; M72715; AAA42528.1; -.
DR PIR; A48550; A48550.
DR HSSP; P03277; LDHX.
DR InterPro; IPR000736; Adeno_hexon.
DR Pfam; PF01065; Adeno_hexon; 1.
KW Coat protein; Hexon protein; Late protein.
FT NON_TER 1
FT SEQUENCE 18 AA; 1938 MW; B9E2AE307A420962 CRC64;

Query Match      25.3%; Score 23; DB 1; Length 18;
Best Local Similarity 57.1%; Pred. No. 7.8e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 YLAMPFA 13
Db || ||:
6 YLRTFPS 12

RESULT 3
MARI_ALTSP
ID MARI_ALTSP STANDARD; PRT; 14 AA.
AC P29399;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Marinosatin C-2 [Marinosatin C-1; Marinosatin D].
OS Alteromonas sp. (Strain B-10-31).
OC Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
OC Alteromonas.
OX NCBI_TaxID=29456;
RN [1]
RP SEQUENCE, AND ACTIVE SITE.
RX MEDLINE=92176155; PubMed=1794974;
RA Takano R., Imada C., Kamei K., Hara S.;
RT "The reactive site of marinosatin, a proteinase inhibitor from
RT marine Alteromonas sp. B-10-31.";
RL J. Biochem. 110:856-858(1991).
CC -!- FUNCTION: INHIBITS SUBTILISIN, CHYMOTRYPSIN, AND ELASTASE, BUT
CC NOT TRYPSIN.
KW Serine protease inhibitor.
FT PEPTIDE 1 14 MARINOSTATIN C-2.
FT PEPTIDE 3 14 MARINOSTATIN C-1.
FT PEPTIDE 4 14 MARINOSTATIN D.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 6 7 REACTIVE BOND.
FT SEQUENCE 14 AA; 1644 MW; 6E7CEE92EF32E44 CRC64;

Query Match      24.2%; Score 22; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFAT 14
Db ||||
2 PFAT 5

RESULT 4
LPF_ECOLI
ID LPF_ECOLI STANDARD; PRT; 15 AA.
AC P03057;
```

```
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Phe leader peptide (Attenuator peptide).
GN PHEL OR PHEAE OR B2598.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=79033820; PubMed=360214;
RA Zurawski G., Brown K., Killingly D., Yanofsky C.;
RT "Nucleotide sequence of the leader region of the phenylalanine operon
RT of Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:4271-4275(1978).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91072346; PubMed=2254312;
RA Gavini N., Davidson B.E.;
RT "pheAO mutants of Escherichia coli have a defective pheA attenuator.";
RL J. Biol. Chem. 265:21532-21535(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
CC OF PHENYLALANINE.
CC -----
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CC -----
DR EMBL; V00314; CAA23600.1; -.
DR EMBL; M10431; AAA24329.1; -.
DR EMBL; M58024; AAA62783.1; -.
DR EMBL; AE000346; AAC75647.1; -.
DR PIR; A03593; LFECF.
DR PIR; B36494; B36494.
DR EcoGene; EG11271; pheL.
KW Leader peptide; Complete proteome.
SQ SEQUENCE 15 AA; 1924 MW; CFE14AE3BFF935E0 CRC64;

Query Match      23.1%; Score 21; DB 1; Length 15;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 4 LEFYLAMPFATP 15
Db : | : | : |
4 IPFFFAFFFTFP 15

RESULT 5
UN01_PINPS
ID UN01_PINPS STANDARD; PRT; 15 AA.
AC P81106;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of needles (S1247/S1248) (N150/N151)
DE (Fragment).
OS Pinus pinaster (Maritime pine).
```


OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RA Plomion C., Costa P., Bahrman N., Frigerio J.M.;
RT "Genetic analysis of needle proteins in maritime pine. 1. Mapping
RT dominant and codominant protein markers assayed on diploid tissue, in
RT a haploid-based genetic map.";
RL Silvae Genetica 46:161-165(1997).
RN [2]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.5, ITS MW IS: 62 kDa.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1670 MW; 29CE44CD51E98FCF CRC64;

Query Match 23.1%; Score 21; DB 1; Length 15;
Best Local Similarity 42.9%; Pred. No. 1.4e+03;
Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 5 EFYLAMPFATPMEA 18
Db 2 EEQITQPSATNDEA 15
| : ||| ||
2 EEQITQPSATNDEA 15

RESULT 6
CRBL_ICASP STANDARD; PRT; 13 AA.
AC PI7237;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Chemotactic peptide (I-CP).
OS Icaria sp. (Ropalidian wasp).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Vespoidea; Vespidae; Polistinae; Icaria.
OX NCBI_TaxID=7495;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Yasuhara T., Itokawa H., Suzuki N., Nakamura H., Nakajima T.;
RL (In) Izumiya N. (eds.);
RL Peptide chemistry 1984, pp.177-182, Protein Research Foundation,
RL Osaka (1985).
CC -!- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. INDUCES THE CHEMOTAXIS
CC OF NEUTROPHILS.
KW Mast cell degranulation; Chemotaxis; Venom; Amidation.
FT MOD_RES 13 13
FT SEQUENCE 13 AA; 1353 MW; 348DBC7AA30A3768 CRC64;

Query Match 22.0%; Score 20; DB 1; Length 13;
Best Local Similarity 42.9%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 10 MPFATPM 16
Db 2 VPFLGPL 8
: || |:
2 VPFLGPL 8

RESULT 7

DRPH_UCAPU STANDARD; PRT; 18 AA.
ID DRPH_UCAPU
AC P08871;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Pigment-dispersing hormone (PDH) (Light adapting distal retinal
DE pigment hormone) (DRPH).
OS Uca pugilator (Atlantic sand fiddler crab) (Celuca pugilator).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Ocypodoidea; Ocypodidae; Ocypodinae; Uca complex;
OC Celuca.
OX NCBI_TaxID=6772;
RN [1]
RP SEQUENCE.
RA Rao K.R., Riehm J.P., Zahnow C.A., Kleinholz L.H., Tarr G.E.,
RA Johnson L., Norton S., Landau M., Semmes O.J., Satttelberg R.M.,
RA Jorenbey W.H., Hintz M.F.;
RT "Characterization of a pigment-dispersing hormone in eyestalks of the
RT fiddler crab Uca pugilator.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:5319-5322(1985).
RN [2]
RP SEQUENCE.
RX MEDLINE=93230895; PubMed=8472537;
RA Loehr J., Klein J., Webster S.G., Dircksen H.;
RT "Quantification, immunoaffinity purification and sequence analysis of
RT a pigment-dispersing hormone of the shore crab, Carcinus maenas
RT (L.).";
RL Comp. Biochem. Physiol. 104B:699-706(1993).
CC -!- FUNCTION: CAUSES THE MIGRATION OF THE DISTAL RETINAL PIGMENT
CC INTO THE PROXIMAL END OF THE PIGMENT CHROMATOPHORE CELLS AND
CC THUS DECREASES THE AMOUNT OF LIGHT ENTERING THE RETINULAS.
CC -!- SIMILARITY: TO THE PDH OF OTHER ARTHROPODS.
DR PIR; A25144; DRUFPD.
KW Hormone; Amidation.
FT DOMAIN 6 9
FT MOD_RES 18 18
FT SEQUENCE 18 AA; 1928 MW; 25D5CE8D016F544E CRC64;

Query Match 22.0%; Score 20; DB 1; Length 18;
Best Local Similarity 36.4%; Pred. No. 2.4e+03;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 SRLLEFYLAMP 11
Db 2 SELINSILGLP 12
| | : | : |
2 SELINSILGLP 12

RESULT 8
MGMT_BOVIN STANDARD; PRT; 9 AA.
AC P29177;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) (6-O-
DE methylguanine-DNA methyltransferase) (Fragment).
GN MGMT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Thymus;
RX MEDLINE=90174912; PubMed=23088822;
RA Rydberg B., Hall J., Karran P.;
RT "Active site amino acid sequence of the bovine O6-methylguanine-DNA
RT methyltransferase.";
RL Nucleic Acids Res. 18:17-21(1990).

```
CC -!- FUNCTION: REPAIR OF ALKYLATED GUANINE IN DNA BY STOICHIOMETRICALLY
CC TRANSFERRING THE ALKYL GROUP AT THE O-6 POSITION TO A CYSTEINE
CC RESIDUE IN THE ENZYME. THIS IS A SUICIDE REACTION: THE ENZYME IS
CC IRREVERSIBLY INACTIVATED.
CC -!- CATALYTIC ACTIVITY: DNA (containing 6-O-methylguanine) +
CC [protein]-L-cysteine = DNA (without 6-O-methylguanine) + protein
CC S-methyl-L-cysteine.
CC -!- SIMILARITY: WITH SEGMENTS OF E.COLI ADA AND OGT METHYLTRANSFERASE
CC WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.
DR InterPro; IPR001497; Methyltransf_1.
DR PROSITE; PS00374; MGMT; PARTIAL.
KW DNA repair; Transferase; Methyltransferase.
FT NON_TER 1 1
FT ACT_SITE 9 9 ALKYL GROUP ACCEPTOR (BY SIMILARITY).
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 967 MW; 325171A720476047 CRC64;

Query Match 20.9%; Score 19; DB 1; Length 9;
Best Local Similarity 50.0%; Pred. No. 1e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 MPFATP 15
Db :| ||
3 IPILTP 8

RESULT 9
COXQ_SHEEP STANDARD; PRT; 10 AA.
ID COXQ_SHEEP
AC P80337;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Cytochrome c oxidase polypeptide VIII-liver/heart (EC 1.9.3.1)
DE (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart, and Liver;
RA Freund R., Kadenbach B.;
RL Submitted (MAR-1994) to the SWISS-PROT data bank.
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) -> 4 ferricytochrome
CC c + 2 H(2)O.
KW Oxidoreductase; Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1027 MW; C4E95CA33DC7633D CRC64;

Query Match 20.9%; Score 19; DB 1; Length 10;
Best Local Similarity 57.1%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 AMPFATP 15
Db | | ||
3 AKPAKTP 9

RESULT 10
PA2B_VIPBO STANDARD; PRT; 12 AA.
ID PA2B_VIPBO
AC P31859;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Phospholipase A2, basic (EC 3.1.1.4) (Phosphatidylcholine
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```
DE 2-acylhydrolase) (Fragment).
OS Vipera berus orientalis (Viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Vipera.
OX NCBI_TaxID=31157;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=74128698; PubMed=4206446;
RA Delori P.J.;
RT "Purification and physiochemical, chemical and biological properties
RT of a toxic A2 phospholipase isolated from the venom of viperidae
RT snakes: Vipera berus.";
RL Biochimie 55:1031-1045(1973).
CC -!- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE
CC 2-ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O -> 1-
CC acylglycerophosphocholine + a fatty acid anion.
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
DR InterPro; IPR001211; PLP_A2.
DR PROSITE; PS00118; PA2_HIS; PARTIAL.
DR PROSITE; PS00119; PA2_ASP; PARTIAL.
KW Hydrolase; Lipid degradation; Calcium; Venom.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1412 MW; D054351A89969879 CRC64;

Query Match 20.9%; Score 19; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLEF 6
Db ||||
2 LLEF 5

RESULT 11
LMT4_LOCMI STANDARD; PRT; 13 AA.
ID LMT4_LOCMI
AC P41490;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Locustamyotropin 4 (LOM-MT-4).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
OC Acridomorpha; Acridoidea; Acrididae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
RA de Loof A.;
RT "Isolation, identification and synthesis of locustamyotropin III and
RT IV, two additional neuropeptides of Locusta migratoria: members of the
RT locustamyotropin peptide family.";
RL Insect Biochem. Mol. Biol. 22:447-452(1992).
CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY). LOM-MT IV SEEMS TO BE A MORE POTENT MUSCLE
CC STIMULATOR THAN LOM-MT I, II AND III.
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1553 MW; 20861943824D6698 CRC64;

Query Match 20.9%; Score 19; DB 1; Length 13;
```

Best Local Similarity 75.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 10 MPFA 13
Db 7 MPFS 10

RESULT 12
MCRA_METTE STANDARD; PRT; 15 AA.
AC P22948;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Methyl-coenzyme M methylreductase alpha subunit (EC 1.8.-.-)
DE (Fragment).
OS Methanosarcina thermophila.
OC Archaea; Euryarchaeota; Methanosarcinales; Methanosarcinaceae;
OC Methanosarcina.
OX NCBI_TaxID=2210;
RN [1]
RP SEQUENCE.
RC STRAIN=DSM 1825 / TM-1;
RX MEDLINE=91193204; PubMed=2013570;
RA Jablonski P.E., Ferry J.G.;
RT "Purification and properties of methyl coenzyme M methylreductase
from acetate-grown Methanosarcina thermophila.";
RL J. Bacteriol. 173:2481-2487(1991).
CC -!- FUNCTION: THIS ENZYME COMPLEX CATALYZES THE FINAL STEP IN
METHANOGENESIS, WHICH IS THE TERMINAL STEP OF ANAEROBIC
DEGRADATION OF BIOMASS.
CC -!- CATALYTIC ACTIVITY: REDUCTION OF METHYL-COENZYME M (2-(METHYLTHIO)
ETHANESULFONIC ACID) WITH 7-MERCAPTOHEPTANOYLTHREONINE PHOSPHATE
TO METHANE AND AN HETERODISULFIDE (CH(3)-S-COM + H-S-HTP = CH(4) +
COM-S-S-HTP).
CC -!- COFACTOR: THE ENZYME COMPLEX BINDS TIGHTLY (BUT NOT COVALENTLY)
TO ONE MOLECULE OF COENZYME F430. F430 IS A YELLOW NICKEL
PORPHINOID.
CC -!- SUBUNIT: TRIMER OF AN ALPHA, A BETA, AND A GAMMA SUBUNIT.
CC -!- MISCELLANEOUS: THE OPTIMAL TEMPERATURE FOR ENZYME ACTIVITY IS 60
DEGREES CELSIUS.
CC -!- MISCELLANEOUS: REDUCED FERREDOXIN COULD REDUCTIVELY REACTIVATE THE
ENZYME.
KW Methanogenesis; Oxidoreductase.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1686 MW; D5D59892FCA5F63C CRC64;

Query Match 20.9%; Score 19; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 3e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 FATPME 17
Db 8 FKTSME 13

RESULT 13
ANP8_ELEGR STANDARD; PRT; 16 AA.
AC P11921;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-APR-1990 (Rel. 14, Last annotation update)
DE Antifreeze glycoprotein 8R.
OS Eleginus gracilis (Saffron cod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadoidae;
OC Eleginus.
OX NCBI_TaxID=8047;
RN [1]

RP SEQUENCE.
RX MEDLINE=86196057; PubMed=3700395;
RA Burcham T.S., Osuga D.T., Rao B.N.N., Bush C.A., Feeney R.E.;
RT "Purification and primary sequences of the major arginine-containing
antifreeze glycopeptides from the fish Eleginus gracilis.";
RL J. Biol. Chem. 261:6384-6389(1986).
CC -!- FUNCTION: ANTIFREEZE PROTEINS LOWER THE BLOOD FREEZING POINT.
DR PIR; A25213; A25213.
KW Antifreeze protein; Glycoprotein.
SQ SEQUENCE 16 AA; 1413 MW; 8EF45D9324E88994 CRC64;

Query Match 20.9%; Score 19; DB 1; Length 16;
Best Local Similarity 66.7%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 ATPMEA 18
Db 11 ATPARA 16

RESULT 14
UPAA_HUMAN STANDARD; PRT; 8 AA.
AC P30096;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 36) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 7, ITS MW IS: 12 kDa.
DR SWISS-2DPAGE; P30096; HUMAN.
FT NON_TER 1 1 F -> P.
FT VARIANT 5 5 /FTID=VAR_000004.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 909 MW; 86677B59D1A72042 CRC64;

Query Match 19.8%; Score 18; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 1e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LLEFY 7
Db 2 ILTFY 6

RESULT 15
NS1_MYCTU STANDARD; PRT; 10 AA.
AC P81135;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 30 kDa non-secretory protein 1 (Fragment).
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;


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RN [1]
RP SEQUENCE.
RC STRAIN=H37RV;
RA Prasad H.K., Annapurna P.S.;
RL Submitted (DEC-1997) to the SWISS-PROT data bank.
CC -!- CAUTION: We are unable to find this protein in the translation of
CC the genome of strain H37RV.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1042 MW; 8767FE6AB2C73771 CRC64;

Query Match 19.8%; Score 18; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 13 ATPM 16
Db 2 ATPL 5

Search completed: July 3, 2002, 11:41:55
Job time: 836 sec
```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:41:21 ; Search time 100.54 Seconds
(without alignments)
30.972 Million cell upd

Title: US-09-165-546A-12
Perfect score: 91
Sequence: 1 SRLLEFYLAMPFATPMEA 18

Scoring table: BLOSUM62
Gapop 10.0 ; Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters:	4250
--	------

```
Minimum DB seq length: 0
Maximum DB seq length: 18
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

```
Database : ,
SPTRMBL_19:*
1:  sp_archea:*
2:  sp_bacteria:*
3:  sp_fungi:*
4:  sp_human:*
5:  sp_invertebrate:*
6:  sp_mammal:*
7:  sp_mhc:*
8:  sp_organelle:*
9:  sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archheap:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	32	35.2		17	4	Q9UCN0	Q9ucn0 homo sapien
2	29	31.9		17	4	Q16309	Q16309 homo sapien
3	29	31.9		17	4	Q16310	Q16310 homo sapien
4	27	29.7		17	10	Q9S8Y2	Q9s8y2 lupinus arb
5	25	27.5		16	2	Q30985	O30985 rhodobacter
6	25	27.5		17	2	Q9ZG33	Q9zg33 chlamydia t
7	24	26.4		15	2	Q9R5A0	Q9r5a0 micrococcus
8	23	25.3		18	2	Q9ZG42	Q9zg42 chlamydia t
9	23	25.3		18	4	Q9UCF9	Q9ucf9 homo sapien
10	22	24.2		11	2	Q9R7U8	Q9r7u8 pseudomonas
11	22	24.2		16	10	Q9SPV1	Q9spv1 nicotiana t
12	22	24.2		17	7	O19716	O19716 homo sapien
13	22	24.2		18	6	Q9TRG2	Q9trg2 oryctolagus
14	21	23.1		10	11	O70580	O70580 mus musculu
15	21	23.1		10	12	Q9J1G8	Q9j1g8 tt virus. o
16	21	23.1		13	2	Q9WW72	Q9ww72 enterococcu

17	21	23.1	13	2	Q9WW71	Q9ww71
18	21	23.1	13	2	Q9X5I4	Q9x5i4
19	21	23.1	15	8	Q36727	Q36727
20	21	23.1	16	2	Q9R596	Q9r596
21	21	23.1	17	4	Q96RT3	Q96rt3
22	21	23.1	17	5	Q61238	Q61238
23	21	23.1	18	2	Q9LAP4	Q9lap4
24	21	23.1	18	5	Q9I7N8	Q9i7n8
25	20	22.0	10	10	Q9S905	Q9s905
26	20	22.0	10	12	Q90347	Q90347
27	20	22.0	10	12	Q90348	Q90348
28	20	22.0	12	8	Q9XNR6	Q9xnr6
29	20	22.0	14	11	Q70599	Q70599
30	20	22.0	15	10	Q9S8K7	Q9s8k7
31	20	22.0	15	10	P83141	P83141
32	20	22.0	16	4	Q9UP51	Q9up51
33	20	22.0	17	4	Q9HB76	Q9hb76
34	20	22.0	17	12	Q9QPC8	Q9qpc8
35	20	22.0	18	2	Q9R5B0	Q9r5b0
36	20	22.0	18	5	Q9TWW7	Q9tww7
37	19	20.9	10	12	Q90349	Q90349
38	19	20.9	11	12	Q9J1G3	Q9j1g3
39	19	20.9	13	2	Q9L8K1	Q9l8k1
40	19	20.9	14	4	Q75692	Q75692
41	19	20.9	15	1	Q9UWH3	Q9uwh3
42	19	20.9	15	2	Q9R565	Q9r565
43	19	20.9	15	7	Q9TNQ5	Q9tnq5
44	19	20.9	15	11	Q62531	Q62531
45	19	20.9	15	13	Q9PS10	Q9ps10

ALIGNMENTS

RESULT	1
Q9UCN0	
ID	PRELIMINARY; PRT; 17 AA.
AC	Q9UCN0;
DT	01-MAY-2000 (TReMBLrel. 13, Created)
DT	01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT	01-MAY-2000 (TReMBLrel. 13, Last annotation update)

Query Match	35.2%;	Score 32;	DB 4;	Length 17;
Best Local Similarity	26.7%;	Pred. No. 73;		
Matches 4;	Conservative	6;	Mismatches	5; Indels 0; Gaps 0;

Qy 4 LEFYLAMPFATPMEA 18
 :|:: |:: :|||:

Dd 2 VEYHFLSPYVSPKES 16

RESULT	2
Q16309	
ID	Q16309
AC	Q16309;
DT	01-NOV-1996 (TReMBLrel. 01, Created)
DT	01-JAN-1999 (TReMBLrel. 09, Last sequence up
DT	01-MAY-1999 (TReMBLrel. 10, Last annotation

```
DE GC*1F PROTEIN (FRAGMENT).
GN GC*1F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95242701; PubMed=7725672;
RA Kofler A., Braun A., Jenkins T., Serjeantson S.W., Cleve H.;
RT "Characterization of mutants of the vitamin-D-binding protein/group
RT specific component: GC aborigine (1A1) from Australian aborigines and
RT South African blacks, and 2A9 from south Germany.";
RL Vox Sang. 68:50-54(1995).
DR EMBL; S77129; AAD14249.1; -.
FT NON_TER 17
SQ SEQUENCE 17 AA; 1852 MW; BB2982750293722C CRC64;

Query Match 31.9%; Score 29; DB 4; Length 17;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 MPFATPME 17
Db |||||
1 MPDATPTE 8

RESULT 3
Q16310
ID Q16310 PRELIMINARY; PRT; 17 AA.
AC Q16310;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-JAN-1999 (TReMBLrel. 09, Last sequence update)
DT 01-MAY-1999 (TReMBLrel. 10, Last annotation update)
DE GC*2 PROTEIN (FRAGMENT).
GN GC*2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95242701; PubMed=7725672;
RA Kofler A., Braun A., Jenkins T., Serjeantson S.W., Cleve H.;
RT "Characterization of mutants of the vitamin-D-binding protein/group
RT specific component: GC aborigine (1A1) from Australian aborigines and
RT South African blacks, and 2A9 from south Germany.";
RL Vox Sang. 68:50-54(1995).
DR EMBL; S77130; AAD14250.1; -.
FT NON_TER 17
SQ SEQUENCE 17 AA; 1845 MW; BB26CAD60293722C CRC64;

Query Match 31.9%; Score 29; DB 4; Length 17;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 MPFATPME 17
Db |||||
1 MPDATPKE 8

RESULT 4
Q9S8Y2
ID Q9S8Y2 PRELIMINARY; PRT; 17 AA.
AC Q9S8Y2;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE L-ASPARAGINASE ISOFORM A (EC 3.5.1.1).
OS Lupinus arboreus (Tree lupine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
```

```
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Genisteae; Lupinus.
OX NCBI_TaxID=3872;
RN [1]
RP SEQUENCE.
RX MEDLINE=92344803; PubMed=1368361;
RA Lough T.J., Chang K.S., Carne A., Monk B.C., Reynolds P.H.,
RA Farnden K.J.;
RL Phytochemistry 31:1519-1527(1992).
SQ SEQUENCE 17 AA; 1877 MW; DB7925924D5F46AF CRC64;

Query Match 29.7%; Score 27; DB 10; Length 17;
Best Local Similarity 71.4%; Pred. No. 5.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 LAMPFAT 14
Db :|||||
1 IAMPFNT 7

RESULT 5
O30985
ID O30985 PRELIMINARY; PRT; 16 AA.
AC O30985;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE PUTATIVE AMMONIA TRANSPORTER (FRAGMENT).
GN AMTB.
OS Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).
OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
OC Rhodobacter.
OX NCBI_TaxID=1063;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=16PHC;
RC MEDLINE=98389683; PubMed=9721307;
RA Qian Y., Tabita F.R.;
RT "Expression of glnB and a glnB-like gene (glnK) in a ribulose
RT biphosphate carboxylase/oxygenase-deficient mutant of Rhodobacter
RT sphaeroides.";
RL J. Bacteriol. 180:4644-4649(1998).
DR EMBL; AF023909; AAC34723.1; -.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1812 MW; EDB859A962D6FEEA CRC64;

Query Match 27.5%; Score 25; DB 2; Length 16;
Best Local Similarity 36.4%; Pred. No. 1.2e+03;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 SRLLEFYLAMP 11
Db |:|||::|
4 STVLVFFMILP 14

RESULT 6
Q9ZG33
ID Q9ZG33 PRELIMINARY; PRT; 17 AA.
AC Q9ZG33;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TReMBLrel. 10, Last annotation update)
DE SUBTILISIN/CHYMOTRYPSIN INHIBITOR (FRAGMENT).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=L2 434B;
RA Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;
RT "Gene identification of Chlamydia trachomatis by random DNA
```


RT sequencing."
RL Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF087336; AAD04110.1; -
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 2043 MW; 4FEE704EE041E120 CRC64;

Query Match 27.5%; Score 25; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 YLAMPFAT 14
: | | | |
Db 2 FLGQPFCT 9

RESULT 7
Q9R5A0 PRELIMINARY; PRT; 15 AA.
AC Q9R5A0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE DNA TOPOISOMERASE I (FRAGMENT).
OS Micrococcus luteus (Micrococcus lysodeikticus).
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Micrococcineae; Micrococcaceae; Micrococcus.
OX NCBI_TaxID=1270;
RN [1]
RP SEQUENCE.
RX MEDLINE=93249439; PubMed=8387285;
RA Anderluzzi D., Pedrini A.M.;
RT "Structural similarities between M. luteus and E. coli DNA topoisomerase I.";
RL Biochem. Biophys. Res. Commun. 192:657-664(1993).
SQ SEQUENCE 15 AA; 1602 MW; 2B5457836F151383 CRC64;

Query Match 26.4%; Score 24; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 9 AMPFATPMEA 18
: | | | |
Db 2 AVPAQTPVYA 11

RESULT 8
Q9ZG42 PRELIMINARY; PRT; 18 AA.
AC Q9ZG42;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE PROLINE TRANSPORT PROTEIN (FRAGMENT).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=L2 434B;
RA Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;
RT "Gene identification of Chlamydia trachomatis by random DNA sequencing."
RL Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF087325; AAD04100.1; -
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 2236 MW; 55C4A82FD42CC261 CRC64;

Query Match 25.3%; Score 23; DB 2; Length 18;

Best Local Similarity 50.0%; Pred. No. 3e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 FYLAMPPFA 13
: | | | |
Db 10 FYKALKFS 17

RESULT 9
Q9UCF9 PRELIMINARY; PRT; 18 AA.
AC Q9UCF9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE C1-INHIBITOR-SERINE PROTEINASE INHIBITOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93264944; PubMed=8495195;
RA Aulak K.S., Davis A.E.III., Donaldson V.H., Harrison R.A.;
RT "Chymotrypsin inhibitory activity of normal C1-inhibitor and a p1 Arg to His mutant: evidence for the presence of overlapping reactive centers.";
RL Protein Sci. 2:727-732(1993).
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
SQ SEQUENCE 18 AA; 2120 MW; 6A614E7BF9F54A85 CRC64;

Query Match 25.3%; Score 23; DB 4; Length 18;
Best Local Similarity 50.0%; Pred. No. 3e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 LLEFYLAMPF 12
: | | | |
Db 5 LLVFEVQQPF 14

RESULT 10
Q9R7U8 PRELIMINARY; PRT; 11 AA.
AC Q9R7U8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DNR PROTEIN (A REGULATORY PROTEIN FOR THE EXPRESSION OF THE NIR AND NOR GENES) (FRAGMENT).
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PA01;
RX MEDLINE=95226457; PubMed=7711073;
RA Arai H., Igarashi Y., Kodama T.;
RT "The structural genes for nitric oxide reductase from Pseudomonas aeruginosa.";
RL Biochim. Biophys. Acta 1261:279-284(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=PA01;
RX MEDLINE=95394152; PubMed=7664887;
RA Arai H., Igarashi Y., Kodama T.;
RT "Expression of the nir and nor genes for denitrification of Pseudomonas aeruginosa requires a novel CRP/FNR-related transcriptional regulator, DNR, in addition to ANR.";
RL FEBS Lett. 371:73-76(1995).
DR EMBL; D50019; BAA08746.1; -.

FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1543 MW; DF363CAE141B5736 CRC64;

Query Match 24.2%; Score 22; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 2.7e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RLLEFY 7
Db 1 RLQLY 6

RESULT 11
Q9SPV1
ID Q9SPV1 PRELIMINARY; PRT; 16 AA.
AC Q9SPV1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE HYPOTHETICAL 1.7 KDA PROTEIN (FRAGMENT).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20023723; PubMed=10561067;
RA Foster E., Hattori J., Labbe H., Ouellet T., Fobert P.R., James L.E.,
RA Iyer V.N., Miki B.L.;
RT "A tobacco cryptic constitutive promoter, tCUP, revealed by T-DNA
tagging.";
RL Plant Mol. Biol. 41:45-55(1999).
DR EMBL; AF133844; AAD56607.1; -.
KW Hypothetical protein.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1725 MW; 6A4C8A093666240D CRC64;

Query Match 24.2%; Score 22; DB 10; Length 16;
Best Local Similarity 38.5%; Pred. No. 4e+03;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 SRLLEFYLAMPFA 13
Db 3 SQAVETLYSPPPFA 15

RESULT 12
O19716
ID O19716 PRELIMINARY; PRT; 17 AA.
AC O19716;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HUMAN HISTOCOMPATIBILITY SYSTEM HLA-DR HEAVY CHAIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82197531; PubMed=6952207;
RA Lee J.S., Trowsdale J., Bodmer W.F.;
RT "cdna clones coding for the heavy chain of human hla-dr antigen.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:545-549(1982).
DR EMBL; J00193; AAA36272.1; -.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 2058 MW; 4874E328EE648F54 CRC64;

Query Match 24.2%; Score 22; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 EFYL.8
Db 11 EFYL 14

RESULT 13
Q9TRG2
ID Q9TRG2 PRELIMINARY; PRT; 18 AA.
AC Q9TRG2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE C1-INHIBITOR=SERINE PROTEINASE INHIBITOR.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=93264944; PubMed=8495195;
RA Aulak K.S., Davis A.E.III., Donaldson V.H., Harrison R.A.;
RT "Chymotrypsin inhibitory activity of normal C1-inhibitor and a p1 Arg
to His mutant: evidence for the presence of overlapping reactive
centers.";
RL Protein Sci. 2:727-732(1993).
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
SQ SEQUENCE 18 AA; 2134 MW; 6A74AE635AF54C5E CRC64;

Query Match 24.2%; Score 22; DB 6; Length 18;
Best Local Similarity 50.0%; Pred. No. 4.5e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 LLEFYLAMPF 12
Db 5 LLIFEVQQPF 14

RESULT 14
O70580
ID O70580 PRELIMINARY; PRT; 10 AA.
AC O70580;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CARBONIC ANHYDRASE III (FRAGMENT).
GN CAR3 OR CAR3 OR CA3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Sowden J., Smith H., Morrison K., Edwards Y.;
RT "Sequence comparisons and functional studies of the proximal promoter
of the carbonic anhydrase 3 (CA3) gene.";
RL Gene 214:157-165(1999).
DR EMBL; AJ006474; CAA07057.1; -.
DR MGD; MGI:1351477; Cars.
DR MGD; MGI:88270; Car3.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1105 MW; 56F7FE71ADC37B13 CRC64;

Query Match 23.1%; Score 21; DB 11; Length 10;
Best Local Similarity 50.0%; Pred. No. 3.7e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 8 LAMPFATP 15
:| :|||
Db 1 MAKEWATP 8

RESULT 15
Q9J1G8
ID Q9J1G8 PRELIMINARY; PRT; 10 AA.
AC Q9J1G8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ORF2.
OS TT virus.
OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TTV-SC232;
RX MEDLINE=20251008; PubMed=10790123;
RA Niel C., Saback F.L., Lampe E.;
RT "Coinfection with Multiple TT Virus Strains Belonging to Different
RT Genotypes Is a Common Event in Brazilian Healthy Adults.";
RL J. Clin. Microbiol. 38:1926-1930(2000).
DR EMBL; AF216453; AAF66889.1; -;
SQ SEQUENCE 10 AA; 1124 MW; 64FE2BD771B5B9CB CRC64;

Query Match 23.1%; Score 21; DB 12; Length 10;
Best Local Similarity 42.9%; Pred. No. 3.7e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 12 FATPMEA 18
|:|:|:
Db 4 FSTPVR 10

Search completed: July 3, 2002, 11:41:22
Job time: 858 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:26:58 ; Search time 128.9 Seconds
(without alignments)
15.511 Million cell updates/sec

Title: US-09-165-546A-12
Perfect score: 91
Sequence: 1 SRLLEFYLLAMPFPATPMEA 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 214377

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	91	100.0	18	21 AAY52439	Human tumour antig
2	91	100.0	18	22 AAU01543	HLA-DR53 recognisi
3	91	100.0	18	22 AAB69943	Human NY-ESO-1 HLA
4	70	76.9	14	22 AAU01549	Human NY-ESO-1 tum
5	54	59.3	10	20 AAY06013	Human cancer antig
6	52	57.1	10	20 AAY06004	Human cancer antig
7	52	57.1	10	20 AAY06007	Human cancer antig
8	52	57.1	10	22 AAG67193	Cancer testis tumo
9	52	57.1	10	22 AAB69925	Human NY-ESO-1 HLA
10	51	56.0	10	20 AAY06010	Human cancer antig
11	48	52.7	9	22 AAG67185	Cancer testis tumo

12	48	52.7	9	22 AAB69917	Human NY-ESO-1 HLA
13	44	48.4	9	20 AAY06021	Human cancer antig
14	44	48.4	9	21 AAY78465	NY-ESO-1 derived H
15	44	48.4	9	22 AAU01545	Human NY-ESO-1 tum
16	39	42.9	9	22 AAG67176	Cancer testis tumo
17	39	42.9	9	22 AAG67181	Cancer testis tumo
18	39	42.9	9	22 AAG67183	Cancer testis tumo
19	39	42.9	9	22 AAB69908	Human NY-ESO-1 HLA
20	39	42.9	9	22 AAB69913	Human NY-ESO-1 HLA
21	39	42.9	9	22 AAB69915	Human NY-ESO-1 HLA
22	37	40.7	11	21 AAB12647	Protein kinase pep
23	37	40.7	15	21 AAY66484	Human MAP kinase S
24	37	40.7	15	21 AAY66485	Human MAP kinase S
25	37	40.7	15	21 AAY66509	Human MAP kinase S
26	37	40.7	15	21 AAY66510	Human MAP kinase S
27	36	39.6	9	21 AAY79757	NY-ESO-1 derived p
28	36	39.6	9	22 AAG67178	Cancer testis tumo
29	36	39.6	9	22 AAB69910	Human NY-ESO-1 HLA
30	35	38.5	9	22 AAG67186	Cancer testis tumo
31	35	38.5	9	22 AAB69918	Human NY-ESO-1 HLA
32	35	38.5	10	22 AAG67194	Cancer testis tumo
33	35	38.5	10	22 AAB69926	Human NY-ESO-1 HLA
34	32	35.2	17	15 AAR49308	Transferrin recept
35	31	34.1	16	18 AAW10317	Beta-subtype retin
36	30	33.0	9	21 AAY79752	NY-ESO-1 derived p
37	30	33.0	10	20 AAY06056	Human cancer antig
38	30	33.0	10	20 AAY05990	Human cancer antig
39	30	33.0	12	18 AAW16119	Peptide containing
40	30	33.0	12	19 AAW68759	Peptide binding in
41	30	33.0	12	19 AAW58246	IL-1RtI binding pe
42	30	33.0	12	20 AAY09890	Interleukin-1 type
43	30	33.0	12	21 AAB17671	IL-1 antagonist pe
44	30	33.0	14	14 AAR36921	Insulin-like growt
45	30	33.0	17	22 AAE01592	Human gene 11 enco

ALIGNMENTS

RESULT 1
AAY52439
ID AAY52439 standard; Protein; 18 AA.
XX
AC AAY52439;
XX
DT 15-FEB-2000 (first entry)
XX Human tumour antigen NY-ESO-1 peptide #12.
DE
XX Cancer; tumour; antigen; MHC; major histocompatibility complex; Class II;
KW T-cell; helper; stimulation; proliferation; treatment;
KW diagnosis; prevention; melanoma; breast cancer; ovarian cancer;
KW prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer;
KW lymphoma.
XX Synthetic.
OS Homo sapiens.
XX
PN WO9953938-A1.
XX
PD 28-OCT-1999.
XX
PF 24-MAR-1999; 99WO-US06875.
XX
PR 17-APR-1998; 98US-0062422.
PR 02-OCT-1998; 98US-0165546.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
PI Gure A, Ritter G;
XX
DR WPI; 2000-038483/03.

XX Novel peptides which bind to MHC class I and MHC class II molecules,
PT useful for therapeutic and diagnostic purposes -
XX
PS Claim 4; Page 22; 49pp; English.
XX
CC Peptides #8-#13 (AAAY52435-Y52440) are peptides derived from the human
CC tumour antigen, NY-ESO-1 (AAAY52430) which can bind to MHC(major
CC histocompatibility Class II HLA-DR53 molecules, thereby stimulating
CC proliferation of helper T-cells. cDNA encoding NY-ESO-1 was initially
CC isolated from an oesophagus squamous cell cancer cDNA library. Tissue
CC localisation studies revealed it to be expressed at high levels
CC in normal ovary and testis but not in normal colon, kidney, liver,
CC brain, oesophagus and skin. It was expressed in certain tumours and
CC tumour cell lines with some degree of frequency - these included
CC melanoma specimens and cell lines, and breast and bladder cancer
CC specimens, with expression in other tumour types being sporadic.
CC These NY-ESO-1-derived peptides may be used in methods and
CC compositions used for the treatment, diagnosis and prevention of
CC cancers (such as melanoma, breast cancer, prostate cancer, lung
CC cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer,
CC or lymphoma) and to stimulate the proliferation of T cells.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 91; DB 21; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLLEFYLAMPFATPMEA 18
Db ||||||
1 srllefyampfatpmea 18

RESULT 2
AAU01543
ID AAU01543 standard; Peptide; 18 AA.
XX
AC AAU01543;
XX
DT 18-JUL-2001 (first entry)
XX
DE HLA-DR53 recognising NY-ESO-1 peptide #5.
XX
KW NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
KW human leukocyte antigen-determining region; disease progression;
KW disease regression; disease onset; body tissue; body fluid; enzyme label;
KW radioactive label; monoclonal antibody.
XX
OS Homo sapiens.
XX
PN WO200123560-A2.
XX
PD 05-APR-2001.
XX
PF 26-SEP-2000; 2000WO-US26411.
XX
PR 29-SEP-1999; 99US-0408036.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Tureci O, Sahin U, Pfreundschuh M;
XX
DR WPI; 2001-266156/27.
XX
PT Polypeptides binding to major histocompatibility complex class II human
PT leukocyte antigen-determining region molecule having amino acid
PT sequence found in tumour rejection antigen precursor used for
PT stimulating proliferation of helper T cells -
XX
PS Example 13; Page 19; 62pp; English.

XX The sequence represents a human NY-ESO-1 tumour rejection antigen
CC precursor fragment which recognises and binds to HLA-DR53. NY-ESO-1 and
CC SSX-2 polypeptides, or fragments of, bind to major histocompatibility
CC complex (MHC) Class II molecules such as human leukocyte
CC antigen-determining region (HLA-DR) molecules and stimulate proliferation
CC of helper T cells. The peptides can be administered to an HLA-DR positive
CC subject in order to stimulate the helper T cells. An MHC Class II
CC HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell or
CC present in free form is useful for this stimulation. The nucleic acid is
CC useful for screening for a cancerous condition, which involves contacting
CC a subject sample to a cell line transfected with the immunoreactive cell
CC (helper T cell), where interaction is indicative of cancer. In addition,
CC a sample from a patient (for example, a body fluid or tissue) can be
CC monitored for the amount of the complex present in the bloodstream. This
CC is useful for determining regression, progression or onset of a cancerous
CC condition. The method involves contacting the sample with a radioactive
CC labelled or enzyme labelled monoclonal antibody which specifically binds
CC with the complex.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 91; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLLEFYLAMPFATPMEA 18
Db ||||||
1 srllefyampfatpmea 18

RESULT 3
AAB69943
ID AAB69943 standard; Peptide; 18 AA.
XX
AC AAB69943;
XX
DT 27-APR-2001 (first entry)
XX
DE Human NY-ESO-1 HLA-DR53 binding motif #5.
XX
KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW non-small cell lung carcinoma; tumour status determination.
XX
OS Homo sapiens.
XX
PN WO200107917-A1.
XX
PD 01-FEB-2001.
XX
PF 14-JUL-2000; 2000WO-US19220.
XX
PR 23-JUL-1999; 99US-0359503.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.
XX
PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
XX
DR WPI; 2001-182822/18.
XX
PT Method useful for determining the status (e.g. progression, regression
PT or stability of the disease) of a cancerous condition, involves
PT determining the levels of NY-ESO-1 specific antibodies in a sample
PT taken from a patient -
XX
PS Example 16; Page 28; 50pp; English.
CC The present sequence is given in a specification relating to a method
CC for determining the status of a cancerous condition in a patient

1

CC with a tumour that expresses NY-ESO-1. The method comprises assaying a
CC sample taken from the patient for antibodies that specifically bind to
CC the NY-ESO-1 and comparing the value obtained to a prior value obtained
CC from assay of a prior sample taken from the patient. Any difference
CC between the values is indicative of a change in status of the cancerous
CC condition. The method is useful for determining whether a cancerous
CC condition is progressing, regressing or remaining stable, in particular
CC in patients receiving treatment for a melanoma, adenocarcinoma,
CC non-small cell lung carcinoma or bladder carcinoma.

XX Sequence 18 AA;
SQ Query Match 100.0%; Score 91; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLLEFYLPMPFATPMEA 18
Db 1 srllefympfptpmea 18
|||||

RESULT 4
AAU01549
ID AAU01549 standard; Peptide; 14 AA.
XX
AC AAU01549;
XX
DT 18-JUL-2001 (first entry)
XX
DE Human NY-ESO-1 tumour rejection antigen precursor peptide #4.
XX
KW NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
KW human leukocyte antigen-determining region; disease progression;
KW disease regression; disease onset; body tissue; body fluid; enzyme label;
KW radioactive label; monoclonal antibody.

XX Homo sapiens.
OS
XX WO200123560-A2.
PN
XX
PD 05-APR-2001.
XX
PF 26-SEP-2000; 2000WO-US26411.
XX
PR 29-SEP-1999; 99US-0408036.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Tureci O, Sahin U, Pfreundschuh M;
XX
DR WPI; 2001-266156/27.

XX Polypeptides binding to major histocompatibility complex class II human
PT leukocyte antigen-determining region molecule having amino acid
PT sequence found in tumour rejection antigen precursor used for
PT stimulating proliferation of helper T cells -

PS Claim 5; Page 38; 62pp; English.
XX
CC The sequence represents a human NY-ESO-1 tumour rejection antigen
CC precursor fragment. NY-ESO-1 and SSX-2 polypeptides, or fragments of,
CC bind to major histocompatibility complex (MHC) Class II molecules such as
CC human leukocyte antigen-determining region (HLA-DR) molecules and
CC stimulate proliferation of helper T cells. The peptides can be
CC administered to an HLA-DR positive subject in order to stimulate the
CC helper T cells. An MHC Class II HLA-DR-NY-ESO-1/SSX-2 complex expressed
CC on the surface of a cell or present in free form is useful for this
CC stimulation. The nucleic acid is useful for screening for a cancerous
CC condition, which involves contacting a subject sample to a cell line
CC transfected with the immunoreactive cell (helper T cell), where
CC interaction is indicative of cancer. In addition, a sample from a patient

CC (for example, a body fluid or tissue) can be monitored for the amount of
CC the complex present in the bloodstream. This is useful for determining
CC regression, progression or onset of a cancerous condition. The method
CC involves contacting the sample with a radioactive labelled or enzyme
CC labelled monoclonal antibody which specifically binds with the complex.

XX Sequence 14 AA;
SQ Query Match 76.9%; Score 70; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLLEFYLPMPFAT 14
Db 1 srllefympfat 14
|||||

RESULT 5
AAY06013
ID AAY06013 standard; Peptide; 10 AA.
XX
AC AAY06013;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; human leukocyte antigen; HLA.
XX
OS Homo sapiens.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US19609.
XX
PR 08-OCT-1997; 97US-0061428.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rosenberg SA, Wang RF;
XX
DR WPI; 1999-277270/23.

PT Cancer antigen NY ESO1/CAG-3
XX
PS Example 10; Page 42; 88pp; English.

XX This peptide was identified as an HLA peptide motif following a
CC screen for epitopes from the coding region of human ESO-1/CAG-3
CC ORF1 (see AAX58599). 30 Epitopes (see AAY05988-Y06017) were identified.
CC The present peptide (ranked 26) corresponds to amino acid residues
CC 91-100 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent
CC tumour antigen capable of eliciting an antigen specific immune
CC response by T cells. Cancer peptides (see AAY05967-87) derived from
CC CAG-3, portions of CAG-3 and their variants, are useful as cancer
CC vaccines. A claimed method of preventing or inhibiting cancer
CC involves administering a cancer peptide, with or without an HLA
CC molecule. The cancer peptides form part of, or are derived
CC from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer and
CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
CC thyroid cancers.

XX

SQ Sequence 10 AA;

Query Match 59.3%; Score 54; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YLAMPFATPM 16
Db 1 ylampfatpm 10
|||||

RESULT 6
AAY06004
ID AAY06004 standard; Peptide; 10 AA.
XX
AC AAY06004;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; human leukocyte antigen; HLA.
XX
OS Homo sapiens.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US19609.
XX
PR 08-OCT-1997; 97US-0061428.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rosenberg SA, Wang RF;
XX
DR WPI; 1999-277270/23.
XX
PT Cancer antigen NY ESO1/CAG-3
XX
PS Example 10; Page 42; 88pp; English.
XX
CC This peptide was identified as an HLA peptide motif following a
CC screen for epitopes from the coding region of human ESO-1/CAG-3
CC ORF1 (see AAX58599). 30 Epitopes (see AAY05988-Y06017) were identified.
CC The present peptide (ranked 17) corresponds to amino acid residues
CC 87-96 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent
CC tumour antigen capable of eliciting an antigen specific immune
CC response by T cells. Cancer peptides (see AAY05967-87) derived from
CC CAG-3, portions of CAG-3 and their variants, are useful as cancer
CC vaccines. A claimed method of preventing or inhibiting cancer
CC involves administering a cancer peptide, with or without an HLA
CC molecule. The cancer peptides form part of, or are derived
CC from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer and
CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
CC thyroid cancers.
XX
SQ Sequence 10 AA;

Query Match 57.1%; Score 52; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLEFYLAMPF 12
Db 1 llefylampf 10
|||||

RESULT 7
AAY06007
ID AAY06007 standard; Peptide; 10 AA.
XX
AC AAY06007;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; human leukocyte antigen; HLA.
XX
OS Homo sapiens.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US19609.
XX
PR 08-OCT-1997; 97US-0061428.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rosenberg SA, Wang RF;
XX
DR WPI; 1999-277270/23.
XX
PT Cancer antigen NY ESO1/CAG-3
XX
PS Example 10; Page 42; 88pp; English.
XX
CC This peptide was identified as an HLA peptide motif following a
CC screen for epitopes from the coding region of human ESO-1/CAG-3
CC ORF1 (see AAX58599). 30 Epitopes (see AAY05988-Y06017) were identified.
CC The present peptide (ranked 20) corresponds to amino acid residues
CC 93-102 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent
CC tumour antigen capable of eliciting an antigen specific immune
CC response by T cells. Cancer peptides (see AAY05967-87) derived from
CC CAG-3, portions of CAG-3 and their variants, are useful as cancer
CC vaccines. A claimed method of preventing or inhibiting cancer
CC involves administering a cancer peptide, with or without an HLA
CC molecule. The cancer peptides form part of, or are derived
CC from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer and
CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
CC thyroid cancers.
XX
SQ Sequence 10 AA;

Query Match 57.1%; Score 52; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AMPFATPMEA 18
Db 1 ampfatpmea 10
|||||

4

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RESULT 8
AAG67193
ID AAG67193 standard; peptide; 10 AA.
XX
AC AAG67193;
XX
DT 13-NOV-2001 (first entry)
XX
DE Cancer testis tumour antigen NY-ESO-1 derived peptide.
XX
KW Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;
KW HLA; HLA binding peptide; major histocompatibility complex; MHC;
KW tumour; cancer; testis tumour.
XX
OS Homo sapiens.
XX
PN WO200162917-A1.
XX
PD 30-AUG-2001.
XX
PF 22-JAN-2001; 2001WO-US02126.
XX
PR 22-FEB-2000; 2000US-0510635.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Lethe B, Boon-Falleur T;
XX
DR WPI; 2001-550091/61.
XX
PT Genomic sequences of tumour associated antigen EY-ESO-1 (LAGE-2) useful
PT for diagnosing testicular tumours -
XX
PS Example 13; Page 26; 50pp; English.
XX
CC AAG67169-AAG67206 represent peptides which are derived from cancer
CC testis tumour antigen NY-ESO-1 (also called LAGE-2). The peptides
CC bind to human leukocyte antigens (HLAs). NY-ESO-1 is a molecule that
CC is processed to at least one human leukocyte antigen (HLA) binding
CC peptide, which binds to Class I and Class II major histocompatibility
CC complex (MHC). NY-ESO-1 is expressed in tumour mRNA and in testis,
CC but not normal colon, kidney, liver or brain tissue. The presence or
CC level of expression of NY-ESO-1 may be assayed for the diagnosis of
CC cancer, especially testis tumours.
XX
SQ Sequence 10 AA;

Query Match 57.1%; Score 52; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLEFYLAMPF 12
Db 1 llefylampf 10

RESULT 9
AAB69925
ID AAB69925 standard; Peptide; 10 AA.
XX
AC AAB69925;
XX
DT 27-APR-2001 (first entry)
XX
DE Human NY-ESO-1 HLA binding motif #25.
XX
KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW non-small cell lung carcinoma; tumour status determination.
XX
OS Homo sapiens.
XX

Query Match 57.1%; Score 52; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLEFYLAMPF 12
Db 1 llefylampf 10

RESULT 10
AAY06010
ID AAY06010 standard; Peptide; 10 AA.
XX
AC AAY06010;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; human leukocyte antigen; HLA.
XX
OS Homo sapiens.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US19609.
XX
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PN WO200107917-A1.
XX
PD 01-FEB-2001.
XX
PF 14-JUL-2000; 2000WO-US19220.
XX
PR 23-JUL-1999; 99US-0359503.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK ) SLOAN KETTERING INST CANCER RES.
PA (CORR ) CORNELL RES FOUND INC.
XX
PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
XX
DR WPI; 2001-182822/18.
XX
PT Method useful for determining the status (e.g. progression, regression
PT or stability of the disease) of a cancerous condition, involves
PT determining the levels of NY-ESO-1 specific antibodies in a sample
PT taken from a patient -
XX
PS Example 14; Page 25; 50pp; English.
XX
CC The present sequence is given in a specification relating to a method
CC for determining the status of a cancerous condition in a patient
CC with a tumour that expresses NY-ESO-1. The method comprises assaying a
CC sample taken from the patient for antibodies that specifically bind to
CC the NY-ESO-1 and comparing the value obtained to a prior value obtained
CC from assay of a prior sample taken from the patient. Any difference
CC between the values is indicative of a change in status of the cancerous
CC condition. The method is useful for determining whether a cancerous
CC condition is progressing, regressing or remaining stable, in particular
CC in patients receiving treatment for a melanoma, adenocarcinoma,
CC non-small cell lung carcinoma or bladder carcinoma.
XX
SQ Sequence 10 AA;

Query Match 57.1%; Score 52; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLEFYLAMPF 12
Db 1 llefylampf 10

RESULT 10
AAY06010
ID AAY06010 standard; Peptide; 10 AA.
XX
AC AAY06010;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; human leukocyte antigen; HLA.
XX
OS Homo sapiens.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US19609.
XX
```

PR 08-OCT-1997; 97US-0061428.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA Rosenberg SA, Wang RF;
XX WPI; 1999-277270/23.
XX Cancer antigen NY ESO1/CAG-3
PT Example 10; Page 42; 88pp; English.
XX This peptide was identified as an HLA peptide motif following a
CC screen for epitopes from the coding region of human ESO-1/CAG-3
CC ORF1 (see AAX58599). 30 Epitopes (see AAY05988-Y06017) were identified.
CC The present peptide (ranked 23) corresponds to amino acid residues
CC 86-95 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent
CC tumour antigen capable of eliciting an antigen specific immune
CC response by T cells. Cancer peptides (see AAY05967-87) derived from
CC CAG-3, portions of CAG-3 and their variants, are useful as cancer
CC vaccines. A claimed method of preventing or inhibiting cancer
CC involves administering a cancer peptide, with or without an HLA
CC molecule. The cancer peptides form part of, or are derived
CC from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer and
CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
CC thyroid cancers.
XX Sequence 10 AA;
SQ

Query Match 56.0%; Score 51; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 RLLEFYLAAMP 11
Db |||||||
1 rllefylamp 10

RESULT 11
AAG67185
ID AAG67185 standard; peptide; 9 AA.
XX
AC AAG67185;
XX
DT 13-NOV-2001 (first entry)
XX
DE Cancer testis tumour antigen NY-ESO-1 derived peptide.
XX
KW Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;
KW HLA; HLA binding peptide; major histocompatibility complex; MHC;
KW tumour; cancer; testis tumour.
XX
OS Homo sapiens.
XX
PN WO200162917-A1.
XX
PD 30-AUG-2001.
XX
PF 22-JAN-2001; 2001WO-US02126.
XX
PR 22-FEB-2000; 2000US-0510635.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Lethe B, Boon-Falleur T;
XX
DR WPI; 2001-550091/61.
XX
PT Genomic sequences of tumour associated antigen EY-ESO-1 (LAGE-2) useful
PT for diagnosing testicular tumours -

XX Example 13; Page 26; 50pp; English.
XX
CC AAG67169-AAG67206 represent peptides which are derived from cancer
CC testis tumour antigen NY-ESO-1 (also called LAGE-2). The peptides
CC bind to human leukocyte antigens (HLAs). NY-ESO-1 is a molecule that
CC is processed to at least one human leukocyte antigen (HLA) binding
CC peptide, which binds to Class I and Class II major histocompatibility
CC complex (MHC). NY-ESO-1 is expressed in tumour mRNA and in testis,
CC but not normal colon, kidney, liver or brain tissue. The presence or
CC level of expression of NY-ESO-1 may be assayed for the diagnosis of
CC cancer, especially testis tumours.
XX
SQ Sequence 9 AA;
Query Match 52.7%; Score 48; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 LEFYLAAMPF 12
Db |||||||
1 lefylampf 9

RESULT 12
AAB69917
ID AAB69917 standard; Peptide; 9 AA.
XX
AC AAB69917;
XX
DT 27-APR-2001 (first entry)
XX
DE Human NY-ESO-1 HLA binding motif #17.
XX
KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW non-small cell lung carcinoma; tumour status determination.
XX
OS Homo sapiens.
XX
PN WO200107917-A1.
XX
PD 01-FEB-2001.
XX
PF 14-JUL-2000; 2000WO-US19220.
XX
PR 23-JUL-1999; 99US-0359503.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX (CORR) CORNELL RES FOUND INC.
PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
XX
DR WPI; 2001-182822/18.
XX
PT Method useful for determining the status (e.g. progression, regression
PT or stability of the disease) of a cancerous condition, involves
PT determining the levels of NY-ESO-1 specific antibodies in a sample
PT taken from a patient -
XX
PS Example 14; Page 25; 50pp; English.
XX
CC The present sequence is given in a specification relating to a method
CC for determining the status of a cancerous condition in a patient
CC with a tumour that expresses NY-ESO-1. The method comprises assaying a
CC sample taken from the patient for antibodies that specifically bind to
CC the NY-ESO-1 and comparing the value obtained to a prior value obtained
CC from assay of a prior sample taken from the patient. Any difference
CC between the values is indicative of a change in status of the cancerous
CC condition. The method is useful for determining whether a cancerous
CC condition is progressing, regressing or remaining stable, in particular

CC in patients receiving treatment for a melanoma, adenocarcinoma,
CC non-small cell lung carcinoma or bladder carcinoma.
XX
SQ Sequence 9 AA;

Query Match 52.7%; Score 48; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LEFYLAMPF 12
| | | | | | | |
Db 1 lefylampf 9

RESULT 13
AAY06021
ID AAY06021 standard; Peptide; 9 AA.

XX AAY06021;

DT 16-AUG-1999 (first entry)

XX Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.

DE
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; human leukocyte antigen; HLA.

XX Homo sapiens.

XX WO9918206-A2.

PN 15-APR-1999.

XX 21-SEP-1998; 98WO-US19609.

PF 08-OCT-1997; 97US-0061428.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Rosenberg SA, Wang RF;

XX WPI; 1999-277270/23.

XX Cancer antigen NY ESO1/CAG-3

XX Example 10; Page 43; 88pp; English.

CC This peptide was identified as an HLA peptide motif following a
CC screen for epitopes from the coding region of human ESO-1/CAG-3
CC ORF1 (see AAX58599). 30 Epitopes (see AAY06018-47) were identified.
CC The present peptide (ranked 4) corresponds to amino acid residues
CC 86-94 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent
CC tumour antigen capable of eliciting an antigen specific immune
CC response by T cells. Cancer peptides (see AAY05967-87) derived from
CC CAG-3, portions of CAG-3 and their variants, are useful as cancer
CC vaccines. A claimed method of preventing or inhibiting cancer
CC involves administering a cancer peptide, with or without an HLA
CC molecule. The cancer peptides form part of, or are derived
CC from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer and
CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
CC thyroid cancers.

XX Sequence 9 AA;

Query Match 48.4%; Score 44; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLLEFYLAM 10
| | | | | | | |
Db 1 rllefylam 9

RESULT 14
AAY78465
ID AAY78465 standard; Peptide; 9 AA.

XX AAY78465;

XX 10-MAY-2000 (first entry)

XX NY-ESO-1 derived HLA binding peptide #1.

DE
XX
KW Cancer; SSX family; SSX-1; SSX-2; SSX-3; SSX-4; SSX-5; NY-ESO-1;
KW HLA binding; human leukocyte antigen; cytolytic T cell; CTL;
KW cytostatic; melanoma; synovial sarcoma.

XX Homo sapiens.

XX WO200000824-A1.

XX 06-JAN-2000.

XX 25-JUN-1999; 99WO-US14493.

XX 26-JUN-1998; 98US-0105839.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Tureci O, Sahin U, Pfreundschuh M, Rammensee G, Stevanovic S;

XX Chen Y, Gure A, Old LJ;

XX WPI; 2000-170933/15.

XX Determining the possible presence of breast, endometrial, colorectal,
XX lung, bladder or head-neck cancer -

XX Claim 34; Page 33; 40pp; English.

CC A method has been developed for determining the possible presence of a
CC cancer, which is not melanoma or synovial sarcoma. The method comprises
CC assaying a sample taken from the subject to determine the expression of
CC an SSX gene, and determining the expression as a determination of the
CC possible presence of cancer. Expression of SSX1 gene indicates possible
CC presence of breast, endometrial, colorectal, lung, bladder or head-neck
CC cancer. These cancers are also detected by SSX2 and SSX4 gene
CC expression. SSX2 gene expression additionally indicates possible presence
CC of lymphoma, renal cell cancer, glioma and prostate cancer. Expression
CC of SSX4 gene also indicates possible presence of ovarian or stomach
CC cancer. SSX5 gene expression indicates the same cancers as SSX1, except
CC breast cancer. Determining expression of SSX gene can be used to monitor
CC progress of melanoma or synovial sarcoma, which is not cancer. The
CC SSX-derived peptide complex stimulates proliferation of cytolytic T
CC cells. This is useful for treating cancer, especially melanoma. AAY78464
CC to AAY78468 represent specifically claimed HLA binding peptides for use
CC in the method of the invention. AAZ88452 to AAZ88465 represent PCR
CC primers used in the isolation of SSX genes in the exemplification of the
CC present invention. AAY78469 to AAY78500, and AAY79684 to AAY79762
CC represent peptides derived from SSX proteins or NY-ESO-1, which are used
CC in the exemplification of the present invention.

XX Sequence 9 AA;

Query Match 48.4%; Score 44; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLLEFYLAM 10
| | | | | | | |
Db 1 rllefylam 9

Search completed: July 3, 2002, 11:26:59
Job time: 956 sec

RESULT 15
AAU01545
ID AAU01545 standard; Peptide; 9 AA.
XX
AC AAU01545;

XX
DT 18-JUL-2001 (first entry)
XX
DE Human NY-ESO-1 tumour rejection antigen precursor peptide #1.

XX
KW NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
KW human leukocyte antigen-determining region; disease progression;
KW disease regression; disease onset; body tissue; body fluid; enzyme label;
KW radioactive label; monoclonal antibody.

XX
OS Homo sapiens.

XX
PN WO200123560-A2.

XX
PD 05-APR-2001.

XX
PF 26-SEP-2000; 2000WO-US26411.

XX
PR 29-SEP-1999; 99US-0408036.

XX
PA (LUDW-) LUDWIG INST CANCER RES.

PI Tureci O, Sahin U, Pfreundschuh M;

XX
DR WPI; 2001-266156/27.

XX
PT Polypeptides binding to major histocompatibility complex class II human
PT leukocyte antigen-determining region molecule having amino acid
PT sequence found in tumour rejection antigen precursor used for
PT stimulating proliferation of helper T cells -

PS Example 21; Page 31; 62pp; English.

XX
CC The sequence represents a human NY-ESO-1 tumour rejection antigen
CC precursor fragment. NY-ESO-1 and SSX-2 polypeptides, or fragments of,
CC bind to major histocompatibility complex (MHC) Class II molecules such as
CC human leukocyte antigen-determining region (HLA-DR) molecules and
CC stimulate proliferation of helper T cells. The peptides can be
CC administered to an HLA-DR positive subject in order to stimulate the
CC helper T cells. An MHC Class II HLA-DR-NY-ESO-1/SSX-2 complex expressed
CC on the surface of a cell or present in free form is useful for this
CC stimulation. The nucleic acid is useful for screening for a cancerous
CC condition, which involves contacting a subject sample to a cell line
CC transfected with the immunoreactive cell (helper T cell), where
CC interaction is indicative of cancer. In addition, a sample from a patient
CC (for example, a body fluid or tissue) can be monitored for the amount of
CC the complex present in the bloodstream. This is useful for determining
CC regression, progression or onset of a cancerous condition. The method
CC involves contacting the sample with a radioactive labelled or enzyme
CC labelled monoclonal antibody which specifically binds with the complex.

XX
SQ Sequence 9 AA;

Query Match 48.4%; Score 44; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLLEFYLAM 10
| | | | | | | |
Db 1 rllefylam 9

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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:38:25 ; Search time 560.51 Seconds
(without alignments)
11.303 Million cell updates/sec

Title: US-09-165-546A-12
Perfect score: 91
Sequence: 1 SRLLEFYLAMPFATPMEA 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 451056

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	91	100.0	18	15 US-09-165-546A-12	Sequence 12, Appl
2	91	100.0	18	18 US-09-408-036B-11	Sequence 11, Appl
3	70	76.9	14	18 US-09-408-036B-31	Sequence 31, Appl
4	54	59.3	10	19 US-09-529-206-101	Sequence 101, App
5	54	59.3	10	19 US-09-529-206A-101	Sequence 101, App
6	54	59.3	10	19 US-09-529-206B-101	Sequence 101, App
7	52	57.1	10	19 US-09-529-206-93	Sequence 93, Appl

8	52	57.1	10	19	US-09-529-206-96	Sequence 96, Appl
9	52	57.1	10	19	US-09-529-206A-93	Sequence 93, Appl
10	52	57.1	10	19	US-09-529-206A-96	Sequence 96, Appl
11	52	57.1	10	19	US-09-529-206B-93	Sequence 93, Appl
12	52	57.1	10	19	US-09-529-206B-96	Sequence 96, Appl
13	51	56.0	10	19	US-09-529-206-98	Sequence 98, Appl
14	51	56.0	10	19	US-09-529-206A-98	Sequence 98, Appl
15	51	56.0	10	19	US-09-529-206B-98	Sequence 98, Appl
16	47	51.6	9	2	US-06-670-456A-2	Sequence 2, Appli
17	44	48.4	9	17	US-09-344-040B-20	Sequence 20, Appl
18	44	48.4	9	18	US-09-408-036B-27	Sequence 27, Appl
19	44	48.4	9	18	US-09-409-455A-19	Sequence 19, Appl
20	44	48.4	9	19	US-09-529-206-63	Sequence 63, Appl
21	44	48.4	9	19	US-09-529-206A-63	Sequence 63, Appl
22	44	48.4	9	19	US-09-529-206B-63	Sequence 63, Appl
23	44	48.4	9	22	US-09-833-039-19	Sequence 19, Appl
24	37	40.7	15	21	US-09-700-253-4	Sequence 4, Appli
25	37	40.7	15	21	US-09-700-253-5	Sequence 5, Appli
26	36	39.6	9	18	US-09-409-455A-124	Sequence 124, App
27	36	39.6	9	22	US-09-833-039-124	Sequence 124, App
28	34	37.4	9	2	US-06-670-456A-4	Sequence 4, Appli
29	32	35.2	17	3	US-07-925-460A-18	Sequence 18, Appl
30	32	35.2	17	4	US-08-077-255-18	Sequence 18, Appl
31	32	35.2	17	4	US-08-077-255A-18	Sequence 18, Appl
32	32	35.2	17	8	US-08-475-399-18	Sequence 18, Appl
33	32	35.2	17	8	US-08-475-399A-18	Sequence 18, Appl
34	32	35.2	17	8	US-08-476-877-18	Sequence 18, Appl
35	32	35.2	17	8	US-08-476-877A-18	Sequence 18, Appl
36	32	35.2	17	8	US-08-487-505-18	Sequence 18, Appl
37	32	35.2	17	8	US-08-487-505A-18	Sequence 18, Appl
38	32	35.2	17	8	US-08-488-377-18	Sequence 18, Appl
39	32	35.2	17	14	US-09-072-163A-18	Sequence 18, Appl
40	32	35.2	17	14	US-09-072-163B-18	Sequence 18, Appl
41	31	34.1	16	6	US-08-264-243-4	Sequence 4, Appli
42	31	34.1	16	6	US-08-264-243A-4	Sequence 4, Appli
43	31	34.1	16	10	US-08-670-781-8	Sequence 8, Appli
44	30	33.0	9	18	US-09-409-455A-119	Sequence 119, App
45	30	33.0	9	22	US-09-833-039-119	Sequence 119, App

ALIGNMENTS

RESULT 1

US-09-165-546A-12
; Sequence 12, Application US/09165546A

GENERAL INFORMATION:

APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao, Canlan, Matt; Gure, Ali, Old, Lloyd, Ritter, Gerd

TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CLASS II MOLECULES, AND USES THEREOF

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: FULBRIGHT & JAWORSKI LLP

STREET: 666 Fifth Avenue

CITY: New York City

STATE: New York

COUNTRY: USA

ZIP: 10158

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage

COMPUTER: IBM

OPERATING SYSTEM: PC-DOS

SOFTWARE: WordPerfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/165,546A

FILING DATE: 02-Oct-1998

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/062,422

FILING DATE: April 17, 1998

APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
APPLICATION NUMBER: US 08/752,182
FILING DATE: 03-October-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, Norman D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-165-546A-12

Query Match 100.0%; Score 91; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLEFFYLAMPFPMEA 18
|||||

Db 1 SRLEFFYLAMPFPMEA 18

RESULT 2

US-09-408-036B-11
Sequence 11, Application US/09408036B
GENERAL INFORMATION:
APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Pfreundschuh, Michael
TITLE OF INVENTION: Isolated Peptides Which Bind to MHC Class II Molecules and Uses T
FILE REFERENCE: LUD 5624
CURRENT APPLICATION NUMBER: US/09/408,036B
CURRENT FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 09/344,040
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 09/165,546
PRIOR FILING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 38
SEQ ID NO 11
LENGTH: 18
TYPE: PRT
ORGANISM: Homo sapiens
US-09-408-036B-11

Query Match 100.0%; Score 91; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLEFFYLAMPFPMEA 18
|||||

Db 1 SRLEFFYLAMPFPMEA 18

RESULT 3

US-09-408-036B-31
Sequence 31, Application US/09408036B
GENERAL INFORMATION:
APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Pfreundschuh, Michael
TITLE OF INVENTION: Isolated Peptides Which Bind to MHC Class II Molecules and Uses T
FILE REFERENCE: LUD 5624
CURRENT APPLICATION NUMBER: US/09/408,036B
CURRENT FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 09/344,040

PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 09/165,546
PRIOR FILING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 38
SEQ ID NO 31
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-09-408-036B-31

Query Match 76.9%; Score 70; DB 18; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLEFFYLAMPFAT 14
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Db 1 SRLEFFYLAMPFAT 14

RESULT 4

US-09-529-206-101
Sequence 101, Application US/09529206
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America as
TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
TITLE OF INVENTION: Encoding Same
FILE REFERENCE: 20264269PC
CURRENT APPLICATION NUMBER: US/09/529,206
CURRENT FILING DATE: 2000-06-13
PRIOR APPLICATION NUMBER: US60/061,428
PRIOR FILING DATE: 1997-10-08
NUMBER OF SEQ ID NOS: 106
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 101
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-09-529-206-101

Query Match 59.3%; Score 54; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YLAMPFATPM 16
|||||

Db 1 YLAMPFATPM 10

RESULT 5

US-09-529-206A-101
Sequence 101, Application US/09529206A
GENERAL INFORMATION:
APPLICANT: Wang Rong, Fu
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
TITLE OF INVENTION: Encoding Same
FILE REFERENCE: 20264269US1
CURRENT APPLICATION NUMBER: US/09/529,206A
CURRENT FILING DATE: 2000-06-13
PRIOR APPLICATION NUMBER: PCT/US98/19609
PRIOR FILING DATE: 1998-09-21
PRIOR APPLICATION NUMBER: US60/061,428
PRIOR FILING DATE: 1997-10-08
NUMBER OF SEQ ID NOS: 127
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 101
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-09-529-206A-101

Query Match 59.3%; Score 54; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YLAMPFATPM 16
| | | | | | | |
Db 1 YLAMPFATPM 10

RESULT 6
US-09-529-206B-101
; Sequence 101, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 101
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-101

Query Match 59.3%; Score 54; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YLAMPFATPM 16
| | | | | | | |
Db 1 YLAMPFATPM 10

RESULT 7
US-09-529-206-93
; Sequence 93, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-93

Query Match 57.1%; Score 52; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLEFYLAMPF 12
| | | | | | | |
Db 1 LLEFYLAMPF 10

RESULT 8
US-09-529-206-96
; Sequence 96, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 96
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-96

Query Match 57.1%; Score 52; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AMPFATPMEA 18
| | | | | | | |
Db 1 AMPFATPMEA 10

RESULT 9
US-09-529-206A-93
; Sequence 93, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206A-93

Query Match 57.1%; Score 52; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLEFYLAMPF 12
| | | | | | | |
Db 1 LLEFYLAMPF 10

RESULT 10
US-09-529-206A-96
; Sequence 96, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A

; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 96
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206A-96

Query Match 57.1%; Score 52; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AMPFATPMEA 18
| | | | | | | | | |
Db 1 AMPFATPMEA 10

RESULT 11
US-09-529-206B-93
; Sequence 93, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-93

Query Match 57.1%; Score 52; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLEFYLAMPF 12
| | | | | | | | | |
Db 1 LLEFYLAMPF 10

RESULT 12
US-09-529-206B-96
; Sequence 96, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 96
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-96

Query Match 57.1%; Score 52; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AMPFATPMEA 18
| | | | | | | | | |
Db 1 AMPFATPMEA 10

RESULT 13
US-09-529-206-98
; Sequence 98, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 98
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-98

Query Match 56.0%; Score 51; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLLEFYLAM 11
| | | | | | | | | |
Db 1 RLLEFYLAM 10

RESULT 14
US-09-529-206A-98
; Sequence 98, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206A-98

Query Match 56.0%; Score 51; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLLEFY LAMP 11
1111111111
Db 1 RLLEFY LAMP 10

RESULT 15
US-09-529-206B-98
; Sequence 98, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-98

Query Match 56.0%; Score 51; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLLEFY LAMP 11
| | | | | | | |
Db 1 RLLEFY LAMP 10

Search completed: July 3, 2002, 11:38:26
Job time: 852 sec

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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:39:32 ; Search time 61.64 Seconds
(without alignments)
29.545 Million cell updates/sec

Title: US-09-165-546A-12

Perfect score: 91

Sequence: 1 SRLLEFYLAMPFATPMEA 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 308740 seqs, 101176262 residues

Total number of hits satisfying chosen parameters: 45157

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
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2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
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6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	57.1	10	6 US-10-117-937-175	Sequence 175, App
2	52	57.1	10	6 US-10-117-937-176	Sequence 176, App
3	48	52.7	9	6 US-10-117-937-174	Sequence 174, App
4	48	52.7	9	6 US-10-117-937-177	Sequence 177, App
5	47	51.6	9	5 US-09-670-456A-2	Sequence 2, Appl
6	44	48.4	9	5 US-09-344-040C-19	Sequence 19, Appl
7	44	48.4	9	6 US-10-117-937-173	Sequence 173, App
8	39	42.9	9	6 US-10-117-937-172	Sequence 172, App
9	36	39.6	9	5 US-09-344-040C-124	Sequence 124, App
10	35	38.5	9	6 US-10-117-937-170	Sequence 170, App
11	35	38.5	10	6 US-10-117-937-171	Sequence 171, App
12	34	37.4	9	5 US-09-670-456A-4	Sequence 4, Appl
13	32	35.2	17	1 PCT-US02-09671-922	Sequence 922, App
14	31	34.1	16	1 PCT-US02-09671-80	Sequence 80, Appl
15	31	34.1	17	1 PCT-US02-09671-84	Sequence 84, Appl
16	30	33.0	9	5 US-09-344-040C-119	Sequence 119, App
17	30	33.0	12	5 US-09-563-286B-775	Sequence 775, App
18	28	30.8	9	6 US-10-117-937-169	Sequence 169, App
19	28	30.8	10	5 US-09-563-286B-758	Sequence 758, App
20	28	30.8	18	6 US-10-153-244-211	Sequence 211, App
21	27	29.7	10	5 US-09-563-286B-692	Sequence 692, App
22	27	29.7	10	5 US-09-563-286B-854	Sequence 854, App
23	27	29.7	11	1 PCT-US02-07487-78	Sequence 78, Appl
24	27	29.7	12	5 US-09-563-286B-740	Sequence 740, App
25	27	29.7	12	5 US-09-563-286B-814	Sequence 814, App
26	27	29.7	12	5 US-09-563-286B-832	Sequence 832, App

27	27	29.7	13	1 PCT-US02-09671-219	Sequence 219, App
28	27	29.7	13	6 US-10-116-252-22	Sequence 22, Appl
29	27	29.7	14	1 PCT-US02-09671-82	Sequence 82, Appl
30	27	29.7	15	1 PCT-US02-09671-79	Sequence 79, Appl
31	27	29.7	16	1 PCT-US02-09671-83	Sequence 83, Appl
32	26	28.6	12	5 US-09-563-286B-742	Sequence 742, App
33	26	28.6	12	5 US-09-563-286B-751	Sequence 751, App
34	26	28.6	12	5 US-09-563-286B-827	Sequence 827, App
35	26	28.6	12	5 US-09-563-286B-842	Sequence 842, App
36	26	28.6	15	5 US-09-563-286B-798	Sequence 798, App
37	26	28.6	15	6 US-10-001-469-2511	Sequence 2511, Ap
38	26	28.6	15	6 US-10-001-469-2576	Sequence 2576, Ap
39	26	28.6	15	6 US-10-001-469-2605	Sequence 2605, Ap
40	26	28.6	15	6 US-10-001-469-2685	Sequence 2685, Ap
41	26	28.6	15	6 US-10-001-469-2686	Sequence 2686, Ap
42	26	28.6	15	6 US-10-001-469-2844	Sequence 2844, Ap
43	25	27.5	9	6 US-10-001-469-216	Sequence 216, App
44	25	27.5	9	6 US-10-001-469-459	Sequence 459, App
45	25	27.5	9	6 US-10-001-469-631	Sequence 631, App

ALIGNMENTS

RESULT 1
US-10-117-937-175
; Sequence 175, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPTOPE SEQUENCES
; FILE REFERENCE: CTLM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-175

Query Match 57.1%; Score 52; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 LLEFYLAMPF 12
| | | | | | | | | |
Db 1 LLEFYLAMPF 10

RESULT 2
US-10-117-937-176
; Sequence 176, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPTOPE SEQUENCES
; FILE REFERENCE: CTLM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937

c

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; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-176
```

```
Query Match      57.1%; Score 52; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      9 AMPFATPMEA 18
        |||||||||
Db       1 AMPFATPMEA 10
```

```
RESULT 3
US-10-117-937-174
; Sequence 174, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 174
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-174
```

```
Query Match      52.7%; Score 48; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 LEFYLAMPF 12
        |||||||||
Db       1 LEFYLAMPF 9
```

```
RESULT 4
US-10-117-937-177
; Sequence 177, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
```

```
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 177
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-177
```

```
Query Match      52.7%; Score 48; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      10 MPFATPMEA 18
        |||||||||
Db       1 MPFATPMEA 9
```

```
RESULT 5
US-09-670-456A-2
; Sequence 2, Application US/09670456A
; GENERAL INFORMATION:
; LUD-5668-PCT
; APPLICANT: Gnjatic, Sacha
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA-C MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: LUD 5668
; CURRENT APPLICATION NUMBER: US/09/670,456A
; CURRENT FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-670-456A-2
```

```
Query Match      51.6%; Score 47; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 LAMPFATPM 16
        |||||||||
Db       1 LAMPFATPM 9
```

```
RESULT 6
US-09-344-040C-19
; Sequence 19, Application US/09344040C
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Deter
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gen
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
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; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 19
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-19

Query Match 48.4%; Score 44; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLLEFYLAM 10
| | | | |
Db 1 RLLEFYLAM 9

RESULT 7
US-10-117-937-173
; Sequence 173, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLLMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 173
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-173

Query Match 48.4%; Score 44; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLLEFYLAM 10
| | | | |
Db 1 RLLEFYLAM 9

RESULT 8
US-10-117-937-172
; Sequence 172, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLLMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210

; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 172
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-172

Query Match 42.9%; Score 39; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLLEFYL 8
| | | | |
Db 2 SRLLEFYL 9

RESULT 9
US-09-344-040C-124
; Sequence 124, Application US/09344040C
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Deter
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gen
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 124
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-124

Query Match 39.6%; Score 36; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 FATPMEA 18
| | | | |
Db 1 FATPMEA 7

RESULT 10
US-10-117-937-170
; Sequence 170, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLLMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210

```

; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 170
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-170

Query Match          38.5%; Score 35; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLLEFY 7
Db 3 SRLLEFY 9

RESULT 11
US-10-117-937-171
; Sequence 171, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLLMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 171
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-171

Query Match          38.5%; Score 35; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRLLEFY 7
Db 4 SRLLEFY 10

RESULT 12
US-09-670-456A-4
; Sequence 4, Application US/09670456A
; GENERAL INFORMATION:
; LUD-5668-PCT
; APPLICANT: Gnjatich, Sacha
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA-C MOLECULES AND USES
; FILE REFERENCE: LUD 5668
; CURRENT APPLICATION NUMBER: US/09/670,456A
; CURRENT FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
```

```

US-09-670-456A-4

Query Match          37.4%; Score 34; DB 5; Length 9;
Best Local Similarity 55.6%; Pred. No. 2.8e+05;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 8 LAMPFATPM 16
Db 1 ITMPFSSPM 9

RESULT 13
PCT-US02-09671-922
; Sequence 922, Application PC/TUS0209671
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT APPLICATION NUMBER: PCT/US02/09671
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 922
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09671-922

Query Match          35.2%; Score 32; DB 1; Length 17;
Best Local Similarity 26.7%; Pred. No. 54;
Matches 4; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 4 LEFYLAMPFATPMEA 18
Db 2 VEYHFLSPYVSPKES 16

RESULT 14
PCT-US02-09671-80
; Sequence 80, Application PC/TUS0209671
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT APPLICATION NUMBER: PCT/US02/09671
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
```

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09671-80

Query Match 34.1%; Score 31; DB 1; Length 16;
Best Local Similarity 28.6%; Pred. No. 74;
Matches 4; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 4 LEFYLAMPPATPME 17
:|:: |:||
Db 3 VEYHFLSPVSPKE 16

RESULT 15
PCT-US02-09671-84
; Sequence 84, Application PC/TUS0209671
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT APPLICATION NUMBER: PCT/US02/09671
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09671-84

Query Match 34.1%; Score 31; DB 1; Length 17;
Best Local Similarity 28.6%; Pred. No. 79;
Matches 4; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 4 LEFYLAMPPATPME 17
:|:: |:||
Db 4 VEYHFLSPVSPKE 17

Search completed: July 3, 2002, 11:39:33
Job time: 884 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:28:57 ; Search time 57.51 Seconds
(without alignments)
30.075 Million cell updates/sec

Title: US-09-165-546A-13

Perfect score: 88

Sequence: 1 TVSGNLTIRLTAADHRQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 3210

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	28.4	11	2 I65231	CCK-B gastrin rece
2	23	26.1	16	2 S36876	aquacobalamin redu
3	22	25.0	12	2 S17540	agglutinin-III lec
4	21	23.9	14	2 B39111	Ig heavy chain V r
5	21	23.9	14	2 PT0259	Ig heavy chain CRD
6	21	23.9	15	2 A56786	pimeloyl-CoA synth
7	21	23.9	15	2 PA0063	ubiquitin - fungus
8	21	23.9	16	2 I51879	cystathionine beta
9	21	23.9	16	2 I46275	hemoglobin beta-x
10	20	22.7	6	2 S71349	beta-crystallin B2
11	20	22.7	9	2 A39841	sucrose 3-glucosyl
12	20	22.7	9	2 PH0902	T-cell receptor be
13	20	22.7	11	2 S66196	alcohol dehydrogen
14	20	22.7	11	2 A34243	H-hyosophorin - Ja
15	20	22.7	12	2 PC4377	telomeric and tetr
16	20	22.7	12	4 PC2121	aminotransferase c
17	20	22.7	16	2 A42291	tail fiber protein
18	20	22.7	17	2 E28587	T-cell receptor be
19	20	22.7	17	2 H53284	T-cell receptor be
20	19	21.6	11	2 B43669	hypothetical prote
21	19	21.6	11	2 PH0906	T-cell receptor be
22	19	21.6	12	2 A37933	Ig lambda chain J
23	19	21.6	13	2 S22761	Ig lambda-2 chain
24	19	21.6	14	2 S19803	ubiquitin - potato
25	19	21.6	15	2 PA0090	protein QF10022 -
26	19	21.6	15	2 PH1342	Ig heavy chain DJ
27	19	21.6	15	2 G41299	T-cell receptor al
28	19	21.6	15	2 S10741	phosphoglucomutase
29	19	21.6	15	2 A35141	T-cell receptor de

30	19	21.6	16	2 PH1778	T cell receptor al
31	19	21.6	16	2 F41299	T-cell receptor al
32	19	21.6	16	2 S59901	pyruvate dehydroge
33	19	21.6	16	2 S68730	bleomycin-binding
34	19	21.6	16	2 B89821	hypothetical prote
35	19	21.6	17	2 B44923	carboxypeptidase 3
36	19	21.6	18	2 B57789	kidney stone matri
37	19	21.6	18	2 PX0081	dipeptidyl-peptida
38	18	20.5	9	2 B39841	dextranucrase (EC
39	18	20.5	10	2 A61617	ecdysteroid UDPglu
40	18	20.5	10	2 A58365	neuropeptide FFRfa
41	18	20.5	10	2 A59173	nuclease Bh1 (EC 3
42	18	20.5	11	2 D58502	27K bile and gallb
43	18	20.5	12	2 A54315	entactin/nidogen -
44	18	20.5	12	2 S65730	hemoglobin, extrac
45	18	20.5	13	2 H44957	protein p18 - comm

ALIGNMENTS

RESULT 1
I65231
CCK-B gastrin receptor isoform - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: I65231
R;Miyake, A.
Biochem. Biophys. Res. Commun. 208, 230-237, 1995
A;Title: A truncated isoform of human CCK-B/gastrin receptor generated by alternative
A;Reference number: I52307; MUID:95194412
A;Accession: I65231
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-11 <RES>
A;Cross-references: GB:S76072; NID:g913752; PIDN:AAB33740.1; PID:g913753
C;Genetics:
A;Gene: CCK-B

Query Match 28.4%; Score 25; DB 2; Length 11;
Best Local Similarity 55.6%; Pred. No. 4.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 9
:||||:|
Db 2 SVGGNMLII 10

RESULT 2
S36876
aquacobalamin reductase (NADPH) (EC 1.6.99.11) - Euglena gracilis (fragment)
C;Species: Euglena gracilis
C;Date: 10-Dec-1993 #sequence_revision 09-May-1997 #text_change 07-May-1999
C;Accession: S36876
R;Watanabe, F.; Yamaji, R.; Isegawa, Y.; Yamamoto, T.; Tamura, Y.; Nakano, Y.
Arch. Biochem. Biophys. 305, 421-427, 1993
A;Title: Characterization of aquacobalamin reductase (NADPH) from Euglena gracilis.
A;Reference number: S36876; MUID:93384296
A;Accession: S36876
A;Molecule type: protein
A;Residues: 1-16 <WAT>
C;Keywords: flavoprotein; NADP; oxidoreductase

Query Match 26.1%; Score 23; DB 2; Length 16;
Best Local Similarity 71.4%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 SGNILTI 9
|||:|
Db 5 SGNHVTI 11

```
RESULT 3
S17540
agglutinin-III lectin - European elder (fragment)
C;Species: Sambucus nigra (European elder)
C;Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
C;Accession: S17540
R;Mach, L.; Scherf, W.; Ammann, M.; Poetsch, J.; Bertsch, W.; Maerz, L.; Gloessl, J.
Biochem. J. 278, 667-671, 1991
A;Title: Purification and partial characterization of a novel lectin from elder (Sambucus
A;Reference number: S17540; MUID:91378923
A;Accession: S17540
A;Molecule type: protein
A;Residues: 1-12 <MAC>
A;Experimental source: fruit
C;Keywords: glycoprotein; lectin

Query Match 25.0%; Score 22; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSGNIL 7
:|l|:
Db 5 ITGNII 10

RESULT 4
B39111
Ig heavy chain V region - Pacific hagfish (fragment)
C;Species: Eptatretus stouti (Pacific hagfish)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-1996
C;Accession: B39111
R;Varner, J.; Neame, P.; Litman, G.W.
Proc. Natl. Acad. Sci. U.S.A. 88, 1746-1750, 1991
A;Title: A serum heterodimer from hagfish (Eptatretus stoutii) exhibits structural simil
A;Reference number: A39111; MUID:91156684
A;Accession: B39111
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14 <VAR>
C;Keywords: heterotetramer; immunoglobulin

Query Match 23.9%; Score 21; DB 2; Length 14;
Best Local Similarity 40.0%; Pred. No. 2.8e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 TVSGNILTIR 10
| | | | |
Db 2 TAYGNLAAIQ 11

RESULT 5
PT0259
Ig heavy chain CRD3 region (clone 2-118C) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0259
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and i
A;Reference number: PT0222; MUID:91108337
A;Accession: PT0259
A;Molecule type: DNA
A;Residues: 1-14 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 23.9%; Score 21; DB 2; Length 14;
Best Local Similarity 36.4%; Pred. No. 2.8e+03;
Matches 4; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
;
```

```
QY 6 ILTIRLTAADH 16
: | | |
Db 3 LTTIAAAGIDH 13

RESULT 6
A56786
pimeloyl-CoA synthase - Bacillus sphaericus (fragment)
C;Species: Bacillus sphaericus
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 18-Aug-1995
C;Accession: A56786
R;Ploux, O.; Soularue, P.; Marquet, A.; Gloeckler, R.; Lemoine, Y.
Biochem. J. 287, 685-690, 1992
A;Title: Investigation of the first step of biotin biosynthesis in Bacillus sphaericu
A;Reference number: A56786; MUID:93075017
A;Accession: A56786
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <PLO>
A;Experimental source: Bacillus sphaericus protein overexpressed in Escherichia coli
A;Note: sequence extracted from NCBI backbone (NCBIP:117639)
C;Genetics:
A;Gene: biow
C;Keywords: biotin biosynthesis; homodimer

Query Match 23.9%; Score 21; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 3e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 8 TIRLTAAD 15
: | | | |
Db 6 SIRMRAAE 13

RESULT 7
PA0063
ubiquitin - fungus (Fusarium sporotrichioides) (fragment)
C;Species: Fusarium sporotrichioides
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C;Accession: PA0063
R;Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotr
A;Reference number: PA0051
A;Accession: PA0063
A;Molecule type: protein
A;Residues: 1-15 <ACC>

Query Match 23.9%; Score 21; DB 2; Length 15;
Best Local Similarity 33.3%; Pred. No. 3e+03;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 TVSGNILTII 9
| : : | : | :
Db 7 TLTGKTITL 15

RESULT 8
I51879
cystathionine beta-synthase - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
C;Accession: I51879
R;Sebastio, G.; Sperandeo, M.P.; Panico, M.; de Franchis, R.; Kraus, J.P.; Andria, G.
Am. J. Hum. Genet. 56, 1324-1333, 1995
A;Title: The molecular basis of homocystinuria due to cystathionine beta-synthase def
A;Reference number: I51879; MUID:95282779
A;Accession: I51879
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
```

A;Residues: 1-16 <RES>
A;Cross-references: GB:S78267; NID:g999349; PIDN:AAB34404.1; PID:g999350

Query Match 23.9%; Score 21; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 11 LTAADH 16
Db 1 ITGVDH 6

RESULT 9
I46275 hemoglobin beta-x chain - goat (fragment)
C;Species: Capra aegagrus hircus (domestic goat)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-Nov-1999
C;Accession: I46275
R;Haynes, J.R.; Rosteck, P.R.; Schon, E.A.; Gallagher, P.M.; Burks, D.J.; Smith, K.; Lin J. Biol. Chem. 255, 6355-6367, 1980
A;Title: The isolation of the beta-a-, beta-c-, and gamma-globin genes and a presumptive A;Reference number: I46273; MUID:80227766
A;Accession: I46275
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-16 <HAY>
A;Cross-references: GB:K00659; NID:gl64151; PIDN:AAA30919.1; PID:gl64156

Query Match 23.9%; Score 21; DB 2; Length 16;
Best Local Similarity 62.5%; Pred. No. 3.2e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GNILTIRL 11
Db 3 GKILVITL 10

RESULT 10
S71349 beta-crystallin B2 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 07-May-1999
C;Accession: S71349
R;Dirks, R.P.H.; Kraft, H.J.; van Genesen, S.T.; Klok, E.J.; Pfundt, R.; Schoenmakers, J Eur. J. Biochem. 239, 23-32, 1996
A;Title: The cooperation between two silencers creates an enhancer element that controls A;Reference number: S71349; MUID:96305362
A;Accession: S71349
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-6 <DIR>
A;Cross-references: EMBL:X83671
A;Experimental source: strain Wistar; lens epithelial cells
C;Genetics:
A;Gene: CRYBB2

Query Match 22.7%; Score 20; DB 2; Length 6;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 AADHR 17
Db 2 ASDHQ 6

RESULT 11
A39841 sucrose 3-glucosyltransferase (EC 2.4.1.-) - Streptococcus sobrinus (fragment)
C;Species: Streptococcus sobrinus
C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 21-Mar-1996

C;Accession: A39841
R;Mooser, G.; Hefta, S.A.; Paxton, R.J.; Shively, J.E.; Lee, T.D.
J. Biol. Chem. 266, 8916-8922, 1991
A;Title: Isolation and sequence of an active-site peptide containing a catalytic aspa A;Reference number: A39841; MUID:91224988
A;Accession: A39841
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <MOO>
C;Keywords: glycosyltransferase; hexosyltransferase

Query Match 22.7%; Score 20; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 8 TIRLTAAD 15
Db 2 SIRVDAVD 9

RESULT 12
PH0902 T-cell receptor beta chain V-D-J region (hybridoma S23F4F4) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0902
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B. J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental alle A;Reference number: PH0891; MUID:92078857
A;Accession: PH0902
A;Molecule type: mRNA
A;Residues: 1-9 <GOL>
A;Experimental source: myelin basic protein-immunized T-cell
C;Keywords: T-cell receptor

Query Match 22.7%; Score 20; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVSGNI 6
Db 4 STSGNV 9

RESULT 13
S66196 alcohol dehydrogenase (EC 1.1.1.1) class III high affinity form - cod (Gadus sp.) (fr C;Species: Gadus sp. (cod)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 12-Jun-1998
C;Accession: S66196
R;Hjelmqvist, L.; Hackett, M.; Shafqat, J.; Danielsson, O.; Iida, J.; Hendrickson, R. FEBS Lett. 367, 237-240, 1995
A;Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogenases nzyme.
A;Reference number: S66191; MUID:95331382
A;Accession: S66196
A;Molecule type: protein
A;Residues: 1-11 <HJE>
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology C;Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 22.7%; Score 20; DB 2; Length 11;
Best Local Similarity 71.4%; Pred. No. 3.2e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 TIRLTAA 14
Db 1 TIRCRAA 7

RESULT 14
A34243
H-hyosophorin - Japanese flounder (fragment)
C;Species: Paralichthys olivaceus (Japanese flounder)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 12-Feb-1999
C;Accession: A34243
R;Seko, A.; Kitajima, K.; Iwasaki, M.; Inoue, S.; Inoue, Y.
J. Biol. Chem. 264, 15922-15929, 1989
A;Title: Structural studies of fertilization-associated carbohydrate-rich glycoproteins
of a novel penta-antennary N-linkedglycan chain in the tandem repeating glycopeptide unit
A;Reference number: A34243; MUID:89380184
A;Accession: A34243
A;Molecule type: protein
A;Residues: 1-11 <SEK>
A;Note: 3-Ala, 4-Ala, 5-Pro or Gln, and 6-Val were also found

Query Match 22.7%; Score 20; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVSGNI 6
:| | |:
Db 3 SVGGNV 8

RESULT 15
PC4377
telomeric and tetraplex DNA binding protein qTBP42 VIII - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 07-May-1999
C;Accession: PC4377
R;Sarig, G.; Weisman-Shomer, P.; Fry, M.
Biochem. Biophys. Res. Commun. 237, 617-623, 1997
A;Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the CA
A;Reference number: PC4371; MUID:97445086
A;Accession: PC4377
A;Molecule type: protein
A;Residues: 1-12 <SAR>
C;Comment: This protein binds either strand of the telomeric DNA as well as unimolecular

Query Match 22.7%; Score 20; DB 2; Length 12;
Best Local Similarity 80.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGN 5
| | | |:
Db 6 TVSGS 10

Search completed: July 3, 2002, 11:28:57
Job time: 398 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:41:55 ; Search time 27.94 Seconds
(without alignments)
24.945 Million cell updates/sec

Title: US-09-165-546A-13
Perfect score: 88
Sequence: 1 TVSGNILTIRLTAADHRQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 923

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	27.3	12	1	DCML_PSECA
2	21	23.9	15	1	CDN4_LITCE
3	20	22.7	15	1	CDN2_LITGI
4	19	21.6	13	1	TEMC_RANTE
5	19	21.6	13	1	TEMD_RANTE
6	19	21.6	13	1	TEME_RANTE
7	18	20.5	10	1	FARP_MYTED
8	18	20.5	15	1	CDN3_LITGI
9	18	20.5	15	1	FRE2_LITIN
10	18	20.5	15	1	UC13_MAIZE
11	17	19.3	10	1	NEMS_DROME
12	17	19.3	15	1	ACT_PINPS
13	17	19.3	15	1	R13A_SPIOL
14	17	19.3	15	1	RKGG_CARCR
15	17	19.3	15	1	SODP_PINPS
16	17	19.3	16	1	PGTL_PELAC
17	17	19.3	17	1	AU33_LITRA
18	17	19.3	17	1	PH3_PERAM
19	17	19.3	17	1	RM35_YEAST
20	17	19.3	18	1	MU21_LITGE
21	16	18.2	9	1	IPYR_RHOVI
22	16	18.2	10	1	LABA_JATMU
23	16	18.2	10	1	TPIS_NICPL
24	16	18.2	11	1	LADD_ONCMY
25	16	18.2	13	1	IDHA_CANFA
26	16	18.2	15	1	KLOM_LUNTE
27	16	18.2	15	1	PH2_PERAM
28	16	18.2	15	1	TRPA_LEUMA
29	16	18.2	16	1	FIBA_MANLE
30	16	18.2	17	1	NU4M_TRIRU
31	16	18.2	17	1	TPIS_PINPS
32	16	18.2	18	1	HEX_ADECU
33	15	17.0	11	1	PQQC_PSEFL

34	15	17.0	11	1	RE41_LITRU
35	15	17.0	12	1	OPS3_DROVI
36	15	17.0	12	1	SOI5_BACSU
37	15	17.0	12	1	V23K_WSSV
38	15	17.0	13	1	CRBL_VESTR
39	15	17.0	14	1	GR75_CANFA
40	15	17.0	14	1	HCYA_MEGCR
41	15	17.0	14	1	LECB_PSOSC
42	15	17.0	15	1	EFIA_MICCR
43	15	17.0	15	1	ESTB_SCHGA
44	15	17.0	15	1	MILT_ONCKE
45	15	17.0	15	1	PGKH_PHYPA

P82074	litoria rub
P17645	drosophila
P80863	bacillus su
P82005	white spot
P17231	vespa tropi
P99502	canis famil
Q10583	megathura c
P22584	psophocarpu
P81266	microplitis
P81011	schizaphis
P81037	oncorhynchu
P80659	physcomitre

ALIGNMENTS

RESULT 1
DCML_PSECA
ID DCML_PSECA STANDARD; PRT; 12 AA.
AC P19919;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Carbon monoxide oxygenase [cytochrome B-561] large chain (EC 1.2.2.4)
DE (Fragment).
OS Pseudomonas carboxydovorans.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Bradyrhizobium group; Oligotrophia.
OX NCBI_TaxID=40137;
RN [1]
RP SEQUENCE.
RC STRAIN=OM5;
RX MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in carboxydotrophic bacteria.";
RL Arch. Microbiol. 152:335-341(1989).
CC -!- CATALYTIC ACTIVITY: CO + H(2)O + ferrocyclochrome b-561 = CO(2) + 2 H(+) + ferrocyclochrome b-561.
CC -!- COFACTOR: MOLYBDENUM.
CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND SMALL.
DR PIR; P10138; P10138.
KW Oxidoreductase; Molybdenum.
FT VARIANT 11 12 GE -> EK.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1289 MW; 9B170C688E6B02D1 CRC64;

Query Match 27.3%; Score 24; DB 1; Length 12;
Best Local Similarity 45.5%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY	5	NILTIRLTAAD	15
		:	
Db	2	NIQTVPTAGE	12

RESULT 2
CDN4_LITCE
ID CDN4_LITCE STANDARD; PRT; 15 AA.
AC P82076;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Caeridin 4.
OS Litoria caerulea (Green tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=30344;
RN [1]

```
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Parotoid gland;
RA Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. Structures of the caeridins from
RT Litoria caerulea.";
RL J. Chem. Soc. perkin Trans. 1:573-576(1993).
CC -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC ANTIBIOTIC ACTIVITY.
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
CC GLANDS.
CC -!- MASS SPECTROMETRY: MW=1504; METHOD=FAB.
KW Amphibian skin; Amidation.
FT MOD_RES 15 15 AMIDATION.
SQ SEQUENCE 15 AA; 1506 MW; 06F1BBFFBBC5195F CRC64;

Query Match 23.9%; Score 21; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 9.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSGNIL 7
Db 5 VVGNVL 10

RESULT 3
CDN2_LITGI
ID CDN2_LITGI STANDARD; PRT; 15 AA.
AC P56247;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Caeridin 2.
OS Litoria gilleni (Centralian tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=39405;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Parotoid gland;
RA Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structures of the caerins and
RT caeridins from Litoria gilleni.";
RL J. Chem. Res. 139:937-961(1993).
CC -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC ANTIBIOTIC ACTIVITY.
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
CC GLANDS.
CC -!- MASS SPECTROMETRY: MW=1408; METHOD=FAB.
KW Amphibian skin; Amidation.
FT MOD_RES 15 15 AMIDATION.
SQ SEQUENCE 15 AA; 1410 MW; 06F1BBF272550CBF CRC64;

Query Match 22.7%; Score 20; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSGNIL 7
Db 5 VVGNVL 10

RESULT 4
TEMC_RANTE
ID TEMC_RANTE STANDARD; PRT; 13 AA.
AC P56918;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Temporin C.
OS Rana temporaria (European common frog).
```

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
RT temporaria.";
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE
CC BACTERIA.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC FAMILY.
KW Amphibian skin; Antibiotic; Amidation; Multigene family.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1363 MW; 2201403A655B2448 CRC64;

Query Match 21.6%; Score 19; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSGNIL 7
Db 4 ILGNLL 9

RESULT 5
TEMD_RANTE
ID TEMD_RANTE STANDARD; PRT; 13 AA.
AC P56919;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Temporin D.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Skin;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
RT temporaria.";
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: HAS NO ANTIBACTERIAL ACTIVITY.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC FAMILY.
KW Amphibian skin; Amidation; Multigene family.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1379 MW; 3EF35DFA655B2448 CRC64;

Query Match 21.6%; Score 19; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSGNIL 7
Db 4 IVGNLL 9

RESULT 6
TEME_RANTE
ID TEME_RANTE STANDARD; PRT; 13 AA.
```



```
AC P56920;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Temporin E.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
RT temporaria.";
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE
CC BACTERIA.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC FAMILY.
KW Amphibian skin; Antibiotic; Amidation; Multigene family.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1379 MW; 26505DFA79A92448 CRC64;

Query Match 21.6%; Score 19; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSGNIL 7
Db 4 IIGNLL 9

RESULT 7
FARP_MYTED
ID FARP_MYTED STANDARD; PRT; 10 AA.
AC P42560;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE FMRamide-like neuropeptide ALAGDHFFRF-amide.
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE.
RX MEDLINE=93047883; PubMed=1358534;
RA Walker R.J.;
RT "Neuroactive peptides with an RFamide or Famide carboxyl terminal.";
RL Comp. Biochem. Physiol. 102C:213-222(1992).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1180 MW; C2F80CC9C1EAA87D CRC64;

Query Match 20.5%; Score 18; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 AADH 16
Db 3 AGDH 6

RESULT 8
CDN3_LITGI
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ID CDN3_LITGI STANDARD; PRT; 15 AA.
AC P56248;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Caeridin 3.
OS Litoria gilleni (Centralian tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=39405;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Parotoid gland;
RA Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structures of the caerins and
RT caeridins from Litoria gilleni.";
RL J. Chem. Res. 139:937-961(1993).
CC -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC ANTIBIOTIC ACTIVITY.
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
CC GLANDS.
CC -!- MASS SPECTROMETRY: MW=1428; METHOD=FAB.
KW Amphibian skin; Amidation.
FT MOD_RES 15 15 AMIDATION.
SQ SEQUENCE 15 AA; 1430 MW; 06E90A797AF70CBF CRC64;

Query Match 20.5%; Score 18; DB 1; Length 15;
Best Local Similarity 75.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GNIL 7
Db 7 GNLL 10

RESULT 9
FRE2_LITIN
ID FRE2_LITIN STANDARD; PRT; 15 AA.
AC P82022;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Frenatin 2.
OS Litoria infrenata (Giant tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=61195;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=97368637; PubMed=9225251;
RA Raftery M.J., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "The structures of the frenatin peptides from the skin secretion of
RT the giant tree frog Litoria infrenata.";
RL J. Pept. Sci. 2:117-124(1996).
CC -!- FUNCTION: WIDE SPECTRUM ANTIMICROBIAL PEPTIDE.
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
CC GLANDS.
CC -!- MASS SPECTROMETRY: MW=1423; METHOD=FAB.
KW Antibiotic; Amphibian skin; Amidation.
FT MOD_RES 15 15 AMIDATION.
SQ SEQUENCE 15 AA; 1425 MW; 06ED4B7BB1650CBF CRC64;

Query Match 20.5%; Score 18; DB 1; Length 15;
Best Local Similarity 75.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GNIL 7
Db 7 GNLL 10
```

Db 7 GNLL 10

RESULT 10
UC13_MAIZE
ID UC13_MAIZE STANDARD; PRT; 15 AA.
AC P80619;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 243)
DE (Fragment).
OS zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP.. SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program."
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.8, ITS MW IS: 56.9 kDa.
CC -!- SIMILARITY: TO GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASES.
DR Maize-2DPAGE; P80619; COLEOPTILE.
DR MaizeDB; 123946; -. 1
FT NON_TER 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1739 MW; 02038EE7471AE038 CRC64;

Query Match 20.5%; Score 18; DB 1; Length 15;
Best Local Similarity 36.4%; Pred. No. 3.1e+03;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5 NILTIRLTAAD 15
I III ::
Db 4 NEFVIRLQXSE 14

RESULT 11
NEMS_DROME
ID . NEMS_DROME STANDARD; PRT; 10 AA.
AC P41494;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Dromyosuppressin (Neomyosuppressin) (NEB-MS).
GN DMS OR NEMS.
OS Drosophila melanogaster (Fruit fly), and
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227, 7385;
RN [1]
RP SEQUENCE.
RC SPECIES=D.melanogaster;
RX MEDLINE=93002195; PubMed=1390001;
RA Nichols R.;
RT "Isolation and structural characterization of Drosophila
RT TDVDFVFLRFamide and FMRFamide-containing neural peptides.";
RL J. Mol. Neurosci. 3:213-218(1992).
RN [2]
RP SEQUENCE.
RC SPECIES=S.bullata; TISSUE=Head;
RX MEDLINE=93047886; PubMed=1358537;
RA Fonagy A., Schoofs L., Proost P., Van Damme J., Bueds H., De Loof A.;
RT "Isolation, primary structure and synthesis of neomyosuppressin, a

RT myoinhibiting neuropeptide from the grey fleshfly, Neobellieria
RT bullata.";
RL Comp. Biochem. Physiol. 102C:239-245(1992).
CC -!- FUNCTION: MYOINHIBITING NEUROPEPTIDE.
DR FlyBase; FBgn0011581; Dms.
KW Neuropeptide; Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1248 MW; D3C00329D2C1EAB2 CRC64;

Query Match 19.3%; Score 17; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 TAADH 16
I ||
Db 1 TDVDH 5

RESULT 12
ACT_PINPS
ID ACT_PINPS STANDARD; PRT; 15 AA.
AC P81085;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Actin (Water stress responsive protein 5) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=98418576; PubMed=9747804;
RA Costa P., Bahrman N., Frigerio J.-M., Kremer A., Plomion C.;
RT "Water-deficit-responsive proteins in maritime pine.";
RL Plant Mol. Biol. 38:587-596(1998).
RN [2]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED
CC IN ALL EUKARYOTIC CELLS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- INDUCTION: BY WATER STRESS.
CC -!- SIMILARITY: BELONGS TO THE ACTIN FAMILY.
DR HSSP; P02570; 2BTF.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; actin; 1.
DR PROSITE; PS00406; ACTINS_1; PARTIAL.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; PARTIAL.
DR PROSITE; PS00432; ACTINS_2; PARTIAL.
KW Structural protein.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1574 MW; 4712F0146D5B4DE3 CRC64;

Query Match 19.3%; Score 17; DB 1; Length 15;
Best Local Similarity 75.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GNIL 7
III:
Db 4 GNIV 7

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RESULT 13
R13A_SPIOL
ID R13A_SPIOL STANDARD; PRT; 15 AA.
AC P82454;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE 60S ribosomal protein L13a (Fragment).
GN RPL13A.
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RC STRAIN=CV. ALVARO; TISSUE=Leaf;
RA Yamaguchi K., Subramanian A.R.;
RT "N-terminal sequence of spinach cytosolic 60S ribosomal protein
RT L13a."
RL Submitted (APR-2000) to the SWISS-PROT data bank.
CC -!- SIMILARITY: BELONGS TO THE L13P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro; IPR001074; Ribosomal_L13.
DR PROSITE; PS00783; RIBOSOMAL_L13; PARTIAL.
KW Ribosomal protein.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1489 MW; C7B9C80F5A099EB3 CRC64;
```

Query Match 19.3%; Score 17; DB 1; Length 15;
Best Local Similarity 28.6%; Pred. No. 4.7e+03;
Matches 4; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

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QY 2 VSGNLTIRLTAAD 15
|||: : : |
Db 1 VSGSGIMAKRVVVD 14
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RESULT 14
RKGG_CARCR
ID RKGG_CARCR STANDARD; PRT; 15 AA.
AC P21586;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-AUG-1991 (Rel. 19, Last annotation update)
DE Rathke's gland glycoprotein (Fragment).
OS Carretta caretta (Loggerhead).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Chelonioidae; Cheloniidae; Carretta.
OX NCBI_TaxID=8467;
RN [1]
RP SEQUENCE.
RC TISSUE=Rathke's gland;
RX MEDLINE=90075703; PubMed=2591198;
RA Radhakrishna G., Chin C.C.Q., Wold F., Weldon P.J.;
RT "Glycoproteins in Rathke's gland secretions of loggerhead (Carretta
RL caretta) and Kemp's ridley (Lepidochelys kempi) sea turtles.";
RL Comp. Biochem. Physiol. 94B:375-378(1989).
CC -!- FUNCTION: RATHKE'S GLAND SECRETIONS MAY FUNCTION AS PHEROMONES,
CC AS PREDATOR REPELLANTS, OR CONTRIBUTE TO THE MAINTENANCE OF THE
CC TURTLE SHELL.
CC -!- SIMILARITY: WITH RATHKE'S GLAND GLYCOPROTEIN FROM KEMP'S RIDLEY
CC SEA TURTLE.
DR PIR; PL0154; PL0154.
KW Glycoprotein.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1477 MW; CC893BAAA1B1B5ED CRC64;
```

Query Match 19.3%; Score 17; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 4.7e+03;

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Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 TVSGNI 6
| | | |
Db 10 TTSGPI 15

RESULT 15
SODP_PINPS
ID SODP_PINPS STANDARD; PRT; 15 AA.
AC P81082;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Probable superoxide dismutase [Cu-Zn], Chloroplast (EC 1.15.1.1)
DE (Water stress responsive protein 15) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=98418576; PubMed=9747804;
RA Costa P., Bahrman N., Frigerio J.-M., Kremer A., Plomion C.;
RT "Water-deficit-responsive proteins in maritime pine.";
RL Plant Mol. Biol. 38:587-596(1998).
RN [2]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins."
RL Electrophoresis 20:1098-1108(1999).
CC -!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Copper and zinc (By similarity).
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- INDUCTION: BY WATER STRESS.
CC -!- SIMILARITY: BELONGS TO THE CU-ZN SUPEROXIDE DISMUTASE FAMILY.
DR HSSP; P07505; ISRD.
DR InterPro; IPR001424; SOD_CU_ZN.
DR Pfam; PF00080; sodcu; 1.
DR PROSITE; PS00087; SOD_CU_ZN_1; PARTIAL.
DR PROSITE; PS00332; SOD_CU_ZN_2; PARTIAL.
KW Oxidoreductase; Copper; Zinc; Chloroplast.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1381 MW; 0369BF9DBBB69CA8 CRC64;
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Query Match 19.3%; Score 17; DB 1; Length 15;
Best Local Similarity 75.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 4 GNIL 7
| | |
Db 6 GNIV 9
```

Search completed: July 3, 2002, 11:41:56
Job time: 837 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:41:22 ; Search time 100.54 Seconds
(without alignments)
30.972 Million cell updates/sec

Title: US-09-165-546A-13
Perfect score: 88
Sequence: 1 TVSGNILTIRLTAADHRQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 4250

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_19:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_invertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archheap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	30.7	18	2 Q53503	Q53503 lactobacill
2	26	29.5	15	2 Q53541	Q53541 bacillus sp
3	25	28.4	15	1 Q9UWH9	Q9uwh9 thermococcu
4	24	27.3	15	11 Q05694	Q05694 mus musculu
5	23	26.1	13	2 Q9R5U4	Q9r5u4 pseudomonas
6	23	26.1	16	2 Q52901	Q52901 rhizobium m
7	23	26.1	16	13 Q9PRQ0	Q9prq0 oncorhynchu
8	23	26.1	17	7 Q31213	Q31213 mus musculu
9	23	26.1	18	3 Q02414	Q02414 aspergillus
10	23	26.1	18	3 Q01672	Q01672 pneumocysti
11	22	25.0	12	10 Q9S931	Q9s931 sambucus ni
12	22	25.0	16	6 P79137	P79137 cercopitheci
13	22	25.0	18	15 Q9QKJ7	Q9qkj7 human immun
14	21	23.9	9	13 Q9PS68	Q9ps68 gallus gall
15	21	23.9	11	7 O77899	O77899 oreochromis
16	21	23.9	11	7 O77900	O77900 oreochromis

17	21	23.9	11	7 O77901	O77901 oreochromis
18	21	23.9	11	7 O77902	O77902 oreochromis
19	21	23.9	11	7 O77903	O77903 oreochromis
20	21	23.9	11	7 O77904	O77904 oreochromis
21	21	23.9	11	7 O77905	O77905 oreochromis
22	21	23.9	11	7 O77916	O77916 oreochromis
23	21	23.9	11	7 O77917	O77917 oreochromis
24	21	23.9	11	7 O77921	O77921 pseudotroph
25	21	23.9	14	4 Q99902	Q99902 homo sapien
26	21	23.9	15	13 P82076	P82076 litoria cae
27	21	23.9	16	4 Q16350	Q16350 homo sapien
28	21	23.9	16	6 Q28324	Q28324 capra hircu
29	21	23.9	18	4 Q9P0M3	Q9p0m3 homo sapien
30	20	22.7	15	1 Q9UWH6	Q9uwh6 thermococcu
31	20	22.7	15	1 Q9UWH4	Q9uwh4 pyrococcus.
32	20	22.7	15	3 Q9UR80	Q9ur80 saccharomyc
33	20	22.7	15	6 Q9TRR9	Q9trr9 oryctolagus
34	20	22.7	15	6 Q9TRN7	Q9trn7 sus scrofa
35	20	22.7	17	6 O62645	O62645 saguinus oe
36	20	22.7	17	15 Q9QEY2	Q9qey2 human immun
37	20	22.7	17	15 Q9QEY1	Q9qey1 human immun
38	20	22.7	18	2 Q9S1H7	Q9slh7 synechococc
39	20	22.7	18	4 Q13665	Q13665 homo sapien
40	20	22.7	18	11 Q924N7	Q924n7 rattus norv
41	19	21.6	10	4 Q9H1I5	Q9h1i5 homo sapien
42	19	21.6	10	4 Q9NP07	Q9np07 homo sapien
43	19	21.6	11	11 Q9Z1H5	Q9z1h5 mus musculu
44	19	21.6	13	15 O92820	O92820 chimpanzee
45	19	21.6	14	10 P82335	P82335 pisum sativ

ALIGNMENTS

RESULT 1
Q53503 ID Q53503 PRELIMINARY; PRT; 18 AA.
AC Q53503;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ORF PROTEIN (FRAGMENT).
GN ORF.
OS Lactobacillus paracasei.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1597;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95219758; PubMed=7704831;
RA Djordjevic G., Bojovic B., Banina A., Topisirovic L.;
RT "Cloning of promoter-like sequences from Lactobacillus paracasei subsp. paracasei CG11 and their expression in Escherichia coli, Lactococcus lactis, and Lactobacillus reuteri.";
RL Can. J. Microbiol. 40:1043-1050(1994).
DR EMBL; S76789; AAB33948.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2113 MW; 4D893098227E619F CRC64;

Query Match 30.7%; Score 27; DB 2; Length 18;
Best Local Similarity 45.5%; Pred. No. 6e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 7 LTIRLTAADHR 17
:|: ||:| |
Db 1 MTLALTQSDFR 11

RESULT 2
Q53541 ID Q53541 PRELIMINARY; PRT; 15 AA.
AC Q53541;

RA Holloway P., McCormick W., Watson R.J., Chan Y.K.;
RT "Identification and analysis of the dissimilatory nitrous oxide
RT reduction genes, nosRZDFY, of Rhizobium meliloti.";
RL J. Bacteriol. 178:1505-1514(1996).
DR EMBL; U47133; AAC44026.1; -.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1735 MW; 0CF7165CF62AA3B8 CRC64;

Query Match 26.1%; Score 23; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NILTI 9
Db 3 NILTI 7

RESULT 7
Q9PRQO PRELIMINARY; PRT; 16 AA.
AC Q9PRQO;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE SULFIDE LINKED SERUM AMYLOID P-COMPONENT (FRAGMENT).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RX MEDLINE=96192413; PubMed=8617401;
RA Jensen L.E., Petersen T.E., Thiel S., Jensenius J.C.;
RT "Isolation of a pentraxin-like protein from rainbow trout serum.";
RL Dev. Comp. Immunol. 19:305-314(1995).
SQ SEQUENCE 16 AA; 1764 MW; B6817B064852C2FA CRC64;

Query Match 26.1%; Score 23; DB 13; Length 16;
Best Local Similarity 36.4%; Pred. No. 2.7e+03;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 VSGNLTIRLT 12
Db 5 LSGKVFVIPMT 15

RESULT 8
Q31213 PRELIMINARY; PRT; 17 AA.
AC Q31213;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE INTEGRAL MEMBRANE PROTEIN (FRAGMENT).
GN J-ALPHA TA61.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPH-NODE;
RX MEDLINE=92165347; PubMed=1371499;
RA Nakajima P.B., Di Vincenzo J.P., Jameson S.C., Gascoigne N.R.J.;
RT "Chromosome 14 in B10.A (18R) mice is recombinant and includes Tcra-V
RT alleles.";
RL Immunogenetics 35:190-198(1992).
DR EMBL; M55634; AAA39702.1; -.
FT NON_TER 1
SQ SEQUENCE 17 AA; 1748 MW; 427C4F4FFD162173 CRC64;

Query Match 26.1%; Score 23; DB 7; Length 17;
Best Local Similarity 42.9%; Pred. No. 2.9e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 GNILTIR 10
Db 10 GTVLTVK 16

RESULT 9
Q02414 PRELIMINARY; PRT; 18 AA.
AC Q02414;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE OROTIDINE-5'-MONOPHOSPHATE DECARBOXYLASE (FRAGMENT).
GN PYRG.
OS Aspergillus niger var. awamori.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=105351;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96031709; PubMed=7553938;
RA Gouka R.J., Hession J.G., Stam H., Musters W., van den Hondel C.A.;
RT "A novel strategy for the isolation of defined pyrG mutants and the
RT development of a site-specific integration system for Aspergillus
RT awamori.";
RL Curr. Genet. 27:536-540(1995).
DR EMBL; S79674; AAB35350.1; -.
FT NON_TER 1
SQ SEQUENCE 18 AA; 1891 MW; E1A0E34C7D23688E CRC64;

Query Match 26.1%; Score 23; DB 3; Length 18;
Best Local Similarity 41.2%; Pred. No. 3.1e+03;
Matches 7; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

QY 1 TVSGNLTIR--LTAAD 15
Db 2 TVSADVTTKELDLAD 18

RESULT 10
Q01672 PRELIMINARY; PRT; 18 AA.
AC Q01672;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MAJOR SURFACE GLYCOPROTEIN (FRAGMENT).
GN MSG.
OS Pneumocystis carinii.
OC Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
OC Pneumocystis.
OX NCBI_TaxID=4754;
RN [1]
RP SEQUENCE FROM N.A.
RA Garbe T.R., Stringer J.R.;
RT "Molecular characterization of P. carinii antigens in natural
RT infection.";
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U17113; AAA67754.1; -.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2020 MW; 4BDD012D046F1923 CRC64;

Query Match 26.1%; Score 23; DB 3; Length 18;
Best Local Similarity 44.4%; Pred. No. 3.1e+03;

Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 VSGNLTIR 10
: || | : |
Db 10 IPGNCLRL 18

RESULT 11
Q9S931 ID Q9S931 PRELIMINARY; PRT; 12 AA.
AC Q9S931;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE SNA-III=AGLUTININ-III.
OS Sambucus nigra (European elder).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Adoxaceae; Sambucus.
OX NCBI_TaxID=4202;
RN [1]
RP SEQUENCE.
RX MEDLINE=91378923; PubMed=1910334;
RA Mach L., Scherf W., Ammann M., Poetsch J., Bertsch W., Marz L.,
RA Glossl J.;
RT "purification and partial characterization of a novel lectin from
RT elder (Sambucus nigra L.) fruit.";
RL Biochem. J. 278:667-671(1991).
SQ SEQUENCE 12 AA; 1241 MW; 1C4D369F004861A0 CRC64;

Query Match 25.0%; Score 22; DB 10; Length 12;
Best Local Similarity 50.0%; Pred. No. 3e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSGNIL 7
: || | : |
Db 5 ITGNII 10

RESULT 12
P79137 ID P79137 PRELIMINARY; PRT; 16 AA.
AC P79137;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-JAN-1999 (TReMBLrel. 09, Last annotation update)
DE CYT1 REGION OF MEMBRANE COFACTOR PROTEIN (MCP, CD46) (FRAGMENT).
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE=97149841; PubMed=89966635;
RA Murakami Y., Seya T., Kurita M., Nagasawa S.;
RT "Molecular cloning of a complementary DNA for a membrane cofactor
RT protein (MCP, CD46)/measles virus receptor on Vero cells and its
RT functional characterization.";
RL Biol. Pharm. Bull. 19:1541-1545(1996).
DR EMBL; D78368; BAA11377.1; -.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1953 MW; 60C102ECD778F939 CRC64;

Query Match 25.0%; Score 22; DB 6; Length 16;
Best Local Similarity 50.0%; Pred. No. 4.1e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 11 LTAADHRQ 18
|| : || :

Db 3 LTDENHRE 10

RESULT 13
Q9QKJ7 ID Q9QKJ7 PRELIMINARY; PRT; 18 AA.
AC Q9QKJ7;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=08108V3;
RX MEDLINE=99094949; PubMed=9878014;
RA Van Dyke R.B., Korber B.T., Popek E., Macken C., Widmayer S.M.,
RA Bardeguet A., Hansen I.C., Wiznia A., Luzuriaga K., Viscarello R.R.,
RA Wolinsky S., the Ariel Core Investigators;
RT "The Ariel Project: A prospective cohort study of maternal-child
RT transmission of human immunodeficiency virus type 1 in the era of
RT maternal antiretroviral therapy.";
RL J. Infect. Dis. 179:319-328(1999).
DR EMBL; AF112541; AAF13319.1; -.
FT NON_TER 1
SQ SEQUENCE 18 AA; 1930 MW; 5A1B913B6C479C96 CRC64;

Query Match 25.0%; Score 22; DB 15; Length 18;
Best Local Similarity 50.0%; Pred. No. 4.7e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 GNILTIRL 11
| || : | : |
Db 1 GGILLRLI 8

RESULT 14
Q9PS68 ID Q9PS68 PRELIMINARY; PRT; 9 AA.
AC Q9PS68;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE LOW DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RX MEDLINE=92011685; PubMed=1918027;
RA Stifani S., Barber D.L., Aebersold R., Steyrer E., Shen X., Nimpf J.,
RA Schneider W.J.;
RT "The laying hen expresses two different low density lipoprotein
RT receptor-related proteins.";
RL J. Biol. Chem. 266:19079-19087(1991).
SQ SEQUENCE 9 AA; 1039 MW; 895EC68B5AB2CDC1 CRC64;

Query Match 23.9%; Score 21; DB 13; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.6e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 LTAADH 16
|| | : |
Db 1 LTAVDY 6

RESULT 15
O77899
ID O77899 PRELIMINARY; PRT; 11 AA.
AC O77899;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MHC CLASS II B LOCUS 14 (FRAGMENT).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
RT class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050009; AAC41348.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 23.9%; Score 21; DB 7; Length 11;
Best Local Similarity 44.4%; Pred. NO. 4.2e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 LTIRLTAAD 15
:| | | |
Db 3 MTYRLSRCD 11

Search completed: July 3, 2002, 11:41:22
Job time: 858 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:26:59 ; Search time 128.9 Seconds
(without alignments)
15.511 Million cell updates/sec

Title: US-09-165-546A-13

Perfect score: 88

Sequence: 1 TVSGNLTIRLTAADHRQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 214377

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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15: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1994.DAT:*
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19: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:*
20: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:*
21: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:*
22: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	88	100.0	18	21 AAY52440	Human tumour antig
2	88	100.0	18	22 AAU01544	HLA-DR53 recognisi
3	88	100.0	18	22 AAB69944	Human NY-ESO-1 HLA
4	56	63.6	18	22 AAE07769	Human NY ESO-1 HLA
5	56	63.6	18	22 AAU01540	HLA-DR53 recognisi
6	56	63.6	18	22 AAB69940	Human NY-ESO-1 HLA
7	51	58.0	14	22 AAE07728	Human NY ESO-1 MHC
8	51	58.0	14	22 AAE07788	Human NY ESO-1 pep
9	51	58.0	15	22 AAE07727	Human NY ESO-1 MHC
10	51	58.0	15	22 AAE07787	Human NY ESO-1 pep
11	51	58.0	17	21 AAY52436	Human tumour antig

12	50	56.8	10	20 AAY06055	Human cancer antig
13	50	56.8	10	20 AAY05989	Human cancer antig
14	49	55.7	10	20 AAY06017	Human cancer antig
15	47	53.4	10	20 AAY05988	Human cancer antig
16	47	53.4	10	20 AAY05980	Human cancer antig
17	47	53.4	15	22 AAE07726	Human NY ESO-1 MHC
18	47	53.4	15	22 AAE07786	Human NY ESO-1 pep
19	45	51.1	9	20 AAY06054	Human cancer antig
20	45	51.1	9	20 AAY06038	Human cancer antig
21	45	51.1	9	20 AAY06045	Human cancer antig
22	45	51.1	10	20 AAY06000	Human cancer antig
23	42	47.7	9	20 AAY06053	Human cancer antig
24	42	47.7	9	20 AAY06030	Human cancer antig
25	42	47.7	9	20 AAY06036	Human cancer antig
26	42	47.7	9	21 AAY79758	NY-ESO-1 derived p
27	42	47.7	10	20 AAY06001	Human cancer antig
28	41	46.6	9	20 AAY06028	Human cancer antig
29	41	46.6	9	21 AAY79754	NY-ESO-1 derived p
30	39	44.3	9	20 AAY06034	Human cancer antig
31	38	43.2	9	21 AAY79753	NY-ESO-1 derived p
32	37	42.0	10	22 AAG67202	Cancer testis tumo
33	37	42.0	10	22 AAB69934	Human NY-ESO-1 HLA
34	33	37.5	9	22 AAG67172	Cancer testis tumo
35	33	37.5	9	22 AAB69904	Human NY-ESO-1 HLA
36	32	36.4	9	22 AAG67179	Cancer testis tumo
37	32	36.4	9	22 AAB69911	Human NY-ESO-1 HLA
38	32	36.4	18	21 AAY52435	Human tumour antig
39	32	36.4	18	22 AAE07770	Human NY ESO-1 HLA
40	32	36.4	18	22 AAU01539	HLA-DR53 recognisi
41	32	36.4	18	22 AAB69939	Human NY-ESO-1 HLA
42	31	35.2	14	22 AAB86339	G. suboxydans DSM
43	29	33.0	10	22 AAB72798	Antibacterial pept
44	29	33.0	18	22 AAU01541	HLA-DR53 recognisi
45	29	33.0	18	22 AAB69941	Human NY-ESO-1 HLA

ALIGNMENTS

RESULT 1
AAY52440
ID AAY52440 standard; Protein; 18 AA.
XX
AC AAY52440;
XX
DT 15-FEB-2000 (first entry)
XX
XX Human tumour antigen NY-ESO-1 peptide #13.
DE
XX
KW Cancer; tumour; antigen; MHC; major histocompatibility complex; Class II;
KW T-cell; helper; stimulation; proliferation; treatment;
KW diagnosis; prevention; melanoma; breast cancer; ovarian cancer;
KW prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer;
KW lymphoma.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9953938-A1.
XX
PD 28-OCT-1999.
XX
PF 24-MAR-1999; 99WO-US06875.
XX
PR 17-APR-1998; 98US-0062422.
PR 02-OCT-1998; 98US-0165546.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
PI Gure A, Ritter G;
XX
DR WPI; 2000-038483/03.

XX PT Novel peptides which bind to MHC class I and MHC class II molecules,
PT useful for therapeutic and diagnostic purposes -
XX PS Claim 4; Page 22; 49pp; English.
XX CC Peptides #8-#13 (AAV52435-Y52440) are peptides derived from the human
CC tumour antigen, NY-ESO-1 (AAV52430) which can bind to MHC(major
CC histocompatibility Class II HLA-DR53 molecules, thereby stimulating
CC proliferation of helper T-cells. cDNA encoding NY-ESO-1 was initially
CC isolated from an oesophagus squamous cell cancer cDNA library. Tissue
CC localisation studies revealed it to be expressed at high levels
CC in normal ovary and testis but not in normal colon, kidney, liver,
CC brain, oesophagus and skin. It was expressed in certain tumours and
CC tumour cell lines with some degree of frequency - these included
CC melanoma specimens and cell lines, and breast and bladder cancer
CC specimens, with expression in other tumour types being sporadic.
CC These NY-ESO-1-derived peptides may be used in methods and
CC compositions used for the treatment, diagnosis and prevention of
CC cancers (such as melanoma, breast cancer, prostate cancer, lung
CC cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer,
CC or lymphoma) and to stimulate the proliferation of T cells.
XX SQ Sequence 18 AA;

Query Match 100.0%; Score 88; DB 21; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.9e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLTAADHRQ 18
Db ||||| ||||| ||||| |||||
1 tvsgniltirltaadhrq 18

RESULT 2
AAU01544
ID AAU01544 standard; Peptide; 18 AA.
XX AC AAU01544;
XX DT 18-JUL-2001 (first entry)
XX DE HLA-DR53 recognising NY-ESO-1 peptide #6.
XX NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
KW human leukocyte antigen-determining region; disease progression;
KW disease regression; disease onset; body tissue; body fluid; enzyme label;
KW radioactive label; monoclonal antibody.
XX OS Homo sapiens.
XX PN WO200123560-A2.
XX PD 05-APR-2001.
XX PF 26-SEP-2000; 2000WO-US26411.
XX PR 29-SEP-1999; 99US-0408036.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PI Tureci O, Sahin U, Pfreundschuh M;
XX WPI; 2001-266156/27.
XX Polypeptides binding to major histocompatibility complex class II human
PT leukocyte antigen-determining region molecule having amino acid
PT sequence found in tumour rejection antigen precursor used for
PT stimulating proliferation of helper T cells -
XX Example 13; Page 19; 62pp; English.

XX CC The sequence represents a human NY-ESO-1 tumour rejection antigen
CC precursor fragment which recognises and binds to HLA-DR53. NY-ESO-1 and
CC SSX-2 polypeptides, or fragments of, bind to major histocompatibility
CC complex (MHC) Class II molecules such as human leukocyte
CC antigen-determining region (HLA-DR) molecules and stimulate proliferation
CC of helper T cells. The peptides can be administered to an HLA-DR positive
CC subject in order to stimulate the helper T cells. An MHC Class II
CC HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell or
CC present in free form is useful for this stimulation. The nucleic acid is
CC useful for screening for a cancerous condition, which involves contacting
CC a subject sample to a cell line transfected with the immunoreactive cell
CC (helper T cell), where interaction is indicative of cancer. In addition,
CC a sample from a patient (for example, a body fluid or tissue) can be
CC monitored for the amount of the complex present in the bloodstream. This
CC is useful for determining regression, progression or onset of a cancerous
CC condition. The method involves contacting the sample with a radioactive
CC labelled or enzyme labelled monoclonal antibody which specifically binds
CC with the complex.
XX SQ Sequence 18 AA;

Query Match 100.0%; Score 88; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.9e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLTAADHRQ 18
Db ||||| ||||| ||||| |||||
1 tvsgniltirltaadhrq 18

RESULT 3
AAB69944
ID AAB69944 standard; Peptide; 18 AA.
XX AC AAB69944;
XX DT 27-APR-2001 (first entry)
XX DE Human NY-ESO-1 HLA-DR53 binding motif #6.
XX KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW non-small cell lung carcinoma; tumour status determination.
XX OS Homo sapiens.
XX PN WO200107917-A1.
XX PD 01-FEB-2001.
XX PF 14-JUL-2000; 2000WO-US19220.
XX PR 23-JUL-1999; 99US-0359503.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX PA (CORR) CORNELL RES FOUND INC.
XX PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
XX WPI; 2001-182822/18.
XX DR
XX Method useful for determining the status (e.g. progression, regression
PT or stability of the disease) of a cancerous condition, involves
PT determining the levels of NY-ESO-1 specific antibodies in a sample
PT taken from a patient -
XX Example 16; Page 28; 50pp; English.
XX PS The present sequence is given in a specification relating to a method
CC for determining the status of a cancerous condition in a patient

CC with a tumour that expresses NY-ESO-1. The method comprises assaying a
CC sample taken from the patient for antibodies that specifically bind to
CC the NY-ESO-1 and comparing the value obtained to a prior value obtained
CC from assay of a prior sample taken from the patient. Any difference
CC between the values is indicative of a change in status of the cancerous
CC condition. The method is useful for determining whether a cancerous
CC condition is progressing, regressing or remaining stable, in particular
CC in patients receiving treatment for a melanoma, adenocarcinoma,
CC non-small cell lung carcinoma or bladder carcinoma.

XX Sequence 18 AA;

SQ

Query Match 100.0%; Score 88; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.9e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLTAADHRQ 18
Db 1 tvsgnltirлтаадhrq 18

RESULT 4
AAE07769
ID AAE07769 standard; peptide; 18 AA.
XX
AC AAE07769;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human NY ESO-1 HLA DR restricted T cell cancer peptide #1.
XX
KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.

XX Homo sapiens.
OS
XX
XX WO200155393-A2.
PN
XX
PD 02-AUG-2001.
XX
PF 26-JAN-2001; 2001WO-US02765.
XX
PR 28-JAN-2000; 2000US-0179004.
PR 29-SEP-2000; 2000US-0237107.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
XX
PI Wang R, Rosenberg SA, Zeng G;
XX
XX WPI; 2001-496851/54.
DR
XX
XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -
XX
XX Claim 84; Page 84; 134pp; English.
PS
XX The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also

CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or hapten and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is human
CC NY ESO-1 HLA DR restricted T cell cancer peptide.

XX Sequence 18 AA;

SQ

Query Match 63.6%; Score 56; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLT 12
Db 7 tvsgnltirtlt 18

RESULT 5
AAU01540
ID AAU01540 standard; Peptide; 18 AA.
XX
AC AAU01540;
XX
DT 18-JUL-2001 (first entry)
XX
DE HLA-DR53 recognising NY-ESO-1 peptide #2.
XX
KW NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
KW human leukocyte antigen-determining region; disease progression;
KW disease regression; disease onset; body tissue; body fluid; enzyme label;
KW radioactive label; monoclonal antibody.

XX Homo sapiens.
OS
XX WO200123560-A2.
PN
XX
XX 05-APR-2001.
PD
XX
XX 26-SEP-2000; 2000WO-US26411.
PF
XX
XX 29-SEP-1999; 99US-0408036.
PR
XX (LUDW-) LUDWIG INST CANCER RES.
PA
XX
XX Tureci O, Sahin U, Pfreundschuh M;
PI
XX WPI; 2001-266156/27.
DR
XX
XX Polypeptides binding to major histocompatibility complex class II human
PT leukocyte antigen-determining region molecule having amino acid
PT sequence found in tumour rejection antigen precursor used for
PT stimulating proliferation of helper T cells -
XX
XX Example 13; Page 19; 62pp; English.
PS
XX The sequence represents a human NY-ESO-1 tumour rejection antigen
CC precursor fragment which recognises and binds to HLA-DR53. NY-ESO-1 and
CC SSX-2 polypeptides, or fragments of, bind to major histocompatibility
CC complex (MHC) Class II molecules such as human leukocyte
CC antigen-determining region (HLA-DR) molecules and stimulate proliferation
CC of helper T cells. The peptides can be administered to an HLA-DR positive
CC subject in order to stimulate the helper T cells. An MHC Class II
CC HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell or
CC present in free form is useful for this stimulation. The nucleic acid is
CC useful for screening for a cancerous condition, which involves contacting
CC a subject sample to a cell line transfected with the immunoreactive cell
CC (helper T cell), where interaction is indicative of cancer. In addition,
CC a sample from a patient (for example, a body fluid or tissue) can be
CC monitored for the amount of the complex present in the bloodstream. This
CC is useful for determining regression, progression or onset of a cancerous
CC condition. The method involves contacting the sample with a radioactive

CC labelled or enzyme labelled monoclonal antibody which specifically binds
CC with the complex.
XX
SQ Sequence 18 AA;

Query Match 63.6%; Score 56; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLT 12
| | | | | | | | | |
Db 7 tvsgnltirlt 18

RESULT 6
AAB69940
ID AAB69940 standard; Peptide; 18 AA.
XX
AC AAB69940;

XX 27-APR-2001 (first entry)
DE Human NY-ESO-1 HLA-DR53 binding motif #2.
XX

KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW non-small cell lung carcinoma; tumour status determination.
XX

OS Homo sapiens.
XX WO200107917-A1.
PN

XX 01-FEB-2001.

PF 14-JUL-2000; 2000WO-US19220.

XX 23-JUL-1999; 99US-0359503.

XX (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.

PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
XX WPI; 2001-182822/18.

XX Method useful for determining the status (e.g. progression, regression
PT or stability of the disease) of a cancerous condition, involves
PT determining the levels of NY-ESO-1 specific antibodies in a sample
PT taken from a patient -

XX Example 16; Page 27; 50pp; English.

XX The present sequence is given in a specification relating to a method
CC for determining the status of a cancerous condition in a patient
CC with a tumour that expresses NY-ESO-1. The method comprises assaying a
CC sample taken from the patient for antibodies that specifically bind to
CC the NY-ESO-1 and comparing the value obtained to a prior value obtained
CC from assay of a prior sample taken from the patient. Any difference
CC between the values is indicative of a change in status of the cancerous
CC condition. The method is useful for determining whether a cancerous
CC condition is progressing, regressing or remaining stable, in particular
CC in patients receiving treatment for a melanoma, adenocarcinoma,
CC non-small cell lung carcinoma or bladder carcinoma.

XX Sequence 18 AA;

Query Match 63.6%; Score 56; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLT 12
| | | | | | | | | |
Db 7 tvsgnltirlt 18

RESULT 7
AAE07728
ID AAE07728 standard; peptide; 14 AA.
XX
AC AAE07728;

XX 06-NOV-2001 (first entry)

DE Human NY ESO-1 MHC class II restricted T cell epitope #14.

XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.

XX Homo sapiens.

OS WO200155393-A2.

XX 02-AUG-2001.

PF 26-JAN-2001; 2001WO-US02765.

XX 28-JAN-2000; 2000US-0179004.

PR 29-SEP-2000; 2000US-0237107.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Wang R, Rosenberg SA, Zeng G;

XX WPI; 2001-496851/54.

XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -

PS Claim 4; Page 16; 134pp; English.

XX The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or hapten and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is MHC
CC class II restricted T cell epitope of human NY ESO-1 protein.

XX Sequence 14 AA;

Query Match 58.0%; Score 51; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIRLT 11
| | | | | | | | | |
Db 4 tvsgnltirl 14

RESULT 8
AAE07788
ID AAE07788 standard; peptide; 14 AA.
XX
AC
XX AAE07788;
AC
XX
DT 06-NOV-2001 (first entry)
XX
DE Human NY ESO-1 peptide #22 to characterise epitope recognised by TE4-1.
XX
DE Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.
XX
OS Homo sapiens.
XX WO200155393-A2.
XX
PN
XX
PD 02-AUG-2001.
XX
PF 26-JAN-2001; 2001WO-US02765.
XX
PR 28-JAN-2000; 2000US-0179004.
PR 29-SEP-2000; 2000US-0237107.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang R, Rosenberg SA, Zeng G;
XX WPI; 2001-496851/54.
XX
PT New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -
XX
PS Example 6; Fig 6A; 134pp; English.
XX
CC The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or haptens and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is human
CC NY ESO-1 peptide used in the characterisation of the NY ESO-1 epitope
CC recognised by TE4-1.
XX
SQ Sequence 14 AA;

Query Match 58.0%; Score 51; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIRL 11
Db 4 tvsgnltirl 14

RESULT 9
AAE07727

ID AAE07727 standard; peptide; 15 AA.
XX
AC AAE07727;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human NY ESO-1 MHC class II restricted T cell epitope #13.
XX
KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.
XX
OS Homo sapiens.
XX WO200155393-A2.
XX
PN
XX
PD 02-AUG-2001.
XX
PF 26-JAN-2001; 2001WO-US02765.
XX
PR 28-JAN-2000; 2000US-0179004.
PR 29-SEP-2000; 2000US-0237107.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang R, Rosenberg SA, Zeng G;
XX WPI; 2001-496851/54.
XX
PT New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -
XX
PS Claim 4; Page 16; 134pp; English.
XX
CC The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or haptens and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is MHC
CC class II restricted T cell epitope of human NY ESO-1 protein.
XX
SQ Sequence 15 AA;

Query Match 58.0%; Score 51; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIRL 11
Db 5 tvsgnltirl 15

RESULT 10
AAE07787
ID AAE07787 standard; peptide; 15 AA.
XX
AC AAE07787;
XX

DT 06-NOV-2001 (first entry)
XX Human NY ESO-1 peptide #21 to characterise epitope recognised by TE4-1.
DE
XX
KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.
XX
OS Homo sapiens.
XX
PN WO200155393-A2.
XX
PD 02-AUG-2001.
XX
PF 26-JAN-2001; 2001WO-US02765.
XX
XX 28-JAN-2000; 2000US-0179004.
PR 29-SEP-2000; 2000US-0237107.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Wang R, Rosenberg SA, Zeng G;
PI
XX WPI; 2001-496851/54.
DR
XX
XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -
XX
PS Example 6; Fig 6A; 134pp; English.
XX
CC The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or hapten and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is human
CC NY ESO-1 peptide used in the characterisation of the NY ESO-1 epitope
CC recognised by TE4-1.
XX
SQ Sequence 15 AA;

Query Match 58.0%; Score 51; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIRL 11
Db ||||||
5 tvsgnltirl 15

RESULT 11
AAY52436
ID AAY52436 standard; Protein; 17 AA.
XX
AC AAY52436;
XX
DT 15-FEB-2000 (first entry)
XX
DE Human tumour antigen NY-ESO-1 peptide #9.

XX Cancer; tumour; antigen; MHC; major histocompatibility complex; Class II;
KW T-cell; helper; stimulation; proliferation; treatment;
KW diagnosis; prevention; melanoma; breast cancer; ovarian cancer;
KW prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer;
KW lymphoma.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9953938-A1.
XX
PD 28-OCT-1999.
XX
PF 24-MAR-1999; 99WO-US06875.
XX
PR 17-APR-1998; 98US-0062422.
PR 02-OCT-1998; 98US-0165546.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
PI Gure A, Ritter G;
XX
DR WPI; 2000-038483/03.
XX
PT Novel peptides which bind to MHC class I and MHC class II molecules,
PT useful for therapeutic and diagnostic purposes -
XX
PS Claim 4; Page 22; 49pp; English.
XX
CC Peptides #8-#13 (AAY52435-Y52440) are peptides derived from the human
CC tumour antigen, NY-ESO-1 (AAY52430) which can bind to MHC(major
CC histocompatibility Class II HLA-DR53 molecules, thereby stimulating
CC proliferation of helper T-cells. cDNA encoding NY-ESO-1 was initially
CC isolated from an oesophagus squamous cell cancer cDNA library. Tissue
CC localisation studies revealed it to be expressed at high levels
CC in normal ovary and testis but not in normal colon, kidney, liver,
CC brain, oesophagus and skin. It was expressed in certain tumours and
CC tumour cell lines with some degree of frequency - these included
CC melanoma specimens and cell lines, and breast and bladder cancer
CC specimens, with expression in other tumour types being sporadic.
CC These NY-ESO-1-derived peptides may be used in methods and
CC compositions used for the treatment, diagnosis and prevention of
CC cancers (such as melanoma, breast cancer, prostate cancer, lung
CC cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer,
CC or lymphoma) and to stimulate the proliferation of T cells.
XX
SQ Sequence 17 AA;

Query Match 58.0%; Score 51; DB 21; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSGNLTIRLT 12
Db ||||||
7 vsgnltirlt 17

RESULT 12
AAY06055
ID AAY06055 standard; Peptide; 10 AA.
XX
AC AAY06055;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 peptide ESO10-34.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;

KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; cytotoxic T lymphocyte; CTL.
XX
OS Homo sapiens.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US19609.
XX
PR 08-OCT-1997; 97US-0061428.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rosenberg SA, Wang RF;
XX
DR WPI; 1999-277270/23.
XX
PT Cancer antigen NY ESO1/CAG-3
XX
PS Example 10; Page 45; 88pp; English.
XX
CC Peptide ESO10-34 corresponds to amino acid residues 134-143 of
CC human NY ESO-1/CAG-3 ORF1 (see AAY05965), a new and potent tumour
CC antigen capable of eliciting an antigen specific immune response
CC by T cells. It was examined for reactivity to a cytotoxic T
CC lymphocyte (CTL), measured as release of granulocyte macrophage
CC colony stimulating factor. Cancer peptides (see AAY05967-87) derived
CC from CAG-3, portions of CAG-3 and their variants, are useful as
CC cancer vaccines. A claimed method of preventing or inhibiting
CC cancer involves administering a cancer peptide, with or without an
CC HLA molecule. The cancer peptides form part of, or are derived
CC from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer and
CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
CC thyroid cancers.
XX
SQ Sequence 10 AA;

Query Match 56.8%; Score 50; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TIRLTAADHR 17
Db | | | | | | | | | |
1 tirltaadhr 10

RESULT 13
AAY05989
ID AAY05989 standard; Peptide; 10 AA.
XX
AC AAY05989;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; human leukocyte antigen; HLA.
XX
OS Homo sapiens.
XX

PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US19609.
XX
PR 08-OCT-1997; 97US-0061428.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rosenberg SA, Wang RF;
XX
DR WPI; 1999-277270/23.
XX
PT Cancer antigen NY ESO1/CAG-3
XX
PS Example 10; Page 42; 88pp; English.
XX
CC This peptide was identified as an HLA peptide motif following a
CC screen for epitopes from the coding region of human NY ESO-1/CAG-3
CC ORF1 (see AAX58599). 30 Epitopes (see AAY05988-Y06017) were identified.
CC The present peptide (ranked 2) corresponds to amino acid residues
CC 134-143 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent
CC tumour antigen capable of eliciting an antigen specific immune
CC response by T cells. Cancer peptides (see AAY05967-87) derived from
CC CAG-3, portions of CAG-3 and their variants, are useful as cancer
CC vaccines. A claimed method of preventing or inhibiting cancer
CC involves administering a cancer peptide, with or without an HLA
CC molecule. The cancer peptides form part of, or are derived
CC from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer and
CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
CC thyroid cancers.
XX
SQ Sequence 10 AA;

Query Match 56.8%; Score 50; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TIRLTAADHR 17
Db | | | | | | | | | |
1 tirltaadhr 10

RESULT 14
AAY06017
ID AAY06017 standard; Peptide; 10 AA.
XX
AC AAY06017;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; human leukocyte antigen; HLA.
XX
OS Homo sapiens.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US19609.
XX

PR 08-OCT-1997; 97US-0061428.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA Rosenberg SA, Wang RF;
XX WPI; 1999-277270/23.
PI Cancer antigen NY ESO1/CAG-3
XX Example 10; Page 42; 88pp; English.
DR This peptide was identified as an HLA peptide motif following a
XX screen for epitopes from the coding region of human ESO-1/CAG-3
PT ORF1 (see AAX58599). 30 Epitopes (see AAY05988-Y06017) were identified.
XX The present peptide (ranked 30) corresponds to amino acid residues
PS 133-142 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent
XX tumour antigen capable of eliciting an antigen specific immune
CC response by T cells. Cancer peptides (see AAY05967-87) derived from
CC CAG-3, portions of CAG-3 and their variants, are useful as cancer
CC vaccines. A claimed method of preventing or inhibiting cancer
CC involves administering a cancer peptide, with or without an HLA
CC molecule. The cancer peptides form part of, or are derived
CC from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer and
CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
XX thyroid cancers.
SQ Sequence 10 AA;

Query Match 55.7%; Score 49; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0069;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LTIRLTAADH 16
Db |||||||||
1 ltirltaadh 10

RESULT 15
AAY05988
ID AAY05988 standard; Peptide; 10 AA.
XX
AC AAY05988;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; human leukocyte antigen; HLA.
XX
OS Homo sapiens.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US19609.
XX
PR 08-OCT-1997; 97US-0061428.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PI Rosenberg SA, Wang RF;
XX

DR WPI; 1999-277270/23.
XX Cancer antigen NY ESO1/CAG-3
PT Example 10; Page 42; 88pp; English.
XX
CC This peptide was identified as an HLA peptide motif following a
CC screen for epitopes from the coding region of human NY ESO-1/CAG-3
CC ORF1 (see AAX58599). 30 Epitopes (see AAY05988-Y06017) were identified.
CC The present peptide (ranked 1) corresponds to amino acid residues
CC 127-136 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent
CC tumour antigen capable of eliciting an antigen specific immune
CC response by T cells. Cancer peptides (see AAY05967-87) derived from
CC CAG-3, portions of CAG-3 and their variants, are useful as cancer
CC vaccines. A claimed method of preventing or inhibiting cancer
CC involves administering a cancer peptide, with or without an HLA
CC molecule. The cancer peptides form part of, or are derived
CC from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer and
CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
XX thyroid cancers.
SQ Sequence 10 AA;

Query Match 53.4%; Score 47; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
Db |||||||||
1 tvsgnltir 10

Search completed: July 3, 2002, 11:26:59
Job time: 956 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:38:26 ; Search time 560.51 Seconds
(without alignments)
11.303 Million cell updates/sec

Title: US-09-165-546A-13

Perfect score: 88

Sequence: 1 TVSGNLTIRLTAAHRQ 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 451056

Minimum DB seq length: 0

Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 6: /cgn2_6/ptodata/2/paa/US082_COMB.pep:*
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- 10: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*
- 11: /cgn2_6/ptodata/2/paa/US087_COMB.pep:*
- 12: /cgn2_6/ptodata/2/paa/US088_COMB.pep:*
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- 26: /cgn2_6/ptodata/2/paa/US60_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	88	100.0	18	15	US-09-165-546A-13
2	88	100.0	18	18	US-09-408-036B-12
3	56	63.6	18	15	US-09-165-546A-9
4	56	63.6	18	18	US-09-408-036B-8
5	50	56.8	10	19	US-09-529-206-16
6	50	56.8	10	19	US-09-529-206-85
7	50	56.8	10	19	US-09-529-206A-16

8	50	56.8	10	19	US-09-529-206A-85	Sequence 85, Appl
9	50	56.8	10	19	US-09-529-206B-16	Sequence 16, Appl
10	50	56.8	10	19	US-09-529-206B-85	Sequence 85, Appl
11	49	55.7	10	19	US-09-529-206-104	Sequence 104, App
12	49	55.7	10	19	US-09-529-206A-104	Sequence 104, App
13	49	55.7	10	19	US-09-529-206B-104	Sequence 104, App
14	47	53.4	10	19	US-09-529-206-15	Sequence 15, Appl
15	47	53.4	10	19	US-09-529-206-84	Sequence 84, Appl
16	47	53.4	10	19	US-09-529-206A-15	Sequence 15, Appl
17	47	53.4	10	19	US-09-529-206A-84	Sequence 84, Appl
18	47	53.4	10	19	US-09-529-206B-15	Sequence 15, Appl
19	47	53.4	10	19	US-09-529-206B-84	Sequence 84, Appl
20	45	51.1	9	19	US-09-529-206-13	Sequence 13, Appl
21	45	51.1	9	19	US-09-529-206-82	Sequence 82, Appl
22	45	51.1	9	19	US-09-529-206A-13	Sequence 13, Appl
23	45	51.1	9	19	US-09-529-206A-82	Sequence 82, Appl
24	45	51.1	9	19	US-09-529-206A-114	Sequence 114, App
25	45	51.1	9	19	US-09-529-206B-13	Sequence 13, Appl
26	45	51.1	9	19	US-09-529-206B-82	Sequence 82, Appl
27	45	51.1	9	19	US-09-529-206B-114	Sequence 114, App
28	45	51.1	10	19	US-09-529-206-90	Sequence 90, Appl
29	45	51.1	10	19	US-09-529-206A-90	Sequence 90, Appl
30	45	51.1	10	19	US-09-529-206B-90	Sequence 90, Appl
31	42	47.7	9	18	US-09-409-455A-125	Sequence 125, App
32	42	47.7	9	19	US-09-529-206-12	Sequence 12, Appl
33	42	47.7	9	19	US-09-529-206-69	Sequence 69, Appl
34	42	47.7	9	19	US-09-529-206A-12	Sequence 12, Appl
35	42	47.7	9	19	US-09-529-206A-69	Sequence 69, Appl
36	42	47.7	9	19	US-09-529-206A-113	Sequence 113, App
37	42	47.7	9	19	US-09-529-206B-12	Sequence 12, Appl
38	42	47.7	9	19	US-09-529-206B-69	Sequence 69, Appl
39	42	47.7	9	19	US-09-529-206B-113	Sequence 113, App
40	42	47.7	9	22	US-09-833-039-125	Sequence 125, App
41	42	47.7	10	19	US-09-529-206-91	Sequence 91, Appl
42	42	47.7	10	19	US-09-529-206A-91	Sequence 91, Appl
43	42	47.7	10	19	US-09-529-206B-91	Sequence 91, Appl
44	41	46.6	9	18	US-09-409-455A-121	Sequence 121, App
45	41	46.6	9	19	US-09-529-206-67	Sequence 67, Appl

ALIGNMENTS

RESULT 1
US-09-165-546A-13
; Sequence 13, Application US/09165546A
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao,
; Canlan, Matt; Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO
; AMINO ACID SEQUENCES OF NY-ESO-1, WHICH BIND TO
; MHC CLASS I AND MHC CLASS II MOLECULES, AND
; USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,546A
; FILING DATE: 02-Oct-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998

; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-16

Query Match 56.8%; Score 50; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TIRLTAADHR 17
|||||
Db 1 TIRLTAADHR 10

RESULT 10
US-09-529-206B-85
; Sequence 85, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 85
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-85

Query Match 56.8%; Score 50; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TIRLTAADHR 17
|||||
Db 1 TIRLTAADHR 10

RESULT 11
US-09-529-206-104
; Sequence 104, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 104
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-104

Query Match 55.7%; Score 49; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LTIRLTAADH 16
|||||
Db 1 LTIRLTAADH 10

RESULT 12
US-09-529-206A-104
; Sequence 104, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206A-104

Query Match 55.7%; Score 49; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LTIRLTAADH 16
|||||
Db 1 LTIRLTAADH 10

RESULT 13
US-09-529-206B-104
; Sequence 104, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-104

Query Match 55.7%; Score 49; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LTIRLTAADH 16
|||||
Db 1 LTIRLTAADH 10

; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-16

Query Match 56.8%; Score 50; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TIRLTADHR 17
| | | | | | | | | |
Db 1 TIRLTADHR 10

RESULT 10
US-09-529-206B-85
; Sequence 85, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 85
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-85

Query Match 56.8%; Score 50; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TIRLTADHR 17
| | | | | | | | | |
Db 1 TIRLTADHR 10

RESULT 11
US-09-529-206-104
; Sequence 104, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 104
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-104

Query Match 55.7%; Score 49; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 LTIRLTADH 16
| | | | | | | |
Db 1 LTIRLTADH 10

RESULT 12
US-09-529-206A-104
; Sequence 104, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206A-104

Query Match 55.7%; Score 49; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LTIRLTADH 16
| | | | | | | |
Db 1 LTIRLTADH 10

RESULT 13
US-09-529-206B-104
; Sequence 104, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-104

Query Match 55.7%; Score 49; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LTIRLTADH 16
| | | | | | | |
Db 1 LTIRLTADH 10

OY 1 TVSGNLTIRLT 12
| | | | | | | | | |
Db 7 TVSGNLTIRLT 18

RESULT 5
US-09-529-206-16
; Sequence 16, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-16

Query Match 56.8%; Score 50; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 TIRLTADHR 17
| | | | | | | | | |
Db 1 TIRLTADHR 10

RESULT 6
US-09-529-206-85
; Sequence 85, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-85

Query Match 56.8%; Score 50; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 TIRLTADHR 17
| | | | | | | | | |
Db 1 TIRLTADHR 10

RESULT 7
US-09-529-206A-16
; Sequence 16, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene

; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206A-16

Query Match 56.8%; Score 50; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 TIRLTADHR 17
| | | | | | | | | |
Db 1 TIRLTADHR 10

RESULT 8
US-09-529-206A-85
; Sequence 85, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 85
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206A-85

Query Match 56.8%; Score 50; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 TIRLTADHR 17
| | | | | | | | | |
Db 1 TIRLTADHR 10

RESULT 9
US-09-529-206B-16
; Sequence 16, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428

RESULT 14
US-09-529-206-15
; Sequence 15, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-15

Query Match 53.4%; Score 47; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNILTIR 10
|||||
Db 1 TVSGNILTIR 10

RESULT 15
US-09-529-206-84
; Sequence 84, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-84

Query Match 53.4%; Score 47; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNILTIR 10
|||||
Db 1 TVSGNILTIR 10

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:39:33 ; Search time 61.64 Seconds
(without alignments)
29.545 Million cell updates/sec

Title: US-09-165-546A-13

Perfect score: 88
Sequence: 1 TVSGNILTIRLTAAADHRQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 308740 seqs, 101176262 residues

Total number of hits satisfying chosen parameters: 45157

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	42	47.7	9	5	US-09-344-040C-125
2	42	47.7	9	6	US-10-117-937-185
3	42	47.7	10	6	US-10-117-937-186
4	41	46.6	9	5	US-09-344-040C-121
5	38	43.2	9	5	US-09-344-040C-120
6	37	42.0	10	6	US-10-117-937-195
7	32	36.4	9	6	US-10-117-937-192
8	27.5	31.2	13	1	PCT-US02-04329-17
9	27.5	31.2	13	1	PCT-US02-04329-31
10	27	30.7	17	5	US-09-511-939-56
11	27	30.7	17	5	US-09-968-561A-56
12	25	28.4	9	5	US-09-722-250-253
13	25	28.4	9	5	US-09-722-250-253
14	25	28.4	11	5	US-09-924-889-4
15	25	28.4	11	6	US-10-039-645-6
16	25	28.4	15	6	US-10-001-469-2577
17	25	28.4	15	6	US-10-001-469-2700
18	25	28.4	15	6	US-10-001-469-2845
19	25	28.4	16	6	US-10-014-436-5
20	24	27.3	13	5	US-09-988-493-46
21	24	27.3	13	6	US-10-120-604-60
22	24	27.3	13	6	US-10-120-604-79
23	24	27.3	14	6	US-10-014-340-520
24	24	27.3	16	7	US-60-368-671-63
25	24	27.3	16	7	US-60-368-671-99
26	24	27.3	16	7	US-60-371-420-63

27	24	27.3	16	7	US-60-371-420-99	Sequence 99, Appl
28	23	26.1	11	5	US-09-050-359B-40	Sequence 40, Appl
29	23	26.1	11	5	US-09-069-827A-40	Sequence 40, Appl
30	23	26.1	12	6	US-10-115-123-376	Sequence 376, App
31	23	26.1	13	7	US-60-368-671-80	Sequence 80, Appl
32	23	26.1	13	7	US-60-371-420-80	Sequence 80, Appl
33	23	26.1	18	6	US-10-116-252-33	Sequence 33, Appl
34	22	25.0	9	5	US-09-580-339B-74	Sequence 74, Appl
35	22	25.0	10	5	US-09-554-467A-20	Sequence 20, Appl
36	22	25.0	10	5	US-09-910-180-11	Sequence 11, Appl
37	22	25.0	12	1	PCT-US02-11167-2	Sequence 2, Appli
38	22	25.0	12	5	US-09-563-286B-1079	Sequence 1079, Ap
39	22	25.0	12	5	US-09-978-309A-72	Sequence 72, Appl
40	22	25.0	12	6	US-10-105-774-2	Sequence 2, Appli
41	22	25.0	13	1	PCT-US02-09257-312	Sequence 312, App
42	22	25.0	13	1	PCT-US02-09370-488	Sequence 488, App
43	22	25.0	13	1	PCT-US02-11167-17	Sequence 17, Appl
44	22	25.0	13	6	US-10-105-774-17	Sequence 17, Appl
45	22	25.0	13	6	US-10-105-299-3985	Sequence 3985, Ap

ALIGNMENTS

RESULT 1
US-09-344-040C-125
; Sequence 125, Application US/09344040C
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Deter
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gen
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 125
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-125

Query Match 47.7%; Score 42; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TVSGNILTIT 9
|||||
Db 1 TVSGNILTIT 9

RESULT 2
US-10-117-937-185
; Sequence 185, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04

; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 185
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-185

Query Match 47.7%; Score 42; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNILT 9
| | | | |
Db 1 TVSGNILT 9

RESULT 3
US-10-117-937-186
; Sequence 186, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 186
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-186

Query Match 47.7%; Score 42; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNILT 9
| | | | |
Db 2 TVSGNILT 10

RESULT 4
US-09-344-040C-121
; Sequence 121, Application US/09344040C
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Determin
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
; TITLE OF INVENTION: Gene, and Uses Thereof

; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 121
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-121

Query Match 46.6%; Score 41; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LTAADHRQ 18
| | | | |
Db 1 LTAADHRQ 8

RESULT 5
US-09-344-040C-120
; Sequence 120, Application US/09344040C
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Deter
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gen
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 120
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-120

Query Match 43.2%; Score 38; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNILT 8
| | | | |
Db 2 TVSGNILT 9

RESULT 6
US-10-117-937-195
; Sequence 195, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04

; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 195
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-195

Query Match 42.0%; Score 37; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TAADHRQ 18
|||||
Db 1 TAADHRQ 7

RESULT 7
US-10-117-937-192
; Sequence 192, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLLM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 192
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-192

Query Match 36.4%; Score 32; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AADHRQ 18
|||||
Db 1 AADHRQ 6

RESULT 8
PCT-US02-04329-17
; Sequence 17, Application PC/TUS0204329
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL GLYCINE RECEPTOR ALPHA SUBUNIT
; TITLE OF INVENTION: IN THE GASTROINTESTINAL TRACT, HGRA4, and SPLICE VARIANT THEREOF
; FILE REFERENCE: D0079 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/04329
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: US 60/269,535
; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 13
; TYPE: PRT
; ORGANISM: homo sapiens
PCT-US02-04329-17

Query Match 31.2%; Score 27.5; DB 1; Length 13;
Best Local Similarity 70.0%; Pred. No. 89;
Matches 7; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 4 GNIL-TIRLT 12
|||||
Db 1 GNVLYSIRLT 10

RESULT 9
PCT-US02-04329-31
; Sequence 31, Application PC/TUS0204329
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL GLYCINE RECEPTOR ALPHA SUBUNIT
; TITLE OF INVENTION: IN THE GASTROINTESTINAL TRACT, HGRA4, and SPLICE VARIANT THEREOF
; FILE REFERENCE: D0079 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/04329
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: US 60/269,535
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 13
; TYPE: PRT
; ORGANISM: homo sapiens
PCT-US02-04329-31

Query Match 31.2%; Score 27.5; DB 1; Length 13;
Best Local Similarity 70.0%; Pred. No. 89;
Matches 7; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 4 GNIL-TIRLT 12
|||||
Db 1 GNVLYSIRLT 10

RESULT 10
US-09-511-939-56
; Sequence 56, Application US/09511939
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligand
; FILE REFERENCE: 8039/1070
; CURRENT APPLICATION NUMBER: US/09/511,939
; CURRENT FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-511-939-56


```

Query Match      30.7%; Score 27; DB 5; Length 17;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 RLTAADHR 17
   | | | | |
Db 1 RITPAGHR 8

RESULT 11
US-09-968-561A-56
; Sequence 56, Application US/09968561A
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-56

Query Match      30.7%; Score 27; DB 5; Length 17;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 RLTAADHR 17
   | | | | |
Db 1 RITPAGHR 8

RESULT 12
US-09-722-250-253
; Sequence 253, Application US/09722250
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; FILE REFERENCE: P-LJ 4514
; CURRENT APPLICATION NUMBER: US/09/722,250
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 253
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-722-250-253
```

```

Query Match      28.4%; Score 25; DB 5; Length 9;
Best Local Similarity 71.4%; Pred. No. 2.8e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 GNILTIR 10
   | | | | |
Db 2 GNLLTRR 8

RESULT 13
US-09-722-250-253
; Sequence 253, Application US/09722250
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 4514
; CURRENT APPLICATION NUMBER: US/09/722,250
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 253
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-722-250-253

Query Match      28.4%; Score 25; DB 5; Length 9;
Best Local Similarity 71.4%; Pred. No. 2.8e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 GNILTIR 10
   | | | | |
Db 2 GNLLTRR 8

RESULT 14
US-09-924-889-4
; Sequence 4, Application US/09924889
; GENERAL INFORMATION:
; APPLICANT: Sakamoto, Kenji
; TITLE OF INVENTION: Methods for searching or producing physiologically active subs
; TITLE OF INVENTION: pharmaceuticals discovered by the method
; FILE REFERENCE: IKU 0106 PUS
; CURRENT APPLICATION NUMBER: US/09/924,889
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: PCT/JP99/01796
; PRIOR FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial polypeptide having inhibitory effect on gastric aci
; OTHER INFORMATION: ecretion
US-09-924-889-4

Query Match      28.4%; Score 25; DB 5; Length 11;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TVSGNILTI 9
   | | | | |
Db 2 SVGGNMLII 10
```

RESULT 15
US-10-039-645-6
; Sequence 6, Application US/10039645
; GENERAL INFORMATION:
; APPLICANT: Kopin, Alan S.
; APPLICANT: Beinborn, Martin
; TITLE OF INVENTION: Constitutively Active, Hypersensitive,
; TITLE OF INVENTION: and Nonfunctional Receptors as Novel Therapeutic Agents
; FILE REFERENCE: 00398/510002
; CURRENT APPLICATION NUMBER: US/10/039,645
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/243,550
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-645-6

Query Match 28.4%; Score 25; DB 6; Length 11;
Best Local Similarity 62.5%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSGNIIIT I 9
: |||||
Db 3 IVGNILVI 10

Search completed: July 3, 2002, 11:39:33
Job time: 884 sec

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OM protein - protein search, using sw model

Run on: July 3, 2002, 11:09:53 ; Search time 29.65 seconds
(without alignments)
23.506 Million cell updates/sec

Title: US-09-165-546A-8
Perfect score: 88
Sequence: 1 AADHRQLQLSISSCLQL 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	88	100.0	180	CTAG_HUMAN	P78358 homo sapien
2	43	48.9	532	CRT1_APHSP	P21134 aphanocapsa
3	40.5	46.0	995	HIPI_HUMAN	O00291 homo sapien
4	40	45.5	123	RNPA_STRBI	P25817 streptomyce
5	39	44.3	242	C217_HUMAN	P57077 homo sapien
6	39	44.3	2014	YJU7_YEAST	P39526 saccharomyc
7	38.5	43.8	2842	APC_RAT	P70478 rattus norv
8	38.5	43.8	2843	APC_HUMAN	P25054 homo sapien
9	38.5	43.8	2845	APC_MOUSE	Q61315 mus musculu
10	38	43.2	309	YHCS_ECOLI	P45691 escherichia
11	38	43.2	373	DEGM_BACSP	Q03069 bacillus sp
12	38	43.2	484	SYE_MYCPN	P75114 mycoplasma
13	38	43.2	1067	LONM_SCHPO	Q09769 schizosacch
14	37	42.0	142	C217_MOUSE	P58500 mus musculu
15	37	42.0	236	SLR1_RALSO	P58590 ralstonia s
16	37	42.0	247	AFAB_ECOLI	P53516 escherichia
17	37	42.0	247	NFAE_ECOLI	P46738 escherichia
18	37	42.0	265	LICD_HAEIN	P14184 haemophilus
19	37	42.0	267	LIAl_HAEIN	P71392 haemophilus
20	37	42.0	308	YIHR_ECOLI	P32139 escherichia
21	37	42.0	330	RIL_CHICK	Q9PW72 gallus gall
22	37	42.0	339	LIA2_HAEIN	P14181 haemophilus
23	37	42.0	491	A2AP_MOUSE	Q61247 mus musculu
24	37	42.0	503	VLI_HPV29	P50792 human papil
25	37	42.0	586	HO_YEAST	P09932 saccharomyc
26	36	40.9	107	SLIB_MESAG	Q60549 mesocricetu
27	36	40.9	241	YRV9_CAEEL	Q09352 caenorhabdi
28	36	40.9	273	PSAB_YERPE	P31523 yersinia pe
29	36	40.9	371	OTX_STRPU	Q26417 strongyloce
30	36	40.9	441	GDF9_MOUSE	Q07105 mus musculu
31	36	40.9	454	GDF9_HUMAN	O60383 homo sapien
32	36	40.9	505	VLI_CRPVK	P03102 cottontail
33	36	40.9	505	VLI_HPV07	Q05136 human papil

34	36	40.9	541	1	DYR4_HUMAN	Q9nr20 homo sapien
35	36	40.9	550	1	SYD_MYCGE	P47282 mycoplasma
36	36	40.9	612	1	YAWD_SCHPO	Q10187 schizosacch
37	36	40.9	778	1	TAST_HUMAN	Q12815 homo sapien
38	36	40.9	960	1	CHP1_SCHPO	Q10103 schizosacch
39	36	40.9	1613	1	VIT2_CAEEL	P05690 caenorhabdi
40	36	40.9	1616	1	VIT1_CAEEL	P55155 caenorhabdi
41	35.5	40.3	327	1	O6Al_HUMAN	O95222 homo sapien
42	35.5	40.3	607	1	LEU1_MYCLE	Q9cb76 mycobacteri
43	35.5	40.3	2245	1	MYSJ_DICDI	P54697 dictyosteli
44	35	39.8	134	1	YAAI_ECOLI	P28696 escherichia
45	35	39.8	158	1	YWID_BACSU	P46910 bacillus su

ALIGNMENTS

RESULT 1					
ID	CTAG_HUMAN	STANDARD;	PRT;	180 AA.	
AC	P78358;				
DT	15-DEC-1998 (Rel. 37, Created)				
DT	15-DEC-1998 (Rel. 37, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Autoimmunogenic cancer/testis antigen NY-ESO-1.				
GN	CTAG.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=97203161; PubMed=9050879;				
RA	Chen Y.-T., Scanlan M.J., Sahin U., Tuereci O., Gure A.O., Tsang S.,				
RA	Williamson B., Stockert E., Pfreundschuh M., Old L.J.;				
RT	"A testicular antigen aberrantly expressed in human cancers detected				
RT	by autologous antibody screening."				
RL	Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Melanoma;				
RX	MEDLINE=98289662; PubMed=9626360;				
RA	Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,				
RA	de Plaen E., Boon T.;				
RT	"LAGE-1 a new gene with tumor specificity."				
RL	Int. J. Cancer 76:903-908(1998).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=98430682; PubMed=9759882;				
RA	Wang R.-F., Johnston S.L., Zeng G., Topalian S.L.,				
RA	Schwartzentruber D.J., Rosenberg S.A.;				
RT	"A breast and melanoma-shared tumor antigen: T cell responses to				
RT	antigenic peptides translated from different open reading frames."				
RL	J. Immunol. 161:3596-3606(1998).				
CC	-!- TISSUE SPECIFICITY: EXPRESSED IN TESTIS AND OVARY AND IN A WIDE				
CC	VARIETY OF CANCERS. DETECTED IN UTERINE MYOMETRIUM.				
CC	-!- SIMILARITY: STRONG, TO LAGE-1.				

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CC	EMBL; U87459; AAB49693.1; -.
DR	EMBL; AJ003149; CAA05908.1; -.
DR	EMBL; AF038567; AAD05202.1; -.
DR	MIM; 300156; -.
KW	Transmembrane; Antigen.
FT	DOMAIN 5 82
FT	TRANSMEM 156 172
FT	GLY-RICH.
FT	POTENTIAL.

SQ SEQUENCE 180 AA; 17992 MW; B122C5C2C8BE1569 CRC64;

Query Match 100.0%; Score 88; DB 1; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQQL 18
Db 139 AADHRQLQLSISSCLQQL 156

RESULT 2
CRTL_APHSP STANDARD; PRT; 532 AA.
AC P21134;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Phytoene dehydrogenase (EC 1.14.99.-) (Phytoene desaturase).
GN CRTI.

OS Aphanocapsa sp.
OC Bacteria; Cyanobacteria; Chroococcales; Aphanocapsa.
OX NCBI_TaxID=1120;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC 6714;
RX MEDLINE=90382685; PubMed=2119326;
RA Schmidt A., Sandmann G.;
RT "Cloning and nucleotide sequence of the crtI gene encoding phytoene
dehydrogenase from the cyanobacterium Aphanocapsa PCC6714.";
RL Gene 91:113-117(1990).
CC -!- FUNCTION: THIS ENZYME CONVERTS PHYTOENE INTO ZETA-CAROTENE VIA THE
INTERMEDIARY OF PHYTOFLUENE BY THE SYMMETRICAL INTRODUCTION OF TWO
DOUBLE BONDS AT THE C-11 AND C-11' POSITIONS OF PHYTOENE.
CC -!- COFACTOR: NAD, NADP, OR FAD (PROBABLE).
CC -!- PATHWAY: CAROTENOID BIOSYNTHESIS.
CC -!- SIMILARITY: BELONGS TO THE PHYTOENE DEHYDROGENASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; M55647; AAA62573.1; -.
DR PIR; JN0084; JN0084.
KW Carotenoid biosynthesis; Oxidoreductase; FAD; Flavoprotein; NAD.
FT NP_BIND 22 49 FAD (ADP PART) (POTENTIAL).
SQ SEQUENCE 532 AA; 56754 MW; 06296C65A914B19F CRC64;

Query Match 48.9%; Score 43; DB 1; Length 532;
Best Local Similarity 50.0%; Pred. No. 4.3;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 ADHRQLQLSISSCLQQL 17
Db 374 ADHRQLQLSISSCLQQL 389

RESULT 3
HIP1_HUMAN STANDARD; PRT; 995 AA.
AC O00291; O00328;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Huntingtin interacting protein 1 (HIP-1) (Fragment).
GN HIP1.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Huq A.H.M., Nichol K., Osborne L., Scherer S.W., Squitieri F.,
RA Hayden M.R.;
RT "Genomic organization of the human HIP1 gene and its exclusion as a
RT candidate gene in a family diagnosed with Huntington disease without
RT CAG expansion.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 82-995 FROM N.A.
RX MEDLINE=97285121; PubMed=9140394;
RA Kalchman M.A., Koide H.B., McCutcheon K., Graham R.K., Nichol K.,
RA Nishiyama K., Kazemi-Esfarjani P., Lynn F.C., Wellington C.,
RA Metzler M., Goldberg Y.P., Kanazawa I., Geitz R.D., Hayden M.R.;
RT "HIP1, a human homologue of S. cerevisiae Sla2p, interacts with
RT membrane-associated huntingtin in the brain.";
RL Nat. Genet. 16:44-53(1997).
RN [3]
RP SEQUENCE OF 82-159 FROM N.A.
RA Bradshaw H., Hinds K., Harrison M.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 203-602 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97227296; PubMed=9147654;
RA Wanker E.E., Rovira C., Scherzinger E., Hasenbank R., Waelter S.,
RA Tait D., Colicelli J., Lehrach H.;
RT "HIP-1: a huntingtin interacting protein isolated by the yeast two-
RT hybrid system.";
RL Hum. Mol. Genet. 6:487-495(1997).
RN [5]
RP ALTERNATIVE SPLICING.
RX MEDLINE=20515263; PubMed=11063258;
RA Chopra V.S., Metzler M., Rasper D.M., Engqvist-Goldstein A.E.Y.,
RA Singaraja R., Gan L., Fichter K.M., McCutcheon K., Drubin D.,
RA Nicholson D.W., Hayden M.R.;
RT "HIP12 is a non-proapoptotic member of a gene family including HIP1,
RT an interacting protein with huntingtin.";
RL Mamm. Genome 11:1006-1015(2000).
CC -!- FUNCTION: MAY PLAY A FUNCTIONAL ROLE IN THE CELL FILAMENT
CC NETWORKS.
CC -!- SUBUNIT: BINDS HUNTINGTIN. THIS INTERACTION IS RESTRICTED TO THE
CC BRAIN.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC. MEMBRANE-ASSOCIATED PROTEIN.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; HIP1-1 AND HIP1-2; ARE PRODUCED
CC BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED WITH THE HIGHEST LEVEL
CC IN BRAIN.
CC -!- MISCELLANEOUS: THE AFFINITY OF THE HUNTINGTIN PROTEIN-HIP1
CC INTERACTION IS INVERSELY CORRELATED TO THE LENGTH OF THE
CC POLYGLUTAMINE TRACT ADDED TO THE HUNTINGTIN PROTEIN IN HUNTINGTON
CC DISEASE.
CC -!- SIMILARITY: BELONGS TO THE SLA2 FAMILY.
CC -----
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CC -----
DR EMBL; AF052288; AAC33564.1; -.
DR EMBL; AF052261; AAC33564.1; JOINED.
DR EMBL; AF052262; AAC33564.1; JOINED.
DR EMBL; AF052263; AAC33564.1; JOINED.
DR EMBL; AF052264; AAC33564.1; JOINED.
DR EMBL; AF052265; AAC33564.1; JOINED.
DR EMBL; AF052266; AAC33564.1; JOINED.
DR EMBL; AF052267; AAC33564.1; JOINED.


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RX SEQUENCE FROM N.A. (ISOFORM D).
RX MEDLINE=21564202; PubMed=11707072;
RA Reymond A., Friedli M., Neergaard Henriksen C., Chapot F.,
RA Deutsch S., Ucla C., Rossier C., Lyle R., Guipponi M.,
RA Antonarakis S.E.;
RT "From PREDS and open reading frames to cDNA isolation: revisiting the
RL human chromosome 21 transcription map.";
RL Genomics 78:46-54(2001).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM D).
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; A (SHOWN HERE), B, C AND D; MAY
CC BE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: Detected in lung and peripheral blood
CC leukocytes.
CC -!- SIMILARITY: STRONG, TO THE C-TERMINAL DOMAIN OF MAP3K7.
CC -----
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CC -----
DR EMBL; AF269161; AAF81751.1; -.
DR EMBL; AF269162; AAF81752.1; -.
DR EMBL; AF269163; AAF81753.1; -.
DR EMBL; AF269164; AAF81754.1; -.
DR EMBL; AL163249; CAB90434.1; ALT_SEQ.
DR EMBL; AY033900; AAK68718.1; -.
DR EMBL; BC008567; AAH08567.1; -.
KW Alternative splicing.
FT VARSPLIC 1 100 MISSING (IN ISOFORM D).
FT VARSPLIC 101 123 GDWMLTLKPKSITVPVEIPSSPL -> MISTARVPADKPVR
FT VARSPLIC 125 138 IAFSLNDAS (IN ISOFORM D).
FT VARSPLIC 139 242 DTPPEDSIPLVFE -> CQWLLCSRCSLVSH (IN
FT VARSPLIC 124 145 ISOFORM B).
FT VARSPLIC 146 242 MISSING (IN ISOFORM B).
FT VARSPLIC 146 242 DTPPEDSIPLVFEPELQQQLQP -> AGRPRRRRLRLCPHD
FT VARSPLIC 146 242 QHSQGTC (IN ISOFORM C).
FT VARSPLIC 146 242 MISSING (IN ISOFORM C).
SQ SEQUENCE 242 AA; 27248 MW; FFED148FE9AB838C CRC64;

Query Match 44.3%; Score 39; DB 1; Length 242;
Best Local Similarity 43.8%; Pred. No. 9.4;
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 3 DHRQLQLSISSCLOQL 18
:| | | | | | | |
Db 213 ENRTLRLAQSQCEQL 228

RESULT 6
YJU7_YEAST
ID YJU7_YEAST STANDARD; PRT; 2014 AA.
AC P39526;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Hypothetical 229.9 kDa protein in NUC1-NCE1 intergenic region.
GN YJL207C OR J0312 OR HRD550.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=95274326; PubMed=7754713;

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RA Purnelle B., Coster F., Goffeau A.;
RT "The sequence of a 36 kb segment on the left arm of yeast chromosome
RT X identifies 24 open reading frames including NUC1, PRP21 (SPP91),
RT CDC6, CRY2, the gene for S24, a homologue to the aconitase gene ACO1
RT and two homologues to chromosome III genes.";
RL Yeast 10:1235-1249(1994).
RN [2]
RP SEQUENCE OF 1465-2014 FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=95242842; PubMed=7725802;
RA Vandenbol M., Durand P., Bolle P.-A., Dion C., Portetelle D.,
RA Hilger F.;
RT "Sequence analysis of a 40.2 kb DNA fragment located near the left
RT telomere of yeast chromosome X.";
RL Yeast 10:1657-1662(1994).
CC -----
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CC -----
DR EMBL; X77688; CAA54749.1; -.
DR EMBL; Z34098; CAA84004.1; -.
DR EMBL; Z49482; CAA89504.1; -.
DR PIR; S46622; S46622.
DR SGD; S0003743; YJL207C.
KW Hypothetical protein.
SQ SEQUENCE 2014 AA; 229898 MW; 6A296796F2FA5791 CRC64;

Query Match 44.3%; Score 39; DB 1; Length 2014;
Best Local Similarity 53.8%; Pred. No. 98;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 DHRQLQLSISSCL 15
| | | | | | |
Db 1927 DHQKASLSIALCL 1939

RESULT 7
APC_RAT
ID APC_RAT STANDARD; PRT; 2842 AA.
AC P70478;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Adenomatous polyposis coli protein (APC protein).
GN APC.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FISCHER 344/N; TISSUE=Brain;
RX MEDLINE=96116966; PubMed=8563176;
RA Toyota M., Ushijima T., Kakiuchi H., Watanabe M., Imai K., Yachi A.,
RA Sugimura T., Nagao M.;
RT "cDNA cloning of the rat APC gene and assignment to chromosome 18.";
RL Mamm. Genome 6:746-748(1995).
RN [2]
RP MUTAGENESIS.
RC STRAIN=SPRAGUE-DAWLEY, AND FISCHER 344/N;
RX MEDLINE=95148647; PubMed=7846077;
RA Kakiuchi H., Watanabe M., Ushijima T., Toyota M., Imai K.,
RA Weisburger J.H., Sugimura T., Nagao M.;
RT "Specific 5'-GGGA-3'-->5'-GGA-3' mutation of the Apc gene in rat colon
RT tumors induced by 2-amino-1-methyl-6-phenylimidazo[4,5-b]pyridine.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:910-914(1995).
CC -!- FUNCTION: TUMOR SUPPRESSOR. ALLOWS THE RAPID TURNOVER OF BETA-
```


CC CATENIN. APC ACTIVITY CORRELATED WITH ITS PHOSPHORYLATION STATE
CC ALLOWS THE DOWN-REGULATION OF CYTOPLASMIC BETA-CATENIN (BY
CC SIMILARITY).
CC -!- SUBUNIT: FORMS HOMOOLOGOMERS AND ASSOCIATES WITH CATENINS (BY
CC SIMILARITY).
CC -!- PTM: PHOSPHORYLATED BY GSK-3B (BY SIMILARITY).
CC -!- SIMILARITY: CONTAINS 7 ARM REPEATS.
CC -----
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CC -----
CC EMBL; D38629; BAA07609.1; -.
CC HSSP; Q02248; 3BCT.
CC InterPro; IPR000225; Armadillo.
CC Pfam; PF00514; Armadillo_seg; 6.
CC SMART; SM00185; ARM; 5.
CC PROSITE; PS50176; ARM_REPEAT; 1.
KW Anti-oncogene; Phosphorylation; Coiled coil; Repeat.
FT DOMAIN 1 728 LEU-RICH.
FT DOMAIN 1 62 COILED COIL (POTENTIAL).
FT DOMAIN 125 260 COILED COIL (POTENTIAL).
FT REPEAT 451 493 ARM 1.
FT REPEAT 503 545 ARM 2.
FT REPEAT 546 589 ARM 3.
FT REPEAT 590 636 ARM 4.
FT REPEAT 637 681 ARM 5.
FT REPEAT 682 723 ARM 6.
FT REPEAT 724 765 ARM 7.
FT DOMAIN 739 2831 SER-RICH.
FT DOMAIN 1130 1155 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 1556 1575 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 1864 1891 HIGHLY CHARGED.
FT MUTAGEN 523 523 C->R: IN AN IQ-INDUCED COLON TUMOR.
SQ SEQUENCE 2842 AA; 310530 MW; 3CBB2EA8A34E8F47 CRC64;

Query Match 43.8%; Score 38.5; DB 1; Length 2842;
Best Local Similarity 56.2%; Pred. No. 1.8e+02;
Matches 9; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 3 DHRQLQLSISSCLQQL 18
| | | | : | : | | |
Db 649 DHRQI-LRENNCLQTL 663

RESULT 8
APC_HUMAN
ID APC_HUMAN STANDARD; PRT; 2843 AA.
AC P25054; Q15162; Q15163;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Adenomatous polyposis coli protein (APC protein).
GN APC OR DP2.5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91335210; PubMed=1651562;
RA Kinzler K.W., Nilbert M.C., Su L.-K., Vogelstein B., Bryan T.M.,
RA Levy D.B., Smith K.J., Preisinger A.C., Hedge P., McKechnie D.,
RA Finnleir R., Markham A., Groffen J., Boguski M.S., Altschul S.F.,
RA Horii A., Ando H., Miyoshi Y., Miki Y., Nishisho I., Nakamura Y.,
RT "Identification of FAP locus genes from chromosome 5q21.";
RL Science 253:661-665(1991).
RN [2]

RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Fetal brain;
RX MEDLINE=91330307; PubMed=1678319;
RA Joslyn G., Carlson M., Thliveris A., Albertsen H., Gelbert L.,
RA Samowitz W., Groden J., Stevens J., Spirio L., Robertson M.,
RA Sargeant L., Krapcho K., Wolff E., Burt R., Hughes J.P.,
RA Warrington J., McPherson J.D., Wasmuth J., Le Paslier D.,
RA Abderrahim H., Cohen D., Leppert M., White R.;
RT "Identification of deletion mutations and three new genes at the
RT familial polyposis locus.";
RL Cell 66:601-613(1991).
RN [3]
RP ASSOCIATION WITH CATENINS.
RX MEDLINE=94082295; PubMed=8259519;
RA Su L.-K., Vogelstein B., Kinzler K.W.;
RT "Association of the APC tumor suppressor protein with catenins.";
RL Science 262:1734-1737(1993).
RN [4]
RP REVIEW ON VARIANTS.
RX MEDLINE=94154728; PubMed=8111410;
RA Nagase H., Nakamura Y.;
RT "Mutations of the APC (adenomatous polyposis coli) gene.";
RL Hum. Mutat. 2:425-434(1993).
RN [5]
RP VARIANTS FAP.
RX MEDLINE=91335211; PubMed=1651563;
RA Nishisho I., Nakamura Y., Miyoshi Y., Miki Y., Ando H., Horii A.,
RA Koyama K., Utsunomiya J., Baba S., Hedge P., Markham A., Krush A.J.,
RA Petersen G., Hamilton S.R., Nilbert M.C., Levy D.B., Bryan T.M.,
RA Preisinger A.C., Smith K.J., Su L.-K., Kinzler K.W., Vogelstein B.;
RT "Mutations of chromosome 5q21 genes in FAP and colorectal cancer
RT patients.";
RL Science 253:665-669(1991).
RN [6]
RP VARIANTS FAP.
RX MEDLINE=93265030; PubMed=1338904;
RA Miyoshi Y., Nagase H., Ando H., Ichii S., Nakatsuru S., Aoki T.,
RA Miki Y., Mori T., Nakamura Y.;
RT "Somatic mutations of the APC gene in colorectal tumors: mutation
RT cluster region in the APC gene.";
RL Hum. Mol. Genet. 1:229-233(1992).
RN [7]
RP VARIANTS FAP.
RX MEDLINE=93244793; PubMed=1338691;
RA Nakatsuru S., Yanagisawa A., Ichii S., Tahara E., Kato Y.,
RA Nakamura Y., Horii A.;
RT "Somatic mutation of the APC gene in gastric cancer: frequent
RT mutations in very well differentiated adenocarcinoma and signet-ring
RT cell carcinoma.";
RL Hum. Mol. Genet. 1:559-563(1992).
RN [8]
RP VARIANT FAP W-1348, AND VARIANTS D-1118; M-1292; V-1304 AND S-2502.
RX MEDLINE=93250848; PubMed=1338764;
RA Nagase H., Miyoshi Y., Horii A., Aoki T., Petersen G.M.,
RA Vogelstein B., Maher E., Ogawa M., Maruyama M., Utsunomiya J.,
RA Baba S., Nakamura Y.;
RT "Screening for germ-line mutations in familial adenomatous polyposis
RT patients: 61 new patients and a summary of 150 unrelated patients.";
RL Hum. Mutat. 1:467-473(1992).
RN [9]
RP VARIANT FAP TRP-99.
RC TISSUE=Peripheral blood lymphocytes;
RX MEDLINE=95134544; PubMed=7833149;
RA Dobbie Z., Spycher M., Huerliman R., Ammann R., Roth J.,
RA Mueller A., Mueller H., Scott R.J.;
RT "Mutation analysis of the first 14 exons of the adenomatous
RT polyposis coli (APC) gene.";
RL Eur. J. Cancer 30A:1709-1713(1994).
RN [10]
RP VARIANT FAP GLY-722.
RX MEDLINE=95135430; PubMed=7833931;
RA Stella A., Montero M., Resta N., Marchese C., Susca F., Gentile M.,
RA Romio L., Pilia S., Prete F., Mareni C., Guanti G.;

RT "Four novel mutations of the APC (adenomatous polyposis coli) gene in
RL FAP patients.";
RN Hum. Mol. Genet. 3:1687-1688(1994).
RP [11]
RA ERRATUM.
RA Stella A., Montera M., Resta N., Marchese C., Susca F., Gentile M.,
RL Romio L., Pilia S., Prete F., Mareni C., Guanti G.;
RN Hum. Mol. Genet. 3:1918-1918(1994).
RP [12]
RA VARIANT FAP ILE-171.
RX MEDLINE=97144176; PubMed=89900002;
RA van der Luijt R.B., Meera Khan P., Vassen H.F.A., Tops C.M.J.,
RA van Leeuwen-Cornelisse I.S.J., Wijnen J.T., van der Klift H.M.,
RA Plug R.J., Griffioen G., Fodde R.;
RT "Molecular analysis of the APC gene in 105 Dutch kindreds with
RT familial adenomatous polyposis: 67 germline mutations identified by
RT DGGE, PTT, and southern analysis.";
RL Hum. Mutat. 9:7-16(1997).
RN [13]
RP VARIANT LYS-1307.
RX MEDLINE=98400248; PubMed=9731522;
RA Redston M., Nathanson K.L., Yuan Z.Q., Neuhausen S.L., Satagopan J.,
RA Wong N., Yang D., Nafa D., Abrahamson J., Ozelik H.,
RA Antin-Ozerkis D., Andrulis I., Daly M., Pinsky L., Schrag D.,
RA Gallinger S., Kaback M., King M.-C., Woodage T., Brody L.C.,
RA Godwin A., Warner E., Weber B., Foulkes W., Offit K.;
RT "The APC I1307K allele and breast cancer risk.";
RL Nat. Genet. 20:13-14(1998).
RN [14]
RP VARIANTS LYS-1307 AND GLN-1317.
RC TISSUE=Peripheral blood;
RX MEDLINE=98393712; PubMed=9724771;
RA Frayling I.M., Beck N.E., Ilyas M., Dove-Edwin I., Goodman P.,
RA Pack K., Bell J.A., Williams C.B., Hodgson S.V., Thomas H.J.W.,
RA Talbot I.C., Bodmer W.F., Tomlinson I.P.M.;
RT "The APC variants I1307K and E1317Q are associated with colorectal
RT tumors, but not always with a family history.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:10722-10727(1998).
RN [15]
RP VARIANT LYS-1307.
RX MEDLINE=98400259; PubMed=9731533;
RA Woodage T., King S.M., Wacholder S., Hartge P., Struewing J.P.,
RA McAdams M., Laken S.J., Tucker M.A., Brody L.C.;
RT "The APC I1307K allele and cancer risk in a community-based study of
RT Ashkenazi Jews.";
RL Nat. Genet. 20:62-65(1998).
RN [16]
RP VARIANT LYS-1307.
RX MEDLINE=99138651; PubMed=9973276;
RA Gryfe R., Di Nicola N., Lal G., Gallinger S., Redston M.;
RT "Inherited colorectal polyposis and cancer risk of the APC I1307K
RT polymorphism.";
RL Am. J. Hum. Genet. 64:378-384(1999).
RN [17]
RP VARIANTS FAP CYS-1171 AND THR-2738, AND VARIANTS GLY-1057 AND
RP VAL-1822.
RX MEDLINE=99133859; PubMed=9950360;
RA Wallis Y.L., Morton D.G., McKeown C.M., Macdonald F.;
RT "Molecular analysis of the APC gene in 205 families: extended
RT genotype-phenotype correlations in FAP and evidence for the role of
RT APC amino acid changes in colorectal cancer predisposition.";
RL J. Med. Genet. 36:14-20(1999).
RN [18]
RP VARIANT FAP PRO-1184.
RX MEDLINE=99401091; PubMed=10470088;
RA Lamlum H., Ilyas M., Rowan A., Clark S., Johnson V., Bell J.A.,
RA Frayling I.M., Efstathiou J., Pack K., Payne S., Roylance R.,
RA Gorman P., Sheer D., Neale K., Phillips R., Talbot I.C., Bodmer W.F.,
RA Tomlinson I.P.M.;
RT "The type of somatic mutation at APC in familial adenomatous polyposis
RT is determined by the site of the germline mutation: a new facet to
RT Knudson's 'two-hit' hypothesis.";
RL Nat. Med. 5:1071-1075(1999).

CC -!- FUNCTION: TUMOR SUPPRESSOR. ALLOWS THE RAPID TURNOVER OF BETA-
CC CATENIN. APC ACTIVITY CORRELATED WITH ITS PHOSPHORYLATION STATE
CC ALLOWS THE DOWN-REGULATION OF CYTOPLASMIC BETA-CATENIN.
CC -!- SUBUNIT: FORMS HOMOOLOGOMERS AND ASSOCIATES WITH CATENINS.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES TYPES.
CC -!- PTM: PHOSPHORYLATED BY GSK-3B.
CC -!- DISEASE: DEFECTS IN APC ARE A CAUSE OF FAMILIAL ADENOMATOUS
CC POLYPOSIS (FAP) AND GARDNERS SYNDROME (GS), THAT CONTRIBUTE TO
CC TUMOR DEVELOPMENT IN PATIENTS WITH NONINHERITED FORMS OF
CC COLORECTAL CANCER. FAP IS CHARACTERIZED BY ADENOMATOUS POLYPS OF
CC THE COLON AND RECTUM, BUT ALSO OF UPPER GASTROINTESTINAL TRACT
CC (AMPULLARY, DUODENAL, AND GASTRIC ADENOMAS). THIS IS A VICIOUSLY
CC PREMALIGNANT DISEASE WITH ONE OR MORE POLYPS PROGRESSING THROUGH
CC DYSPLASIA TO MALIGNANCY IN UNTREATED GENE CARRIERS WITH A MEDIAN
CC AGE AT DIAGNOSIS OF 40 YEARS.
CC -!- DISEASE: APC MUTATIONS HAVE LED TO SOME INTERESTING OBSERVATIONS..
CC (1) THE GREAT MAJORITY OF THE MUTATIONS FOUND TO DATE WOULD RESULT
CC IN TRUNCATION OF THE APC PRODUCT. (2) ALMOST ALL THE MUTATIONS
CC HAVE OCCURRED WITHIN THE FIRST HALF OF THE CODING SEQUENCE, AND
CC SOMATIC MUTATIONS IN COLORECTAL TUMORS ARE FURTHER CLUSTERED IN A
CC PARTICULAR REGION, CALLED MCR (MUTATION CLUSTER REGION). (3) MOST
CC IDENTIFIED POINT MUTATIONS IN THE APC GENE ARE TRANSITIONS FROM
CC CYTOSINE TO OTHER NUCLEOTIDES. (4) THE LOCATION OF COLORECTAL POLYPS
CC MUTATIONS TENDS TO CORRELATE WITH THE NUMBER OF COLORECTAL POLYPS
CC IN FAP PATIENTS. INACTIVATION OF BOTH ALLELES OF THE APC GENE
CC SEEMS TO BE REQUIRED AS AN EARLY EVENT TO DEVELOP MOST ADENOMAS
CC AND CARCINOMAS IN THE COLON AND RECTUM AS WELL AS SOME OF THOSE IN
CC THE STOMACH.
CC -!- SIMILARITY: CONTAINS 7 ARM REPEATS.
CC -!- DATABASE: NAME=APC; NOTE=Information about APC mutations;
CC WWW="http://perso.curie.fr/Thierry.Soussi/APC.html".

Query Match 43.8%; Score 38.5; DB 1; Length 2843;
Best Local Similarity 56.2%; Pred. No. 1.8e+02;
Matches 9; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 3 DHRQLQLSISCLQQL 18
| | | | : | : | | |
Db 651 DHRQI-LRENNCLQTL 665

RESULT 9
APC_MOUSE
ID APC_MOUSE STANDARD; PRT; 2845 AA.
AC Q61315; Q62044;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Adenomatous polyposis coli protein (APC protein) (mAPC).
GN APC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANTS.
RC STRAIN=C57BL/6J, AND CAST/EI; TISSUE=Brain;
RX MEDLINE=92263101; PubMed=1350108;
RA Su L.-K., Kinzler K.W., Vogelstein B., Preisinger A.C., Moser A.R.,
RA Luongo C., Gould K.A., Dove W.F.;
RT "Multiple intestinal neoplasia caused by a mutation in the murine
RT homolog of the APC gene.";
RL Science 256:668-670(1992).
RN [2]
RP ERRATUM.
RA Su L.-K., Kinzler K.W., Vogelstein B., Preisinger A.C., Moser A.R.,
RA Luongo C., Gould K.A., Dove W.F.;
RL Science 256:1114-1114(1992).
RN [3]
RP SEQUENCE OF 1-45 FROM N.A.
RC STRAIN=BALB/C; TISSUE=Liver;

RA Dicker F., Lambertz S., Reitnair A., Ballhausen W.G.;

RT "The murine APC gene: alternative splicing of 5' untranslated

RT region segments.;"

RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.

RN [4]

RP ALTERNATIVE SPLICING.

RX MEDLINE=94061824; PubMed=8242607;

RA Oshima M., Sugiyama H., Kitagawa K., Taketo M.;

RT "APC gene messenger RNA: novel isoforms that lack exon 7.;"

RL Cancer Res. 53:5589-5591(1993).

CC -!- FUNCTION: TUMOR SUPPRESSOR. ALLOWS THE RAPID TURNOVER OF BETA-

CC CATENIN. APC ACTIVITY CORRELATED WITH ITS PHOSPHORYLATION STATE

CC ALLOWS THE DOWN-REGULATION OF CYTOPLASMIC BETA-CATENIN (BY

CC SUBMITALITY).

CC -!- SUBUNIT: FORMS HOMOOLOGOMERS AND ASSOCIATES WITH CATENINS (BY

CC SIMILARITY).

CC -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; 1 (SHOWN HERE), 2, 3 AND 4; ARE

CC PRODUCED BY ALTERNATIVE SPLICING.

CC -!- TISSUE SPECIFICITY: EXPRESSED IN LIVER, SPLEEN, KIDNEY, HEART,

CC LUNG, BRAIN, STOMACH, INTESTINE, TESTIS AND OVARY.

CC -!- PTM: PHOSPHORYLATED BY GSK-3B (BY SIMILARITY).

CC -!- SIMILARITY: CONTAINS 7 ARM REPEATS.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL; M88127; AAB59632.1; -.

DR EMBL; U02937; AAA03443.1; -.

DR HSSP; Q02248; 3BCT.

DR MGD; MGI:88039; Apc.

DR InterPro; IPR000225; Armadillo.

DR Pfam; PF00514; Armadillo_seg; 6.

DR SMART; SM00185; ARM; 5.

DR PROSITE; PS0176; ARM_REPEAT; 1.

KW Anti-oncogene; Phosphorylation; Alternative splicing; Repeat;

KW Coiled coil.

FT DOMAIN 1 61 COILED COIL (POTENTIAL).

FT DOMAIN 125 245 COILED COIL (POTENTIAL).

FT DOMAIN 1 728 LEU-RICH.

FT REPEAT 451 493 ARM 1.

FT REPEAT 503 545 ARM 2.

FT REPEAT 546 589 ARM 3.

FT REPEAT 590 636 ARM 4.

FT REPEAT 637 681 ARM 5.

FT REPEAT 682 723 ARM 6.

FT REPEAT 724 765 ARM 7.

FT DOMAIN 739 2834 SER-RICH.

FT DOMAIN 1130 1156 ASP/GLU-RICH (ACIDIC).

FT DOMAIN 1556 1575 ASP/GLU-RICH (ACIDIC).

FT DOMAIN 1864 1891 HIGHLY CHARGED.

FT VARSPLIC 243 276 MISSING (IN ISOFORM 2 AND ISOFORM 4).

FT VARSPLIC 310 410 MISSING (IN ISOFORM 3 AND ISOFORM 4).

FT VARIANT 120 120 T -> A (IN STRAIN CAST/EI).

FT VARIANT 493 493 V -> I (IN STRAIN CAST/EI).

FT VARIANT 797 797 Y -> F (IN STRAIN CAST/EI).

FT VARIANT 1330 1330 A -> T (IN STRAIN CAST/EI).

FT VARIANT 1618 1618 A -> S (IN STRAIN CAST/EI).

FT VARIANT 2294 2294 G -> A (IN STRAIN CAST/EI).

FT VARIANT 2496 2496 H -> Q (IN STRAIN CAST/EI).

FT VARIANT 2523 2523 T -> Q (IN STRAIN CAST/EI).

FT VARIANT 2813 2813 T -> S (IN STRAIN CAST/EI).

SQ SEQUENCE 2845 AA; 311086 MW; 145CA73CF570A499 CRC64;

Query Match 43.8%; Score 38.5; DB 1; Length 2845;

Best Local Similarity 56.2%; Pred. No. 1.8e+02;

Matches 9; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 3 DHRQLQLSISSCLQQL 18

Db 649 DHRQI-LRENNCLQTL 663

RESULT 10

YHCS_ECOLI

ID YHCS_ECOLI STANDARD; PRT; 309 AA.

AC P45691;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical transcriptional regulator yhcs.

GN YHCS OR B3243 OR Z4602 OR ECS4116.

OS Escherichia coli, and

OS Escherichia coli O157:H7.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.

OX NCBI_TaxID=562, 83334;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=K12 / MGI655;

RX MEDLINE=97426617; PubMed=9278503;

RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,

RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

RA Mau B., Shao Y.;

RT "The complete genome sequence of Escherichia coli K-12.;"

RL Science 277:1453-1474(1997).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=O157:H7 / EDL933 / ATCC 700927;

RX MEDLINE=21074935; PubMed=11206551;

RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

RA Welch R.A., Blattner F.R.;

RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.;"

RL Nature 409:529-533(2001).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=O157:H7 / RIMD 0509952;

RX MEDLINE=21156231; PubMed=11258796;

RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

RA Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,

RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;

RT "Complete genome sequence of enterohemorrhagic Escherichia coli

RT O157:H7 and genomic comparison with a laboratory strain K-12.;"

RL DNA Res. 8:11-22(2001).

CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL

CC REGULATORS. STRONG, TO H.INFLUENZAE HI1364.

CC -----

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CC -----

CC EMBL; U18997; AAA58045.1; -.

DR EMBL; AE000403; AAC76275.1; -.

DR EMBL; AE005552; AAG58371.1; -.

DR EMBL; AP002564; BAB37539.1; -.

DR EcoGene; EG12825; yhcs.

DR InterPro; IPR000847; HTH_LysR.

DR Pfam; PF00126; HTH_1; 1.

DR PROSITE; PS00044; HTH_LYSR_FAMILY; 1.

KW Hypothetical protein; Transcription regulation; DNA-binding;

KW Complete proteome.


```
FT  DNA_BIND      19      38      H-T-H MOTIF (POTENTIAL).
SQ  SEQUENCE      309 AA;  34516 MW;  22DF64653AF4BE2F CRC64;

Query Match      43.2%;  Score 38;  DB 1;  Length 309;
Best Local Similarity 66.7%;  Pred. No. 19;
Matches      8;  Conservative  2;  Mismatches  2;  Indels  0;  Gaps  0;

QY  5 RQLQLSISSCLQ 16
Db  24 RQLQMSVSSISQ 35

RESULT 11
DEGM_BACSP
ID  DEGM_BACSP      STANDARD;      PRT;      373 AA.
AC  Q03069;
DT  01-OCT-1996 (Rel. 34, Created)
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  01-MAR-2002 (Rel. 41, Last annotation update)
DE  Sensor protein degM (EC 2.7.3.-).
GN  DEGM.
OS  Bacillus sp. (strain B21-2).
OC  Bacteria; Firmicutes; Bacillus/Clostridium group;
OC  Bacillus/Staphylococcus group; Bacillus.
OX  NCBI_TaxID=1409;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Masui A., Fujiwara N., Takagi M., Imanaka T.;
RT  "Cloning and nucleotide sequence of degM, the regulatory gene, degM,
RT  for minor protease in Bacillus subtilis.";
RL  J. Ferment. Bioeng. 74:230-233(1992).
CC  -!- FUNCTION: INVOLVED IN A SENSORY TRANSDUCTION PATHWAY THAT
CC  ENHANCES THE PRODUCTION OF MINOR PROTEASES.
CC  -!- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
CC  -----
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CC  -----
DR  EMBL; D10690; BAA01532.1; -.
DR  InterPro; IPR003594; HATPase_c.
DR  InterPro; IPR004359; HIS_KIN_sig.
DR  InterPro; IPR003661; His_kinA.
DR  Pfam; PF02518; HATPase_c; 1.
DR  Pfam; PF00512; signal; 1.
DR  SMART; SM00387; HATPase_c; 1.
DR  SMART; SM00388; HSKA; 1.
DR  PROSITE; PS50109; HIS_KIN; 1.
KW  Sensory transduction; Transferase; Kinase; Transmembrane.
FT  DOMAIN      170 370  HISTIDINE KINASE.
FT  DOMAIN      306 315  GLY-RICH.
FT  DOMAIN      330 340  GLY-RICH.
SQ  SEQUENCE      373 AA;  41614 MW;  6494279E0879294B CRC64;

Query Match      43.2%;  Score 38;  DB 1;  Length 373;
Best Local Similarity 41.2%;  Pred. No. 23;
Matches      7;  Conservative  4;  Mismatches  6;  Indels  0;  Gaps  0;

QY  2 ADHRQLQLSISSCLQQL 18
Db  245 AQERSIQLTIGTCEQAI 261

RESULT 12
SYE_MYCPN
ID  SYE_MYCPN      STANDARD;      PRT;      484 AA.
AC  P75114;
```

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DT  01-NOV-1997 (Rel. 35, Created)
DT  01-NOV-1997 (Rel. 35, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
DE  (GluRS).
DE  GLTX OR MPN678 OR MP164.
GN  Mycoplasma pneumoniae.
OS  Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC  Mycoplasmataceae; Mycoplasma.
OX  NCBI_TaxID=2104;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=ATCC 29342 / M129;
RX  MEDLINE=97105885; PubMed=8948633;
RA  Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
RA  Herrmann R.;
RT  "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT  pneumoniae.";
RL  Nucleic Acids Res. 24:4420-4449(1996).
CC  -!- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
CC  diphosphate + L-glutamyl-tRNA(Glu).
CC  -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC  -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC  -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC  -----
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CC  -----
DR  EMBL; AE000017; AAB95812.1; -.
DR  HSSP; P27000; IGLN.
DR  InterPro; IPR000924; tRNA-synt_1c.
DR  InterPro; IPR001412; tRNA-synt_I.
DR  Pfam; PF00749; tRNA-synt_1c; 1.
DR  PRINTS; PR00987; TRNASYNTHGLU.
DR  PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
KW  Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW  Complete proteome.
FT  SITE      10 20  "HIGH" REGION.
FT  SITE      252 256  "KMSKS" REGION.
FT  BINDING    255 255  ATP (BY SIMILARITY).
SQ  SEQUENCE      484 AA;  55621 MW;  FD7B7F4742B09A50 CRC64;

Query Match      43.2%;  Score 38;  DB 1;  Length 484;
Best Local Similarity 53.3%;  Pred. No. 31;
Matches      8;  Conservative  2;  Mismatches  5;  Indels  0;  Gaps  0;

QY  4 HRQLQLSISSCLQQL 18
Db  394 HRELFKEQLQSALQQL 408

RESULT 13
LONM_SCHPO
ID  LONM_SCHPO      STANDARD;      PRT;      1067 AA.
AC  Q09769;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Putative ATP-dependent protease, mitochondrial precursor
DE  (EC 3.4.21.-).
GN  SPAC22F3.06C.
OS  Schizosaccharomyces pombe (Fission yeast).
OC  Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC  Schizosaccharomycetales; Schizosaccharomycetaceae;
OC  Schizosaccharomyces.
OX  NCBI_TaxID=4896;
RN  [1]
```

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RC SEQUENCE FROM N.A.
RC STRAIN=972;
RA Lye G., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: REQUIRED FOR INTRAMITOCHONDRIAL PROTEOLYSIS. CATALYZES
CC THE INITIAL STEPS OF PROTEIN DEGRADATION (POTENTIAL).
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix (Potential).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S16; ALSO KNOWN AS THE
CC LON FAMILY OF ATP-DEPENDENT PROTEASES.
CC -----
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CC -----
DR EMBL; Z54285; CAA91071.1; -.
DR MEROPS; S16.002; -.
DR InterPro; IPR003593; AAA.
DR InterPro; IPR003959; AAA_subfam.
DR InterPro; IPR003111; LON.
DR InterPro; IPR001984; Lon_endopep.
DR Pfam; PF00004; AAA; 1.
DR Pfam; PF02190; LON; 1.
DR PRINTS; PR00830; ENDOLAPTASE.
DR SMART; SM00382; AAA; 1.
DR SMART; SM00464; LON; 1.
DR PROSITE; PS01046; LON_SER; 1.
KW Hypothetical protein; Hydrolase; Serine protease; ATP-binding;
KW Mitochondrion; Transit peptide.
FT TRANSIT 1 ? MITOCHONDRION (POTENTIAL).
FT CHAIN ? 1067 PUTATIVE ATP-DEPENDENT PROTEASE.
FT NP_BIND 578 585 ATP (POTENTIAL).
FT ACT_SITE 946 946 BY SIMILARITY.
FT SEQUENCE 1067 AA; 118641 MW; 215FCFBE9CDC4AAD CRC64;

Query Match 43.2%; Score 38; DB 1; Length 1067;
Best Local Similarity 87.5%; Pred. No. 73;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADHRQLQ 8
Db 395 AADHRELQ 402

RESULT 14
C217_MOUSE STANDARD; PRT; 142 AA.
AC P58500;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Protein C21orf7 homolog.
GN C21ORF7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21564202; PubMed=11707072;
RA Raymond A., Friedli M., Neergaard Henriksen C., Chapot F.,
RA Deutsch S., Ucla C., Rossier C., Lyle R., Guipponi M.,
RA Antonarakis S.E.;
RT "From PREDs and open reading frames to cDNA isolation: revisiting the
RT human chromosome 21 transcription map.";
RL Genomics 78:46-54(2001).
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- SIMILARITY: STRONG, TO THE C-TERMINAL DOMAIN OF MAP3K7.
CC -----
```

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CC -----
DR EMBL; AY033899; AAK68717.1; -.
DR SEQUENCE 142 AA; 16271 MW; 1C7FD9C02B0E7F6B CRC64;

Query Match 42.0%; Score 37; DB 1; Length 142;
Best Local Similarity 37.5%; Pred. No. 12;
Matches 6; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 3 DHRQLQLSISSCLQQL 18
Db 113 ENRTLKMAQSQCQEQL 128

RESULT 15
SLR1_RALSO STANDARD; PRT; 236 AA.
AC P58590;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Transcriptional activator protein solR.
GN SOLR OR RSC3287 OR RS02516.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Sigulier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE LUXR/UHPA FAMILY OF TRANSCRIPTIONAL
CC REGULATORS. AUTOINDUCER REGULATED SUBFAMILY.
CC -----
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CC -----
DR EMBL; AL646074; CAD17075.1; -.
DR PROSITE; PS00622; HTH_LUXR_FAMILY; 1.
KW Transcription regulation; DNA-binding; Activator; Quorum sensing;
KW Autoinducer synthesis; Complete proteome.
FT DNA_BIND 193 212 H-T-H MOTIF (POTENTIAL).
FT SEQUENCE 236 AA; 25926 MW; 4F11E733A4890F5F CRC64;

Query Match 42.0%; Score 37; DB 1; Length 236;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 AADHRQLQLSISSCLQQL 18
Db 15 AADERQLFRQIASVVRQL 32
```

Search completed: July 3, 2002, 11:24:42
Job time: 889 sec
